

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 ; Search time 1435.66 Seconds
(Without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579a-18

Perfect score: 28

Sequence: 1 aaatggtacagatgatacttcgtc 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthm:*
3: em_estln:*
4: em_estlm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	21.6	77.1	481 10	BE059008 sn23h02.y
2	20.2	72.1	600 13	BM078736 MEST123-F
3	20	71.4	495 14	W95055 2h48c01.s1
4	20	71.4	624 10	AV717903 AV717903
5	20	71.4	841 13	BI952375 BI952375
6	20	71.4	878 13	BI906578 BI906578

	7	20	71.4	908	17	CNS077U1	AL433168 T7 end of
C	8	20	71.4	1051	14	BO940394	BO940394 AGENCOURT
	9	19.2	68.6	453	17	AZ990219	AZ990219 2M0273P18
	10	19.2	68.6	457	10	AM942444	AM942444 LD17235.3
	11	19.2	68.6	460	17	PT013M03R	AL446163 Parameteciu
C	12	19	67.9	245	10	BB171446	BB171446 BB171446
C	13	19	67.9	300	9	AV181810	AV181810 AV181810
C	14	19	67.9	330	10	BB223116	BB223116 BB223116
C	15	19	67.9	404	10	AM254027	AM254027 UT-R-B70-
C	16	19	67.9	539	19	AZ139861	AZ139861 SP_0002_B
C	17	19	67.9	649	13	BU151093	BU151093 BU151093
C	18	19	67.9	705	17	AQ367197	AQ367197 tox0002A
C	19	19	67.9	1062	14	BO942400	BO942400 AGENCOURT
C	20	19	67.9	1291	13	BM474170	BM474170 AGENCOURT
C	21	18.6	66.4	408	9	AV125998	AV125998 AV125998
C	22	18.6	66.4	408	14	T95260	T95260 ye39c11.s1
C	23	18.6	66.4	459	14	C21108	C21108 HUMS00204
C	24	18.6	66.4	462	14	D25548	D25548 HUMS02045
C	25	18.6	66.4	476	14	T79804	T79804 yd74f10.s1
C	26	18.6	66.4	514	17	AQ458760	AQ458760 HS_5050_B
C	27	18.6	66.4	639	17	AQ292251	AQ292251 npx0043G
C	28	18.6	66.4	655	17	A2243210	A2243210 RPT-23-3
C	29	18.6	66.4	704	17	AO628396	AO628396 CITR1-E1-
C	30	18.6	66.4	790	12	BC213999	BC213999 RST33625
C	31	18.6	66.4	914	17	BH132277	BH132277 ENTOR86TR
C	32	18.6	66.4	1012	9	AL517643	AL517643 AL517643
C	33	18.4	65.7	337	17	BH617237	BH617237 SALK_0361
C	34	18.4	65.7	363	17	A2857519	A2857519 2M0162A22
C	35	18.4	65.7	386	9	AI394920	AI394920 MA001346
C	36	18.4	65.7	387	9	AL706663	AL706663 DKFP686G
C	37	18.4	65.7	400	9	AA349054	AA349054 EST55612
C	38	18.4	65.7	440	12	BF603367	BF603367 268865 MA
C	39	18.4	65.7	487	10	AM644100	AM644100 cm37d07.w
C	40	18.4	65.7	526	10	AM373663	AM373663 OYA-BT053
C	41	18.4	65.7	528	14	BO289215	BO289215 PJ27c01.Y
C	42	18.4	65.7	534	13	BI932816	BI932816 EST552705
C	43	18.4	65.7	534	13	BI932816	BI932816 EST552705
C	44	18.4	65.7	541	14	BO288634	BO288634 PJ33c01.Y
C	45	18.4	65.7	543	14	BO275899	BO275899 PJ48f06.Y

ALIGNMENTS

RESULT 1
BE059008/c 481 bp mRNA linear EST 03-DEC-2001
LOCUS
DEFINITION
sn23h02.y1 Gm-cl016 Glycine max cDNA clone GENOME SYSTEMS CLONE 1D:
Gm-cl016-12364 5' similar to SW:ROK_HUMAN 007244 HETEROGENEOUS
NUCLEAR RIBONUCLEOPROTEIN K ; mRNA sequence.

ACCESSION
BE059008.1 GI:8403374
VERSION
KEYWORDS
SOURCE
ORGANISM

soybean.
Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
AUTHORS

1 (bases 1 to 481)
Shoemaker,R., Keim,P., Vockin,L., Eppelting,J., Corcelli,V., Khanna

A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
R., Waterston,R. and Wilson,R.

Public Soybean EST Project
Unpublished (1999)

Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

TITLE
JOURNAL
COMMENT

Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccutefresgen.com
 Insert length: 1791 Std Error: 0.00
 Seq primer: -40RP from Gibco
 High quality sequence stop: 423.

FEATURES

source

Location/Qualifiers

1..481
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1016-12364"
 /clone.lib="Gm-c1016"
 /tissue_type="Immature flowers of field grown plants"
 /lab_host="X110-Gold"
 /note="vector: pBluescript II XR; Site_1: EcoRI; Site_2:
 XhoI; This cDNA library was constructed from mRNA isolated
 from immature flowers of field grown plants. The cDNA
 library was prepared using the Stratagene pBluescript II
 XR library construction kit. Complementary DNA was
 synthesized from mRNA using a primer consisting of a poly
 (dT) sequence with a XhoI restriction site. EcoRI adaptors
 were ligated to the blunt-ended cDNA fragments followed by
 XhoI digestion. The cDNA fragments were directionally
 cloned into the EcoRI-XhoI restriction site of the
 pBluescript vector. The ligated cDNA fragments were
 transformed into X110-Gold host cells. This library was
 constructed by Dr. Randy Shoemaker and Dr. John
 Ertelding."

BASE COUNT 141 a 116 c 88 g 136 t
 ORIGIN

Query Match 77.1%; Score 21.6; DB 10; Length 481;
 Best Local Similarity 85.7%; Pred. No. 27;

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AATTGGCTACAGATGATCCTTCCTT 28

Db 203 AAGTTGGCAAAAGATGATCCTTACGTT 176

RESULT 2

BM078736

LOCUS 600 bp mRNA linear EST 14-NOV-2001
 DEFINITION MEST123-F06.T3 ISUM4-TN Zea mays cDNA clone MEST123-F06 3', mRNA

ACCESSION BM078736

VERSION BM078736.1 GI:16925668

KEYWORDS EST.

ORIGIN Zea mays.

ORGANISM Zea mays.

REFERENCE Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:

Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC

clado: Panicoideae: Andropogoneae: Zea.

1 (bases 1 to 600)

Oluf.F., Cui.F., Guo.L., Ashlock,D.A., Men,T.J. and Schnable,P.S.

Expressed Sequence Tags from B73 Maize seedlings and silks

Unpublished (2001)

CONTACT: Patrick S. Schnable

Schnable Laboratory

Iowa State University

4405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA

Tel: 515-294-0975

Fax: 515-294-2299

Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the

Phred software.

(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b

rt>). Overall sequence quality assessment and vector trimming were

conducted using the Lucy software (<http://www.ligr.org/softlab/>).

Lucy parameters were set to ensure an overall trimmed quality of

97.5% or better without any vector fragments in the chosen

high-quality region of each sequence. Low-quality bases between the
 poly-T and the high-quality region were replaced with N's to serve
 as spacers.
 PCR Primers
 FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
 CTA TAC)
 BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
 TAA AG)
 Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES

source

Location/Qualifiers

1..600
 /organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="MEST123-F06"
 /clone.lib="ISUM4-TN"
 /tissue_type="Seedling and silk"
 /lab_host="DH10B"
 /note="vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
 ds-cDNA molecules were generated as follows. First-strand
 cDNA was prepared from oligo-dT selected mRNA by priming
 with a Noli oligo-dT primer (5'
 AACTGAGAGATTCGGCGCGCAGGAATTTTTTTTTTTT). The
 resulting DNA:RNA hybrid was treated with RNase H and used
 as a template for DNA Pol-I-catalyzed second strand
 synthesis. After the addition of EcoRI adaptors, the
 ds-cDNAs were digested with NciI and size-selected. The
 resulting molecules were directionally cloned into the
 EcoRI and NciI sites of the pT73PAC vector. The library
 then went through one round of normalization to C₀t value
 of 5 based on the methods of Marcelo Bento Soares (Genome
 Research 6: 791-806, 1996)."

BASE COUNT 164 a 151 c 101 g 184 t
 ORIGIN

Query Match 72.1%; Score 20.2; DB 13; Length 600;
 Best Local Similarity 88.0%; Pred. No. 1.3e+02;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TTGGGTACAGATGATACCTTCGTT 28

Db 155 TTGGGTCAAAAGATGATACCTTCGTT 179

RESULT 3

W95055

LOCUS 495 bp mRNA linear EST 02-FEB-1997
 DEFINITION clone IMAGE:415296 3', mRNA sequence.

ACCESSION W95055

VERSION W95055.1 GI:1424403

KEYWORDS EST.

ORIGIN human.

ORGANISM human.

REFERENCE Homo sapiens

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.

1 (bases 1 to 495)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chapell,B.,

Chissoe,S., Dietrich,N., Dubugue,T., Favello,A., Gish,W., Hawkins

,M., Hultman,M., Kucaba,T., Laey,M., Le,M., Le,N., Mardis,E., Moore

,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,

Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevisan,E.,

Underwood,R., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LNL ; contact the

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriidae; Drosophilidae; Drosophila.
1 (bases 1 to 457)
Harvey, D., Broksstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S., and Rubin, G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
Other_ESTs: LD17235.5prime
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST/estfruitfly.berkeley.edu>
Based upon the presence of a xhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic A6003796: Drosophila melanogaster genomic scaffold
1420001386047 section 6 of 52, complete sequence.: 02/23/2001
Plate: LD.172 row: C column: 11
High quality sequence stop: 377.

FEATURES
source
1..457
Location/Qualifiers
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="LD17235"
/clone_lib="LD Drosophila melanogaster embryo Bluescript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
/note="Organ: embryo; Vector: Bluescript SK; Site_1: EcoRI
; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis kit. Oligo dt-primed and directionally cloned at
EcoRI and XhoI in Bluescript SK(+/-)";

BASE COUNT
101 a 121 c 127 g 108 t

ORIGIN
Query Match 68.6%; Score 19.2; DB 10; Length 457;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TTGGGTACAGATGATACCTTCCT 27
1 ||||| ||||| ||||| ||||| |||||
DB 78 TGGGGTTCAAGATGATACCATCCT 101

RESULT 11
PT013M03R 460 bp DNA linear GSS 13-JUL-2001
OCUS
FINITION
Paramecium tetraurelia sequence R13G02r of the end of plasmid
PT013M03, genomic survey sequence.
ACCESSION
AL446163.1 GI:11123054
VERSION
GSS.
KEYWORDS
Paramecium tetraurelia.
SOURCE
ORGANISM
Paramecium tetraurelia.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Penicillia;
Paramacium.
1 (bases 1 to 460)
Keller, A.M. and Cohen, J.
An indexed genomic library for Paramecium complementation cloning
J. Eukaryot. Microbiol. 47 (1), 1-6 (2000)
MEDLINE
20114709
PUBMED
10651287
2 (bases 1 to 460)
Dessen, P., Zagulski, M., Gromadka, R., Plattner, H., Kismehl, R.,
Meyer, E., Betermier, M., Schultz, J.E., Linder, D., Pearlman, R.E.,
Kung, C., Forney, J., Satir, B.H., Van Houten, J.L., Keller, A.M.,
Froisard, M., Sperling, L. and Cohen, J.
Paramecium genome survey: a pilot project
Trends Genet. 17 (6), 306-308 (2001)
JOURNAL
MEDLINE
21273563
PUBMED
11377780

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

3 (bases 1 to 460)
Wong, L. and Pearlman, R.E.
Random sequencing of the Paramecium macronuclear genome
Unpublished
Core Molecular Biology Facility, York University, 4700 Keele St.,
Toronto, Canada M3J 1P3
4 (bases 1 to 460)
Cohen, J. and Sperling, L.
Direct Submission
JOURNAL
Submitted (01-NOV-2000) Paramecium Genome Survey Project, Centre de
Genetique Moleculaire, Centre National de la Recherche
Scientifique, 91198 Gif-sur-Yvette, France. E-mail:
sperling@cgm.cnrs-gif.fr
The present survey of the Paramecium tetraurelia macronuclear
genome consists of end sequences of a library of random 4-12 kb
fragments obtained by Sau3A partial digestion of macronuclear DNA
cloned in the BamHI site of pBS1KS-. See [4].
Genes are predicted from matches to other sequences. For more
information about this sequence or the Paramecium Project, see
<http://paramecium.cgm.cnrs-gif.fr>.

FEATURES
source
1..460
Location/Qualifiers
/organism="Paramecium tetraurelia"
/macronuclear
/strain="stock d4-2"
/db_xref="taxon:5888"

BASE COUNT
165 a 62 c 63 g 170 t

ORIGIN
Query Match 68.6%; Score 19.2; DB 17; Length 460;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AATTGGTACAGATGATACCTTC 25
1 ||||| ||||| ||||| ||||| |||||
DB 102 AATTGGATTCATATGATACCTTC 125

RESULT 12
BB171446/c 245 bp mRNA linear EST 29-JUN-2000
LOCUS
BB171446 RIKEN full-length enriched, adult male hypohalamus Mus
musculus cDNA clone A230028C13 3', mRNA sequence.
ACCESSION
BB171446
VERSION
BB171446.1 GI:8830529
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 245)
Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci,
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, U., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata,
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomioka, N., Toya,
T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamanaoka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino,
M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Kono, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.go.jp

FEATURES	Location/Qualifiers
source	1. .245

Query Match

Q. 10

REFERENCE
AUTHORS

1 (bases 1 to 300)
Kohara, Y., Shirai, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H.,
Nishigaki, A., Motokashiri, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano,
M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and
Nomoto, H.

70

FEATURES	Location/Qualifiers
source	1. .300

Query Match

VERSION E

ORGANISM

TITLE
 JOURNAL
 COMMENT
 Contact: Yoshihide Hayashizaki
 RIKEN Mouse ESTs (Konno, H., et al.)
 Unpublished (2000)

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-readgsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carnicelli, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoinactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Kikunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,

PT mRNA -
PS Claim 5; Page 19; 28pp; English.

XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in
CC Staphylococcus aureus) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the mecA gene as template. Also disclosed is a detection
CC method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant S. aureus in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the mecA gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.

XX Sequence 28 BP; 9 A; 4 C; 6 G; 9 T; 0 other;

Query Match 100.0%; Score 28; DB 24; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.0022; Mismatches 0; Gaps 0;

Matches 28; Conservative 0; Indels 0; Gaps 0;
OY 1 AAATTGGGTACAGATGATGATCTTCGTT 28
DB 1 AAATTGGGTACAGATGATGATCTTCGTT 28

RESULT 2
AAAT04536
ID AAAT04536 standard; cDNA to mRNA; 1789 BP.

XX AAT04536;

XX 11-APR-1996 (first entry)

XX Staphylococcus aureus 'mecca' protein coding sequence.

XX methicillin-resistant Staphylococcus aureus; MRSA; 'mecca' protein;
XX antibiotic resistance; ds.

XX Staphylococcus aureus.

Key Location/Qualifiers
CDS 1..1608
/*tag= a
/product= 'mec_A'-protein

JP07209294-A.

11-AUG-1995.

10-JAN-1994; 94JP-0012226.

10-JAN-1994; 94JP-0012226.

(DENK-) DENKA SEIKEN KK.

(KAWA/) KAWANO M.

(MITU) MITSUBISHI CHEM CORP.

WPI: 1995-313917/41.

P-PSDB; AAR80035.

New 'mec A' protein and DNA encoding it - used for the detection of
methicillin-resistant Staphylococcus aureus

PS Claim 5; Page 11-13; 15pp; Japanese.

XX The present sequence codes for the 'mec A' protein which controls
CC methicillin resistance in methicillin-resistant Staph. aureus. The
CC 'mec A' protein (mol. wt. 40000) is useful for preparation of
CC an antiserum specific for MRSA, thereby allowing methicillin-resistant
CC and methicillin-sensitive strains to be distinguished. The coding
CC sequence was obtained by PCR amplification of the mec A sequence
CC (see AAAT04536) using primers AAAT04537 and AAAT04539.
CC N.B. in the sequence listing of the patent specification, the
CC sequence length is stated to be 1785 bp.

XX Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;

Query Match 100.0%; Score 28; DB 16; Length 1789;

Best Local Similarity 100.0%; Pred. No. 0.0036; Mismatches 0; Gaps 0;

Matches 28; Conservative 0; Indels 0; Gaps 0;
OY 1 AAATTGGGTACAGATGATGATCTTCGTT 28
DB 203 AAATTGGGTACAGATGATGATCTTCGTT 230

RESULT 3
AAQ28599

ID AAQ28599 standard; DNA; 2007 BP.

XX AAQ28599;

XX 19-FEB-1993 (first entry)

XX Encodes penicillin binding protein PBP2A-27R.

XX penicillin; antibiotic; bacteria; methicillin; staphylococci;
XX soluble; chelating peptide; MRS infection; methicillin resistant;
XX strain.

XX Staphylococcus aureus strain 27R.

XX Key Location/Qualifiers

FT CDS 1..2007

/*tag= a

EP505151-A.

23-SEP-1992.

18-MAR-1992; 92EP-0302298.

19-MAR-1991; 91US-0672704.

(ELIL) LILLY & CO ELI.

Biaszczak LC, Skatrud PL, Smith MC, Wu CYE;

WPI: 1992-318034/39.

Polynucleotide cpd. encoding PBP 2A-27R protein or its deriv. -
PT contains PBP isolated from Staphylococcus aureus and is used to
PT treat methicillin resistant staphylococci

PS Disclosure; Page 14; 101pp; English.

XX This sequence encodes a PBP2a penicillin binding protein isolated
CC from S. aureus strain 27R. A cDNA library was constructed from
CC S. aureus DNA in lambda phage EMBL3. Packaging extracts from this
CC were then used to infect E. coli Cj236. Plaques were screened for the
CC presence of the mecA-27R gene by a probe produced by PCR amplification
CC of the mecA gene using primers Q28600.1. Positive plaques were purified
CC and digested with HindIII, and this fragment digested with XbaI and
CC cloned into M13amp8 and M13amp19 for sequencing.

XX Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;

Query Match 100.0%; Score 28; DB 13; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 0.0037;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 A A A T T G G G T A C A G A T G A T A C C T T C G T T 28
 |||
 Db 609 A A A T T G G G T A C A G A T G A T A C C T T C G T T 636

RESULT 4
 AAT28568
 ID AAT28568 standard; DNA: 2007 BP.
 XX
 AC AAT28568;
 XX
 DT 01-APR-1997 (first entry)
 XX
 NE Bacterial antibiotic resistance gene, mecA, probe.
 C
 D Detection: probe; amplification primer; bacterial pathogen; pneumonia;
 KW Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
 KW Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
 KW Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
 KW Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
 KW Haemophilus influenzae; Moraxella catarrhalis; septicemia; meningitis;
 KW infection; intra-abdominal infection; skin infection;
 KW bacterial resistance; beta-lactam antibiotic; ds.
 XX
 OS Synthetic.
 XX
 PN W09608582-A2.
 XX
 PD 21-MAR-1996.
 XX
 PE 12-SEP-1995; 95WO-CA00528.
 XX
 PR 12-SEP-1994; 94US-0304732.
 XX
 PA (BERG/) BERGERON M G.
 PA (OUEL/) OUELLETTE M.
 PA (ROYP/) ROY P H.
 XX
 PI Bergeron MG, Ouellette M, Roy PH;
 DR WPI; 1996-179953/18.
 PS
 XX Claim 91; Page 144-145; 216pp; English.
 CC The sequences given in AAT28560-76 represent fragments derived from
 CC bacterial antibiotic resistance genes which were used as probes in the
 CC method of the invention for the detection of bacterial species in a
 CC sample. The method of the invention comprises using probes and/or
 CC amplification primers which are specific, ubiquitous and sensitive for
 CC determining the presence and/or amount of nucleic acids from selected
 CC bacterial species in any sample, where the bacterial nucleic acid
 CC comprises a selected target region hybridisable with the probes or
 CC primers. The method comprises contacting the sample with the probes
 CC or primers and detecting the presence and/or amount of hybridised
 CC primers or amplification products as and indication of the presence
 CC and/or amount of the bacterial species. This method may be used to
 CC detect commonly encountered bacterial pathogens, e.g. Escherichia coli,
 CC Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis,
 CC Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus
 CC epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus,
 CC Streptococcus pyogenes, Haemophilus influenzae and Moraxella
 CC catarrhalis. These bacterial species are associated with approx. 90% of
 CC urinary tract infections and with a high percentage of other severe
 CC infections including septicaemia, meningitis, pneumonia, intra-abdominal

CC infections, skin infections and other severe respiratory tract
 CC infections. The method may also be used to evaluate a bacterial
 CC resistance to beta- lactam antibiotics.
 CC
 XX
 SQ Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;

Query Match 100.0%; Score 28; DB 17; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 0.0037;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 A A A T T G G G T A C A G A T G A T A C C T T C G T T 28
 |||
 Db 608 A A A T T G G G T A C A G A T G A T A C C T T C G T T 635

RESULT 5
 AAV68337
 ID AAV68337 standard; DNA: 2007 BP.
 XX
 AC AAV68337;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Penicillin binding protein PBP2A mecA-27R gene of S. aureus 27R.
 XX
 DE Penicillin binding protein; PBP2A-27A; mecA-27R gene;
 KW methicillin resistance; antibiotic; assay; purification; ss.
 KW
 XX
 OS Staphylococcus aureus.
 XX
 PN EP875578-A2.
 XX
 PD 04-NOV-1998.
 XX
 PE 18-MAR-1992; 92EP-0302298.
 XX
 PR 19-MAR-1991; 91US-0672704.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Blaszczak LC, Skatrud PL, Smith MC, Wu CE;
 DR P-PSDB; AAM81149.
 XX
 PT New Staphylococcus aureus soluble penicillin-binding proteins and
 PT their derivatives - useful for screening for compounds effective
 PT against methicillin resistant organisms
 XX
 PS Disclosure: Page 14-16; 97pp; English.
 XX
 CC This mecA-27R gene encodes penicillin binding protein 2A (PBP2A-27R)
 CC responsible for the methicillin resistance of Staphylococcus aureus
 CC strain 27R. The invention provides new PBs of formula SP-L-PBP2As,
 CC where: SP is 0 or a signal peptide (preferably from the ampC, ompA or
 CC beta-lactamase gene product); L is Met-Val or a compound of formula
 CC Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see
 CC AAW61151-58) of formula (His)x-(A)y-(His)z and A-an amino acid,
 CC x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above
 CC polypeptide where each monomer unit is the same or different; Pro
 CC is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see
 CC AAW61159-62). Also claimed are polynucleotides encoding specific
 CC soluble PBP2A compounds. The new PBP2A-27R proteins are useful for
 CC assaying for agents useful as antibiotics against methicillin
 CC resistant Staphylococcus strains by creating a kinetically inert
 CC complex between a support-immobilised transition ion and a modified
 CC soluble PBP2A protein comprising a chelating agent, which screens
 CC for agents which bind to PBP2A proteins (disclosed). Soluble forms
 CC of PBP2A-27R protein facilitate crystallisation as they lack their
 CC transmembrane association region, and so are useful for x-ray
 CC crystallography studies of the protein, assisting in the design of
 CC antibiotic compounds against methicillin resistant staphylococcus
 CC strains (disclosed). The chelating peptide operably linked to the

CC BP2A-27R proteins is useful for purifying PBPs.
XX
SQ Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
Query Match 100.0%; Score 28; DB 19; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAATGGGTACAGATGATACCTTCGTT 28
|||||
DB 609 AAATGGGTACAGATGATACCTTCGTT 636
RESULT 6
ID ABA76993 standard; DNA: 2007 BP.
AC ABA76993;
XX
DT 28-JAN-2002 (first entry)
XX
X Antibiotic resistance detection polynucleotide SEQ ID NO 169.
KM Detection: bacterial species; animal; food; environment;
KM antibiotic resistance; ds.
XX
OS Unidentified.
XX
PN NZ501596-A.
XX
PD 29-JUN-2001.
XX
PF 12-SEP-1995; 95NZ-0501596.
XX
PR 12-SEP-1995; 95NZ-0501596.
XX
PA (IDIT-) IDI INFECTION DIAGNOSTIC INC.
XX
PI Bergeron MG, Ouellette M, Roy PH;
XX
DR WPI: 2001-615034/71.
XX
XX
PT Method for detecting target bacterial species in a sample, comprises
PT detecting the presence or amount of bacterial nucleic acid amplified by
PT a primer derived from bacterial DNA, specific for the target bacterial
PT species -
XX
PS
PS
PS Claim 16: Page 159-160; 168pp; English.
XX
C The invention relates to detecting target bacterial species suspected to
be present in a sample, comprising contacting nucleic acid of target
bacterial species with an amplification primer pair derived from a
bacterial DNA fragment (ABA76825-ABA76861) specific for the target
bacterial species but ubiquitous for different strains, amplifying the
nucleic acid and detecting the presence or amount of an amplified
sequence as an indication of the presence or amount of the target
bacterial species. The invention includes primers and probes
(ABA76862-ABA76984) against the target bacterial species, especially
E.coli, K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae,
S.aureus, S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes,
H.influenzae, M.catalis and/or group A Streptococci producing
exotoxin A gene spe A, suspected to be present in a sample which is
obtained from human patients, animals, environment or food, and which
consists of one or more bacterial colonies. Oligonucleotide
CC probes and primers complementary to the bacterial genes encoding
resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadB,
aacC1, aacC2, aacC3, aacC4, mecA, vanA, vanH, vanX, satA, aacA-aphD, vat,
vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify
commonly encountered and clinically important resistance genes. The
invention provides a rapid method of bacterial identification that can be
achieved, which reduces the time currently required for the
identification of pathogens in the clinical laboratory.
XX

SQ Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
Query Match 100.0%; Score 28; DB 22; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAATGGGTACAGATGATACCTTCGTT 28
|||||
DB 608 AAATGGGTACAGATGATACCTTCGTT 635
RESULT 7
ID ABN92247 standard; DNA: 2028 BP.
AC ABN92247;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.
XX
KM Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KM antibacterial; gene therapy; gene; ds.
XX
OS Staphylococcus epidermidis.
XX
PN US6380370-B1.
XX
PD 30-APR-2002.
XX
PF 13-AUG-1998; 98US-0134001.
XX
PR 14-AUG-1997; 97US-055779P.
XX
PR 08-NOV-1997; 97US-064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucelte-Stamm LA, Bush D;
XX
DR WPI: 2002-381255/41.
XX
DR P-PSDB; ABP39702.
XX
XX
PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
PT polypeptide, useful for diagnosing and treating bacterial infections -
XX
PS Disclosure; SEQ ID 1710; 267pp; English.
XX
CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC antibacterial activity and can be used in gene therapy. The sequences
CC can also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life
CC cycle or inhibit S. epidermidis infection.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site.
XX
SQ Sequence 2028 BP; 861 A; 273 C; 346 G; 547 T; 1 other;
Query Match 100.0%; Score 28; DB 24; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAATGGGTACAGATGATACCTTCGTT 28
|||||
DB 630 AAATGGGTACAGATGATACCTTCGTT 657
RESULT 8
AAQ35213
ID AAQ35213 standard; DNA: 2110 BP.


```
XX AC AAQ35213;
XX DT 06-JUN-1993 (first entry)
XX DE Sequence of the mec A gene.
XX KW Methicillin-resistant staphylococci; detection; primer; PCR; ss.
XX OS Staphylococcus aureus.
XX FH Key
XX FT CDS 105..2110
XX FT /*tag= a
XX PN EP527628-A.
XX PD 17-FEB-1993.
XX PS 10-AUG-1992; 92EP-0307307.
XX PR 13-AUG-1991; 91US-0744770.
XX PA (E.L.I.L.) LILLY & CO E.L.I.
XX PI Skatrud PL, Unal S;
XX DR WPI; 1993-054352/07.
XX DR P-PSDB; AAR30845.
XX PT Detection of methicillin-resistant staphylococci - using
XX PT polymerase chain reaction method, and DNA primers, for rapid,
XX PT sensitive and accurate detection
XX PS Disclosure; pages 7-10; 16pp; English.
XX CC The inventors claim a method for detecting methicillin-resistant
XX CC staphylococcal infections which involves the use of the PCR primed
XX CC by fragments of the Staphylococcus meca gene. More specifically, the
XX CC initial primers used are nucleotides 141-160 and the inverse
XX CC complement of nucleotides 1929-1952 of the S. aureus meca gene. The
XX CC interior primers are nucleotides 568-593 and the inverse complement
XX CC of 1647-1670 of the S. aureus meca gene.
XX SQ Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;
XX
XX Query Match 100.0%; Score 28; DB 14; Length 2110;
XX Best Local Similarity 100.0%; Pred. No. 0.0037;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAATTGGGTACAAAGATGATACCTTCGTT 28
Db 713 AAATTGGGTACAAAGATGATACCTTCGTT 740
RESULT 9
AAQ25905
ID AAQ25905 standard; DNA; 2322 BP.
XX AC AAQ25905;
XX DT 18-JAN-1993 (first entry)
XX DE PBP2'.
XX KW Polymerase chain reaction; PCR; amplification; ss.
XX OS Synthetic.
XX FH Key
XX FT misc_binding 1581..1598
XX FT Location/Qualifiers
XX FT /*tag= a
XX FT /label= Probe_binding_site
```

```
XX PN JP04169200-A.
XX PD 17-JUN-1992.
XX PF 31-OCT-1990; 90JP-0296708.
XX PR 31-OCT-1990; 90JP-0296708.
XX PA (SHIO) SHIONOGI & CO LTD.
XX DR WPI; 1992-253403/31.
XX PT Detection of PBP2' gene for determ. of methicillin-resistance -
XX PT useful esp. for detection of methicillin-resistance
XX PT Staphylococcus aureus
XX PS Disclosure; fig 1; 9pp; Japanese.
XX CC The sequence given is the PBP2' gene. This gene could be detected
XX CC by the primer sequences given in AAQ25897-904. Due to the results of
XX CC this amplification reaction resistance to methicillin in Staphylococcus
XX CC aureus could be determined.
XX SQ Sequence 2322 BP; 940 A; 324 C; 389 G; 669 T; 0 other;
XX
XX Query Match 100.0%; Score 28; DB 13; Length 2322;
XX Best Local Similarity 100.0%; Pred. No. 0.0038;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAATTGGGTACAAAGATGATACCTTCGTT 28
Db 608 AAATTGGGTACAAAGATGATACCTTCGTT 635
RESULT 10
AAT04538
ID AAT04538 standard; cDNA to mRNA; 2455 BP.
XX AC AAT04538;
XX DT 11-APR-1996 (first entry)
XX DE Staphylococcus aureus meca protein coding sequence.
XX KW methicillin-resistant Staphylococcus aureus; MRSA; 'meca protein;
XX KW antibiotic resistance; ds.
XX OS Staphylococcus aureus.
XX FH Key
XX FT CDS 134..2146
XX FT Location/Qualifiers
XX FT /*tag= a
XX FT /product= mec_A-protein
XX PN JP07209294-A.
XX PD 11-AUG-1995.
XX PF 10-JAN-1994; 94JP-0012226.
XX PR 10-JAN-1994; 94JP-0012226.
XX PA (DENK-) DENKA SEIKEN KK.
XX PA (KAWA/) KAWANO M.
XX PA (MITU) MITSUBISHI CHEM CORP.
XX DR WPI; 1995-313917/41.
XX DR P-PSDB; AAR80036.
XX PT New 'mec A protein and DNA encoding it - used for the detection of
XX PT methicillin-resistant Staphylococcus aureus
```

PS Example 2; Page 8-10; 15pp; Japanese.
XX
CC The present sequence codes for the mec A protein. DNA coding for
CC the 'mec A' protein, which controls methicillin resistance in
CC methicillin-resistant Staph. aureus (MRSA), was obtained by PCR
CC amplification of the mec A sequence using primers AA04537 and
CC AA04539. The 'mec A' protein (mol. wt. 40000) is useful for
CC preparation of antiserum specific for MRSA, thereby allowing
CC methicillin-resistant and methicillin-sensitive strains to be
CC distinguished.
XX
SQ Sequence 2455 BP; 997 A; 344 C; 401 G; 713 T; 0 other;
Query Match 100.0%; Score 28; DB 16; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAATTGGGTACAGATGATACCTTCGTT 28
DB 741 AAATTGGGTACAGATGATACCTTCGTT 768
JSLUT 11
AAH01187
ID AAH01187 standard; DNA: 2456 BP.
XX
AC AAH01187;
XX
DT 24-JUL-2001 (first entry)
XX
DE Staphylococcus aureus nucleotide sequence SEQ ID NO:1178.
XX
KM Species specific; genus specific; family specific; probe; detection;
KM identification; algal; archaeal; bacterial; fungal; parasitical;
KM microorganism; diagnosis; translation elongation factor Tuv; toxin;
KM translation elongation factor G; RecA recombinase; resistance;
KM catalytic subunit of proton-translocating ATPase; antimicrobial;
KM vaccine; primer; ds.
XX
OS Staphylococcus aureus.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000MO-CA01150.
XX
PR 28-SEP-1999; 99CA-2283458.
PR 19-MAY-2000; 2000CA-2307010.
PR
(INF-) INFECTIO DIAGNOSTIC (IDI) INC.
AX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
XX WPI; 2001-245006/25.
DR
XX
PT Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasitical species in a test sample -
PT
XX
PS Disclosure; Page 1048-1049; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitical species, genus, family and group. A nucleic acid (1)

CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexa nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (1) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC which are given in the exemplification of the present invention.
XX
SQ Sequence 2456 BP; 1001 A; 344 C; 396 G; 715 T; 0 other;
Query Match 100.0%; Score 28; DB 22; Length 2456;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAATTGGGTACAGATGATACCTTCGTT 28
DB 748 AAATTGGGTACAGATGATACCTTCGTT 775
RESULT 12
ABQ70885
ID ABQ70885 standard; DNA: 3800 BP.
XX
AC ABQ70885;
XX
DT 29-AUG-2002 (first entry)
XX
DE Listeria monocytogenes 4b contig DNA sequence #827.
XX
KM Antibacterial; Listeria; food contamination; mutational analysis;
KM infection; ds.
XX
OS Listeria monocytogenes 4b.
XX
PN WO200228891-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001MO-FR03061.
XX
PR 04-OCT-2000; 2000FR-0012697.
PR
(INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Kunst F, Glaser P;
XX
XX WPI; 2002-332479/37.
DR
XX
PT New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators -
XX
PS Claim 14; SEQ ID 3698; 180pp; French.
XX
XX The present invention relates to nucleic acid sequences
CC (ABQ67188-ABQ7112) from Listeria sp. The sequences are useful as probes
CC and primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in
CC anti-Listeria vaccines.
CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 3800 BP; 1230 A; 768 C; 714 G; 1084 T; 4 other;

Query Match 71.4%; Score 20; DB 24; Length 3800;
Best Local Similarity 82.1%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 AAATTGGGTACAGATGATCTTCGTT 28
||| ||||| ||||| ||||| |||||
Db 2300 AAAATGGGTCCACAGCATGACTTCGTT 2327

RESULT 13
AAT20797/c
ID AAT20797 standard; cDNA to mRNA; 462 BP.

XX
AC AAT20797;
X
T 09-JUL-1996 (first entry)
XX
DE Human gene signature HUMGS02045.

XX
KM Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KM human; cloning; mapping; non-biased library; diagnosis; detection;
KM cell typing; abnormal cell function; ss.

XX
OS Homo sapiens.

XX
PN W09514772-A1.

XX
PD 01-JUN-1995.

XX
PE 11-NOV-1994; 94WO-JP01916.

XX
PR 12-NOV-1993; 93JP-0355504.

XX
PA (MATS/) MATSUBARA K.

XX
PA (OKUB/) OKUBO K.

XX
PI Matsubara K, Okubo K;

XX
DR WPI; 1995-206931/27.

XX
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
T tissues

AX
PS Claim 1; Page 726; 2245pp; Japanese.

XX
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "Gs" sequences
CC given in AA119001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (gene signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.

XX
SQ Sequence 462 BP; 133 A; 82 C; 99 G; 137 T; 11 other;

Query Match 66.4%; Score 18.6; DB 16; Length 462;
Best Local Similarity 80.8%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ATTGGTACAGATGATCTTCGTT 28
||| ||||| ||||| ||||| |||||
Db 305 ATTGGTACAGATGATCTTCGTT 280

RESULT 14
AAF65394
ID AAF65394 standard; cDNA; 381 BP.

XX
AC AAF65394;

XX
DT 09-APR-2001 (first entry)

XX
DE Novel human polynucleotide, SEQ ID NO: 1150.

XX
KM Human; cytostatic; gene therapy; colon cancer; prostate cancer;
KM breast cancer; lung cancer; cancer detection; ss.

XX
OS Homo sapiens.

XX
PN W0200102568-A2.

XX
PD 11-JAN-2001.

XX
PE 30-JUN-2000; 2000WO-US18374.

XX
PR 02-JUL-1999; 99US-0142310.

XX
PR 02-JUL-1999; 99US-0142311.

XX
PA (CHIR) CHIRON CORP.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassam A;

XX
PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Drmanac R;

XX
PI Cerkenjajkov R, Drmanac S, Dickson M, Labat I, Leshkowitz D;

XX
PI Kita D, Garcia V, Jones LW, Strache-Grain B;

XX
DR WPI; 2001-091805/10.

XX
PT Library of polynucleotides for diagnosing a cancerous state of a
PT mammalian cell and detecting cancer, particularly of the colon or
PT prostate, comprises: 3351 human polynucleotide sequences -

XX
PS Claim 9; Page 708-709; 1046pp; English.

XX
CC The present sequence is one of 3351 sequences in a library of human
CC polynucleotides. The library is used to detect differentially expressed
CC genes correlated with a cancerous state of a mammalian cell and can
CC detect colon, prostate, breast and lung cancer. The library can be used
CC to produce probes for detection of mRNA and to produce additional copies
CC of the polynucleotides. The probes can be used for chromosome mapping of
CC the polynucleotide and for detection of transcription levels. Ribozymes
CC or antisense oligonucleotides can be generated. The polynucleotides and
CC their gene products are used as genetic or biochemical markers (e.g. in
CC blood or tissues) that will detect the earliest changes along the
CC carcinogenesis pathway and/or monitor the efficacy of therapies and
CC preventive interventions. The polynucleotides, polypeptides and
CC antibodies against them can be used in pharmaceutical compositions to
CC treat the cancers and proliferative disorders such as neoplasia,
CC dysplasia and hyperplasia.

XX
SQ Sequence 381 BP; 119 A; 92 C; 78 G; 92 T; 0 other;

Query Match 65.7%; Score 18.4; DB 22; Length 381;
Best Local Similarity 78.6%; Pred. No. 79;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATCTTCGTT 28
||| ||||| ||||| ||||| |||||
Db 286 AAATGGGTACAGATCTTAATTGTT 313

Search completed: December 10, 2002, 17:32:27
 Job time : 185.347 secs

```

RESULT 15
AAH10449/c
ID AAH10449 standard; cDNA: 563 BP.
XX
AC AAH10449;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (3'-primer) SEQ ID NO:7284.
XX
KW Human; primer: detection; diagnosis: antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
R 27-AUG-1999; 99JP-0300253.
r 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 3: SEQ ID 7284; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 563 BP; 141 A; 140 C; 109 G; 158 T; 15 other:

Query Match 65.7%; Score 18.4; DB 22; Length 563;
Best Local Similarity 78.6%; Pred. No. 83;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Caps 0;

0Y 1 AAATTGGTACAAGATGATACCTTCGTT 28
1 ||||| ||| || ||||| ||
DB 356 ATATTGGAACATGTCCTACCTCTTT 329

```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 607.084 Seconds

(Without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-18

Perfect score: 28
Sequence: 1 aaatggtgcaagatgatacctcgtt 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

otal number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_cm:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_man:*
37: em_htg_vit:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	AX306859	AX306859 Sequence
2	28	100.0	1789	E09772	E09772 The base se
3	28	100.0	2007	AR089410	AR089410 Sequence
4	28	100.0	2007	AR093610	AR093610 Sequence
5	28	100.0	2322	SABBP	Y00688 Staphylococ
6	28	100.0	2322	E03736	E03736 DNA sequenc
7	28	100.0	2454	SEMECAPB	X52592 S. epidemia
8	28	100.0	2455	E09771	E09771 The base se
9	28	100.0	2456	SAMECAPB	X52593 S. aureus m
10	28	100.0	2456	AX110445	AX110445 Sequence
11	28	100.0	5596	SSKMECA2	Y13096 S.sciuri me
12	28	100.0	6368	SSKMECA2	Y13095 S.sciuri me
13	28	100.0	9047	SAMECAR11	Y14051 Staphylococ
14	28	100.0	21777	AB063173	AB063173 Staphyloc
15	28	100.0	26090	AB063172	AB063172 Staphyloc
16	28	100.0	39332	AB033763	AB033763 Staphyloc
17	28	100.0	58237	D86934	D86934 Staphylococ
18	28	100.0	290250	AP004822	AP004822 Staphyloc
19	28	100.0	298050	AP003129	AP003129 Staphyloc
20	28	100.0	349999	AB003358	AB003358 Staphyloc
21	26.4	94.3	68256	AB037671	AB037671 Staphyloc
22	21.8	77.9	272258	AC123866	AC123866 Mus muscu
23	20.6	73.6	2012	HAM.LTR6BH	M73592 Mesocricetu
24	20.2	72.1	5068	SSK1MECA	Y09223 S.sciuri me
25	20.2	72.1	6684	SSK1MECA	Y13094 S.sciuri me
26	20	71.4	3800	AX416707	AX416707 Sequence
27	20	71.4	103705	AC110641	AC110641 Rattus no
28	20	71.4	161799	AC111516	AC111516 Rattus no
29	20	71.4	186728	AC111099	AC111099 Mus muscu
30	20	71.4	219471	AL772341	AL772341 Mus muscu
31	19.8	70.7	86487	AL592157	AL592157 Human DNA
32	19.8	70.7	147700	AC025344	AC025344 Homo sapi
33	19.6	70.0	194907	AC106835	AC106835 Mus muscu
34	19.6	70.0	198421	AC125180	AC125180 Mus muscu
35	19.2	68.6	112286	AP005556	AP005556 Oryza sat
36	19.2	68.6	117737	F6D8	AC008016 Arabidops
37	19.2	68.6	127824	AC004822	AC004822 Homo sapi
38	19.2	68.6	161955	AC068718	AC068718 Homo sapi
39	19.2	68.6	179993	AC018360	AC018360 Homo sapi
40	19	67.9	30626	CE16A11	281505 Caenorhabdi
41	19	67.9	45350	AC084398	AC084398 Homo sapi
42	19	67.9	60931	AC105113	AC105113 Homo sapi
43	19	67.9	66397	AC117548	AC117548 Mus muscu
44	19	67.9	111851	AC090564	AC090564 Homo sapi
45	19	67.9	125866	OSJN00283	AL731638 Oryza sat

ALIGNMENTS

RESULT 1
AX306859
LOCUS AX306859
DEFINITION Sequence 18 from Patent EP1160333.
ACCESSION AX306859
VERSION AX306859.1 GI:17894681
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.

REFERENCE
AUTHORS Taya, T., Ishiura, T. and Saito, J.
TITLE Oligonucleotides and method for detection of meca gene of methicillin-resistant Staphylococcus aureus
JOURNAL Patent: EP 1160333-A 18 05-DEC-2001;

tosoh Corporation (JP)
Location/Qualifiers
1. 28
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"
9 a 4 c 6 g 9 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATACCTTCGTT 28
|||||
Db 1 AAATTGGGTACAGATGATACCTTCGTT 28

RESULT 2
E09772 1789 bp RNA linear PAT 29-SEP-1997
XCUS The base sequence of modified meca DNA.
DEFINITION E09772
ACCESSION E09772.1 GI:22026401
VERSION JP 1995209294-A/2.
KEYWORDS Staphylococcus aureus.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 1789)
AUTHORS Kono, M., Hiramatsu, K., Sasazu, M., Noguchi, M. and Suguro, K.
TITLE NOVEL "MECA PROMPTIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 2, 11-AUG-1995;
COMMENT KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53, C07K14/31, C12N1/21, C12N15/09, C12P21/02, (C12N1/21, PC C12R1:19);
PC (C12P21/02, C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH key Location/Qualifiers
FH source 1. 1789
FT /organism="Staphylococcus aureus" FT CDS
FT 1. 1608
FT /product="Modified meca".
FEATURES
source Location/Qualifiers
1. 1789
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"
BASE COUNT 735 a 263 c 302 g 489 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATACCTTCGTT 28
|||||
Db 203 AAATTGGGTACAGATGATACCTTCGTT 230

RESULT 3
AR089410 2007 bp DNA linear PAT 07-SEP-2000
LOCUS AR089410
DEFINITION Sequence 169 from patent US 5994066.
ACCESSION AR089410

VERSION AR089410.1 GI:10016167
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron, M.C., Picard, F.J., Ouellette, M. and Roy, P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
FEATURES
source Location/Qualifiers
1. 2007
BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATACCTTCGTT 28
|||||
Db 608 AAATTGGGTACAGATGATACCTTCGTT 635

RESULT 4
AR093610 2007 bp DNA linear PAT 08-SEP-2000
LOCUS AR093610
DEFINITION Sequence 169 from patent US 6001564.
ACCESSION AR093610
VERSION AR093610.1 GI:10020359
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron, M.G., Ouellette, M. and Roy, P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
FEATURES
source Location/Qualifiers
1. 2007
BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATACCTTCGTT 28
|||||
Db 608 AAATTGGGTACAGATGATACCTTCGTT 635

RESULT 5
SABP 2322 bp DNA linear BCT 12-SEP-1993
LOCUS SABP
DEFINITION Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
ACCESSION Y00688
VERSION Y00688.1 GI:46628
KEYWORDS penicillin-binding protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 2322)
AUTHORS Song, M.D., Wachi, M., Doi, M., Ishino, F. and Matsushashi, M.
TITLE Evolution of an inducible penicillin-target protein in

methicillin-resistant *Staphylococcus aureus* by gene fusion
JOURNAL EMBL Lett. 221 (1), 167-171 (1987)
MEDLINE 87304805
PUBMED 3305073
REFERENCE 2 (bases 1 to 2322)
AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
Barberis-Maino, L., Kayser, F. H. and Berger-Bachli, B.
TITLE Sequence comparison of meca genes isolated from
methicillin-resistant *Staphylococcus aureus* and *Staphylococcus*
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT Data kindly reviewed (13.1.88) by Matsubashi.
FEATURES
source
1..2322
Location/Qualifiers
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"
1..2013
/note="penicillin-binding protein (AA 1-670)"
/codon_start=1
/transl_table=1
/protein_id="CAA6684.1"
/db_xref="GI:46629"
/db_xref="SWISS-PROT:P07944"
/translation="MKIKIVPLIVVVGFGIYPAASKDEINNTDAIEDKNEKQ
VYKDSYISKSDNGEVEETPERIKIYNSLQKINIDRKIKRYSKNKKRYDAQYKIK
TNYGIDRNQFNFVEKEDGMKLDMDISYIIPGMKDSIHIEKLSERGLDRNV
ELANTGTHMLGIVPKVSKKQYKAIKEISTEDYINNNKIKYGMIPSPFHKTVK
KMDYSDPAKKFHLTNTFESRNPGLGVGNGIPNINSEELKOKRYKCKDDA
VIGKKLEKLYDKLGHEDYRPTIYVDNK. VTAHTLEKKKKCKDKDQUTIDAV
OKSTYNNKNDYSGTAHPQTELLALVSTPSDYTPFNWGSNEYNLTEDEKRP
LNNFQITTSRPSQKILTFAMIGLNNNTLDDKTSYKIDGQWQKDSWGWYNTRYEV
VNGSIDLQKAIIESDNIETFAVALELSGSKFEKMGKLGVEDIPSPYPMQISNK
NLDEIILADSGGEILINPOILISYALENGNINAPHLKDTKNNKVMKNITS
KENINILNDGMOGVNKTKEIDYRSYANLIGSGTGLKMKOCEETQROGWFIISYDK
DNPMMAIIVKNDQDKMASYNAKISGYDELYENGNKKYDIDE"
BASE COUNT 940 a 324 c 389 g 669 t
ORIGIN
Query Match 100.0%; Score 28; DB 1; Length 2322;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 A A A T T G G T A C A G A T G A T C C T T C G T T 28
|||||
Db 608 A A A T T G G T A C A G A T G A T C C T T C G T T 635
RESULT 6
LOCUS 2454 bp DNA linear BCT 12-SEP-1993
DEFINITION S. epidermidis meca gene for PBP2' (penicillin binding protein 2').
ACCESSION X52592.1 GI:46693
VERSION X52592.1 GI:46693
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2;
Staphylococcus epidermidis.
SOURCE Staphylococcus epidermidis.
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
1 (bases 1 to 2448)
AUTHORS Ryffel, C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE
2 (bases 1 to 2454)
AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
Barberis-Maino, L., Kayser, F. H. and Berger-Bachli, B.
TITLE Sequence comparison of meca genes from methicillin-resistant
Staphylococcus aureus and Staphylococcus epidermidis
JOURNAL Gene (1990) In press
REFERENCE
3 (bases 1 to 2454)
AUTHORS Ryffel, C.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE
4 (bases 1 to 2454)
AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
Barberis-Maino, L., Kayser, F. H. and Berger-Bachli, B.
TITLE Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52593-4> and <X00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source
1..2454
Location/Qualifiers
/organism="Staphylococcus epidermidis"
/strain="WT55"
/db_xref="taxon:1282"
/clone="WT80/WT79"
80..85
/note="-35 region"
101..105
promoter

CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT misc_feature 1..2322
/note="'PBP2' gene for determination of FT
FT methicillin
resistance'
FT
FEATURES
source
Location/Qualifiers
1..2322
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 939 a 324 c 390 g 669 t
ORIGIN
Query Match 100.0%; Score 28; DB 6; Length 2322;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 A A A T T G G T A C A G A T G A T C C T T C G T T 28
|||||
Db 608 A A A T T G G T A C A G A T G A T C C T T C G T T 635
RESULT 7
LOCUS 2454 bp DNA linear BCT 12-SEP-1993
DEFINITION S. epidermidis meca gene for PBP2' (penicillin binding protein 2').
ACCESSION X52592.1 GI:46693
VERSION X52592.1 GI:46693
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2;
Staphylococcus epidermidis.
SOURCE Staphylococcus epidermidis.
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
1 (bases 1 to 2448)
AUTHORS Ryffel, C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE
2 (bases 1 to 2454)
AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
Barberis-Maino, L., Kayser, F. H. and Berger-Bachli, B.
TITLE Sequence comparison of meca genes from methicillin-resistant
Staphylococcus aureus and Staphylococcus epidermidis
JOURNAL Gene (1990) In press
REFERENCE
3 (bases 1 to 2454)
AUTHORS Ryffel, C.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE
4 (bases 1 to 2454)
AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
Barberis-Maino, L., Kayser, F. H. and Berger-Bachli, B.
TITLE Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52593-4> and <X00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source
1..2454
Location/Qualifiers
/organism="Staphylococcus epidermidis"
/strain="WT55"
/db_xref="taxon:1282"
/clone="WT80/WT79"
80..85
/note="-35 region"
101..105
promoter

RBS /note=-10 region"
130..134
/note="ribosome binding site"
precursor_RNA 141..2159
/note="primary transcript"
141..2147
/note="PBP2' (AA 1 - 668)"
/codon_start=1
/transl_table=1
/protein_id="CAA36828.1"
/db_xref="GI:46994"
/db_xref="SPTREMBL:O54113"
/translation="MKKIKIVLILIVVVGGIYFVASKDEINNTIDAIEDKREKO
VYKDSYISKSDNGEVEETERPRIKITYNSLGKODIIOQRKIKKSKNKKRDAQYKIK
TNGNIDNRVQNFPEKEDGMKLDMDHSVLIIPGOKDSDIHTENLSERGKILDRNNV
ELANTGVAIEIGIVPRNVSKDYKAIKELISSEYIIRKQMDQNVQDDTEVPKIKTV
KMDYLSDFPAKKFLITNETESRNPILGKAVSHLIGYGPINSEELKOKEGYKDDA
VYKKGLEKLYDKLQIHEDGYRVTVDNDSNTIAHTLLEKKKDKDGLDTIDAKVOK
SIYNNKNDYSGSTAIHPOTGELLALVSTPSDYVPEMYGMSNEEYKLTEDKKEPIL
NKFOITSPSGSTOKILTMIGLNNKTLDDKTSYKIDGKMGKDKSMGCVNTRYEVN
GNIDLKQAIIESDNIFFARVALELCSKFEKGKMLGVEDIPSDYPRYNAQISKNL
DNEILLADSGYGGCEILINPVQILSIYSALENNNGINAPHLIKDRKNVYMKNIISKE
NINLITDGMQGVNKTHTKEDIYRSYANLIGSGTAELMKOGETGROIQWFIISYDKDN
PNNMAIIVKDVQDKGMASYNKISGKYVDLEYENKKYDIDE"

old_sequence 441..448
/note="altaaac was ac in [1]"
/citation=[1]
old_sequence 641..643
/note="agc was ac in [1]"
/citation=[1]
old_sequence 652..653
/note="ta was tta in [1]"
/citation=[1]
old_sequence 731..733
/note="caa was ca in [1]"
/citation=[1]
old_sequence 780..781
/note="ct was ctt in [1]"
/citation=[1]
BASE COUNT 997 a 345 c 398 g 714 t
ORIGIN

Query Match 100.0%; Score 28; DB 1; Length 2454;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATTGGGTACAAGATGATACCTTCGTT 28
|||||
749 AATTGGGTACAAGATGATACCTTCGTT 776

RESULT 8
LOCUS E09771 2455 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of meca DNA.
ACCESSION E09771
VERSION E09771.1 GI:22026400
KEYWORDS JP 1995209294-A/1.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 2455)
Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
Patent: JP 1995209294-A 1 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/1
PD 11-AUG-1995
PE 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA,

PI SUGURO KAZUHA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,(C12N1/21, PC
C12R1:19),
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..2455
FT 134..2146 /organism="Staphylococcus aureus" FTY CDS
FT 134..2146 /product="meca protein".
FEATURES
source Location/Qualifiers
1..2455
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"
BASE COUNT 997 a 344 c 401 g 713 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATTGGGTACAAGATGATACCTTCGTT 28
|||||
741 AATTGGGTACAAGATGATACCTTCGTT 768

RESULT 9
SAMECAPB 2456 bp DNA linear BCT 12-SEP-1993
LOCUS
DEFINITION S. aureus meca gene for PBP2' (penicillin binding protein 2').
ACCESSION X52593
VERSION X52593.1 GI:46610
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
pen.,illin-binding protein 2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 2456)
Ryffel,C.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE 2 (bases 1 to 2456)
Ryffel,C., Tesch,M., Birch-Machin,I., Reynolds,P.E.,
Barberis-Maino,L., Kayser,F.H. and Berger-Bachi,B.
Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52592> and <X00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source Location/Qualifiers
1..2456
/organism="Staphylococcus aureus"
/strain="NCTC8325, isolate-BB270"
/db_xref="taxon:1280"
/clone_lib="EMBL-3"
80..85
/note="35 region"
101..105
/note="10 region"
130..134
/note="ribosome binding site"
141..2153
/note="primary transcript"
141..2147
/note="PBP2' (AA 1-668)"
/codon_start=1
/transl_table=1


```
/protein_id="CAA36829.1"
/db_xref="GI:46611"
/translaton="MKKIKIVPLIIVVVVFGIIFYASDKKEINNTIDAIEDKNFKQ
VYKDSYISKSDNEVEEMTERIKIVSDIKDINODRKIKVSKKKKRVDAQYKIK
TNYGIDNRVOPNFVEKEDMMKLDMDHSLVILPGMQOSIHEILKSESGKILDRNV
ELANTGHHMLGIYPKNVSKDKYAIKAEKISISDDYINNMKIKGYMISFHKYTK
KMDYELSDPAKKHLLTNTRESRYPLEKATSHLGYCPINSELPKOKEKYKQKDA
VIGKKGLEKLYDKLQHEDEIRYIVDNSNTIAHTLEKKKRGKDIQTLIDAKYVK
SIYNNKNDGSGTAIHPQTELLALVSTPSYDYPYPMYGSNNEYNKLTEDKEPPL
NKFOITPSGSTOKILITAMIGLNKKTLDDSTYKIDGMOQKDSWGVYVTRREVN
GNIDKQAISSDNIFFARVALIEGSKFEKGMKLGQSDIPSDYPPYAOISNNKL
DNELLADSGGCEILINPQILSIYSALENNCININAPHLIKDTYKKNYKNIISKE
NINLNMGOVVKTKHEDIRSYANLICKSGTAELKMKQESGRQIGMFISYDKDN
PNMMAINVADVDKGNASTYNAKISGVYDELYENGNKKYDIDE"

BASE COUNT      1001 a      344 c      396 g      715 t
ORIGIN

Query Match      100.0%; Score 28; DB 1; Length 2456;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AATTGGGTACAGATGATACCTTCCTT 28
|||||
Db 748 AATTGGGTACAGATGATACCTTCCTT 775

RESULT 10
AX110445
LOCUS      AX110145      2456 bp      DNA      linear      PAT 30-Apr-2001
DEFINITION Sequence 1178 from Patent WO0123604.
ACCESSION  AX110445
VERSION     AX110445.1 GI:13926737
KEYWORDS
SOURCE
ORIGIN      Staphylococcus aureus subsp. aureus NCTC 8325.
            Staphylococcus aureus subsp. aureus NCTC 8325.
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
            1 (bases 1 to 2456)
            Bergeron, M.G., Boisset, M., Huletsky, A., m Nard, C., Ouellette, M.,
            Picard, F.J. and Roy, P.H.
            Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
            Patent: WO 0123604-A 1178 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
            Location/Qualifiers
            1..2456
            /organism="Staphylococcus aureus subsp. aureus NCTC 8325"
            /db_xref="taxon:93061"

FEATURES
    source
    ASE COUNT      1001 a      344 c      396 g      715 t
    ORIGIN

Query Match      100.0%; Score 28; DB 6; Length 2456;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AATTGGGTACAGATGATACCTTCCTT 28
|||||
Db 748 AATTGGGTACAGATGATACCTTCCTT 775

RESULT 11
SSK8MECA
LOCUS      SSK8MECA      5596 bp      DNA      linear      BCT 16-Jan-1998
DEFINITION S.sciuri meca gene, strain K8 (ATCC700063).
ACCESSION  Y13096
VERSION     Y13096.1 GI:2791919
KEYWORDS   meca gene; mecI gene; mecR1 gene; NTOF78; ORF142.
SOURCE     Staphylococcus sciuri.
            Staphylococcus sciuri.
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
            1 (bases 1 to 5596)
            Wu, S., de Lencastre, H. and Tomasz, A.
            Genetic organization of the meca region in methicillin-susceptible
            and methicillin-resistant strains of Staphylococcus sciuri
            J. Bacteriol. 180 (2), 236-242 (1998)
            MEDLINE 98101461
            PUBMED 9440511
            REFERENCE 2 (bases 1 to 5596)
            AUTHORS Wu, S.
            DIRECT SUBMISSION
            Submitted (08-Nov-1997) S. Wu, Lab of Microbiology, The Rockefeller
            University, 1230 York Avenue, New York NY 10021, USA
            Related sequences X53818, X54660, L14020, X52593, Y09223.
            Location/Qualifiers
            1..5596
            /organism="Staphylococcus sciuri"
            /strain="K8 (ATCC700063)"
            /sub_species="rodentius"
            /db_xref="taxon:1296"
            1..236
            /gene="NTOF78"
            <1..236
            /gene="NTOF78"
            /codon_start=3
            /transl_table=11
            /protein_id="CAA73550.1"
            /db_xref="GI:2791920"
            /translaton="AFKLKPDCHCTSKYNNI.IBODRHRIKVRKTRYOSINTAKNFKL
            GIEICVLYKKNRRSLQYGFSPCHSISIMLAS"
            complement(485..856)
            /gene="mecI"
            complement(485..856)
            /gene="mecI"
            /codon_start=1
            /transl_table=11
            /product="MecI protein"
            /protein_id="CAA73545.1"
            /db_xref="GI:2791921"
            /db_xref="SPTREMBL:054285"
            /db_xref="SPTREMBL:054285"
            IRTLITRLYKGFIDRKDKNLIFOYISLSESDIKYKSKNFINKYVKGGRNSLVNLF
            VEKEDLSODEIEELRNILNKK"
            complement(join(856..2613,2620..2626,2638..2643))
            /gene="mecR1"
            complement(856..2613)
            /gene="mecR1"
            /codon_start=1
            /transl_table=11
            /product="MecR1 protein"
            /protein_id="CAA73546.1"
            /db_xref="GI:2791922"
            /translaton="WLSGFMLSIISLLTICVIFIVNMYIKYTONIMSHKIMLLVY
            VSTPLIPFYKISNFTSKDMNRRNSDITSSVSHMLDGGQSVTQDLATINQOFK
            SNITMYILLINFGSLCLFEMKAFKAFQIDIVIKSSLESSLYNRLKLVQSKMQFYK
            HITISYSSNIDNPVFGVGLKSOIYPTVVTIMDKREIYILIELSHVSHDILFNO
            LYVFKMIFMFPNAPALYISKTMNDNCEVCDRNLYKILNHEHRIYCESILKCSILKS
            OHINNVAAOYLLFGNSNIKERKVIYALDSMPKPRNKRIYAVIVCSISLLIOAPLSS
            AHVOODKRETVSYKKIQLNOALPYFKGFGDSFLVLENREDAONLANSKRYSVNRYENTKH
            KYIYALMAEPQNLISLNTQODKQHPFKKKNQDONLANSKRYSVNRYENTKH
            LRQDEKVSITDILIEGNEISGENENTMSSLSKISAEQVNLNMMQHNHFNKAI
            EKVENSMTLKQKQDYKYVGTGTGIVNKEANGVFGVETKNTYTFATHLKGEDNA
            NGERAQOISERILKEMELI"
            complement(855..869)
            /gene="mecI"
            complement(865..869)
            /gene="mecI"
            complement(865..869)
            /gene="mecI"
            complement(2620..2626)
            /gene="mecR1"
            complement(2638..2643)
            /gene="mecR1"
            2652..2657
            /gene="meca"
            2652..2657
            /gene="meca"
            complement(2663..2668)

gene
CDS
gene
-35_signal
gene
```

-35_signal /gene="mecR1"
complement(2663..2668)
/gene="mecR1"
gene 2676..4719
/gene="meca"
2676..2681
-10_signal /gene="meca"
2702..2707
RBS /gene="meca"
2713..4719
/gene="meca"
CDS /transl_table=1
/product="Meca protein"
/protein_id="CA73547.1"
/db_xref="GI:2791923"
/db_xref="SPTREMBL:O54286"
/translation="MKRIKIVPLILVVVVGQIVYVASKDEINNTIDATIEDKNFKO
VVKDSSYISKSDNGEVEWTERPIKLYNSLGVKDINTODRKIKKVSNNKRRVDAQYKIK
TNYGNIDRWVQFNFVKEKDMKIDMDSYIIPQMKDOSIHIENLKSESGKILDRNN
ELANTGAVEIGIVPKNVSKKDYKAKALAKELTISEDYIKOQMDQNMVODDEPVLTKV
KMEYISDFAKKRHLTNETESRNPYLEKATSHLIGVGPINSEELKOKEYGYKQDA
VICKKLEKLYDKKLOHEDGYRTIYDQNSNTIAHLIIRKKDKDLOLITDARQK
STNNKNDIGSGTAIHPOGELALVSTPSTQVTFPMQMSNEEYNTKLTEDKKEPL
NKQITTSPOSTQKILTAMGLNNKTLDTKTSYKIDGKMOKDSWGVNVRVEYVN
GNIDLKQALIESSDNIPFARVALELGSKKFEKMGKLVGEDIPSDYPYNAQISNNL
DNEILLADSGYGGEILLINPVOLISYSALENNGINAPHLKDTKNKYNKKIISKE
NINLTEDGMOOVYNTKEDIYRSYANLIGKSGTALMKOGETGRQIQWFIISYKDN
PNMMAINVKDVODKGMASYNAKISGVYDELXENKRYDIDE"
gene complement(4765..5266)
/gene="ORF142"
CDS complement(4765..5193)
/gene="ORF142"
/codon_start=1
/transl_table=11
/protein_id="CA73548.1"
/db_xref="GI:2791924"
/db_xref="SPTREMBL:O54520"
/translation="MKYDIEVGETTKTKSLHITEEETIOFATTFDPQYMHIDKEKAE
QSRKGIILASGMHTLSISFKLWEEGKGEVAVAGQNNNFKIKPYVGNLTLYIAE
ITNKKSIKKENGIVTSLSTYNNENEIVFKEVTALINNS"
RBS complement(5200..5205)
/gene="ORF142"
-10_signal complement(5238..5243)
/gene="ORF142"
-35_signal complement(5261..5266)
/gene="ORF142"
gene complement(5290..5596)
/gene="NTORF101"
CDS complement(5290..>5596)
/gene="NTORF101"
/codon_start=2
/transl_table=11
/protein_id="CA73549.1"
/db_xref="GI:2791925"
/db_xref="SPTREMBL:O54616"
/translation="SFNVYLVLKAEIIMPOYNAVYFHTTSPFEDRRTLLDYCNAKIV
NTEDAKLTAKVMKVEAGVELNWTYNNKPARANOALANNGVDCIIFDNADKKVHLSO"
BASE COUNT 1991 a 856 c 821 g 1928 t
ORIGIN
Query Match 100.0%; Score 28; DB 1; Length 5596;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAATGGCTACAGATACCTTCGTT 28
DB 3321 AAATGGGTACAGATGATACCTTCGTT 3348
RESULT 12
SSK3MECA2
LOCUS SSK3MECA2 6368 bp DNA linear BCT 16-JAN-1998

DEFINITION S. sciuri meca2 gene, strain K3 (MM2).
ACCESSION Y13095
VERSION Y13095.1 GI:2791912
KEYWORDS CTORE261 gene; mecA2 gene; mecI gene; mecR1 gene; NTORF101; ORF142.
SOURCE Staphylococcus sciuri.
ORGANISM Staphylococcus sciuri
REFERENCE 1 (bases 1 to 6368)
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic organization of the meca region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 98101461
PUBMED 9440511
REFERENCE 2 (bases 1 to 6368)
AUTHORS Wu, S.
TITLE Direct Submission
COMMENT Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
FEATURES
source location/qualifiers
1..6368
/organism="Staphylococcus sciuri"
/strain="K3 (MM2)"
/sub_species="rodentius"
/db_xref="taxon:1296"
complement(1..883)
/gene="CTORE261"
complement(<1..784)
/gene="CTORE261"
/codon_start=1
/transl_table=11
/protein_id="CA73539.1"
/db_xref="GI:2791913"
/db_xref="SPTREMBL:O54280"
/translation="MENTININDNEKRVLEIREYNNHNISKROISKNLEINAKTASSIL
NKIKRSLVNEGEGBSTKSGRKPLIKLVNHLGYFISLDITSSVEWNTNPDGAV
NHTESYDLPDEKVSISLTIKRIHIDIOEKLDVNLGVSVSIHGVVNDQHVYLLP
HTEGSIISIAKKIKETYNPVVVENANSALYERFNHNLSYNNILALSIIHKIGIAGL
IINNDLYRGANAGEIGKTLVSKSVDSWEIFPKHIEDIFSQA"
complement(791..797)
/gene="CTORE261"
complement(855..860)
/gene="CTORE261"
complement(878..883)
/gene="CTORE261"
complement(1257..1628)
/gene="mecI"
complement(1257..1628)
/gene="mecI"
/codon_start=1
/transl_table=11
/product="MecI protein"
/protein_id="CA73540.1"
/db_xref="GI:2791914"
/db_xref="SPTREMBL:O54281"
/translation="MDNKTYEISAEHEVYNTIMKKYASANNITEETIQMRDMSPT
ITLTLRLAKKGFIRKKDKNKFQITSLVEESDITKTSKNFINKVTAGGNSLVLP
VEKEDLSODEIELNLINLKK"
complement(join(1628..3385,3392..3398,3410..3415))
/gene="mecR1"
complement(1628..3385)
/gene="mecR1"
/codon_start=1
/transl_table=11
/product="MecR1 protein"
/protein_id="CA73541.1"
/db_xref="GI:2791915"
/db_xref="SPTREMBL:O54282"
/translation="MLSSFLMCIISLITICVIFLVRMYIKXTONIMSHKILVY
VSLIPLIPFYKISNFTSKDMKNNRVSDTSSVYHMLDGOSSYTDLAINVQFET
SNITTHILLIIVFGSLCIFTYIKAFROIIVYKSSLSSESLYNEKLAKCOSKMPYRK
HTTISYSSNIDNPVFGLVKSOIVLPVYVETMMDKRELEYIILHLSHVKSHDIFNQ

Query Match	Best Local Similarity	100.0%	Score 28;	DB 1;	Length 6368;
Matches 28;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY 1	AAATGGGTACAGATGATACCTTGCTT 28				
Db 4093	AAATTGGCTACAGATGATACCTTGCTT 4120				
RESULT 13					
SAMECAR11		9047 bp	DNA	linear	BC1 16-JAN-1998
LOCUS					
DEFINITION	Staphylococcus aureus mecA, mecR1, mecI genes and ORF142, ORF44, ORF145 and ORF224.				
ACCESSION	U14051.1				
VERSION	GI:2791983				
KEYWORDS	mecA gene; mecI gene; mecR1 gene; ORF142; ORF145; ORF224; ORF44; PBE2a; repressor protein; transposase.				
SOURCE	Staphylococcus aureus				
ORGANISM	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
REFERENCE	1 (bases 1 to 9047)				
AUTHORS	Wu, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (27-JUN-1997) S. Wu, Laboratory of Microbiology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA				
AUTHORS	2 (bases 1 to 9047)				
TITLE	Wu, S., de Lencastre, H. and Tomasz, A.				
JOURNAL	Genetic organization of the mecA region in methicillin-susceptible				
MEDLINE	J. Bacteriol. 180 (2), 236-242 (1998)				
PUBMED	98101461				
FEATURES	9440511				
SOURCE	Location/Qualifiers				
	1..9047				
	/organism="Staphylococcus aureus"				
	/strain="BMS-1"				
	/strain="B8270"				
	/db_xref="taxon:1280"				
	complement(<1..505)				
	/note="ORF168"				
	/codon_start=1				
	/transl_table=1				
	/product="putative repressor"				
	/protein_id="CAA74373.1"				
	/db_xref="GI:2791984"				
	/db_xref="SPTREMBL:O53708"				
	/translation="MYNVPDGNVTKHESYLDPEKVSIIISIKKHIDIOEKIDYNG				
	LLGVSISIHGVNDEQHYTILPHFETGCSIAKIKETIWPVVEENALISALYERN				
	FNNH;STNNLIALSIHKIGICAGLIINNQLYRGANGEGEIGKTLVSKVSDNVEIFPKI				
	EDISQA"				
	complement(11244..1615)				
	/gene="mecI"				
	complement(11244..1615)				
	/gene="mecI"				
	/codon_start=1				
	/transl_table=1				
	/product="MecI protein"				
	/protein_id="CAA74374.1"				
	/db_xref="GI:2791985"				
	/translation="MDNKYEISAEWEVNNIIMKKYASANNIIEIOMQKWSPT				
	IRITILRIUKKGFIDRKKDKKILFOYISLVEESDIKITSNFINKYKGGFNSLVNF				
	VEKDLSDDEIEELRNILNK"				
	complement(1615..3372)				
	/gene="mecR1"				

```

CDS      complement(1615. .3372)
        /gene="mecR1"
        /codon_start=-1
        /transl_table=-1
        /product="MecR1 protein"
        /protein_id="CA74375.1"
        /db_xref="GI:2791986"
        /translation="MLSEFLMLSLISLITLCVLFVRLMYIKYTONIMSHKIMLVL
        VSTLPLIPPEYKISNFTPSKDMNRNRVSDTSSHMLDGOSSVTKDLAINNOET
        SNITVYLILIMVGSLLCLPYMIKARQIDYIKSSSESYLNERLKACOSKQYPRK
        HITITSNIDNPMPFGLVKSQIVLPTVVEITNDEIEITILHEISHKSHDILFNO
        LYVFMFTFENFALYISKTMNDNDEKCDRVNLILNHEHIRGESLILKSLILKS
        OHINNAAYQLLGFNSNIKERKYIALYDSMPKPNKRIVAYIVCSISLLIAPLIS
        AHVQODKRETVNSYKKNLQALAPYKGFDSFVLYNERQAYSIYNESKORYSPNST
        YK1YLALMAFDONLILNHTEOQMDKHQYPFKEMDONLNSMKYSVMVYENLAKH
        LRQDEVKSTYLDIEYGNERTSGNENYNESLSKISAIEOVNLLKKNKHMHFDNKA
        I EKVNSMTLKQDTPYKCTGTCGIVNHNKANWPFVGYETKNTPTTFATHLKCEDNA
        NGEKAQOISERILKEMELT"
        3472. .3478
        /gene="meca"
        3472. .5478
        /gene="meca"
        /codon_start=-1
        /transl_table=-1
        /product="pBP2A"
        /protein_id="CA74376.1"
        /db_xref="GI:2791987"
        /db_xref="SPTREMBL:O53707"
        /translation="MKKIRIVPLILIVVVVGQIFYVASKKEINNTIDAIEDKNFKO
        VYKDSYISKSDGEVEMTERPIKIYNSLGVKINIDQRIKKVSKNKRKVDQYQYIK
        TNGNIDRVNVOEFVEKDGMMKLMDHDSYIIPGMQDSIHENLKSERGLIDRVN
        ELANTGIMRLGIVPKNVSKKDYKATAKELSTIEDYINNKWIKIGKIMPSPIEFYK
        KMEYISDPAKKHLITNETESKNYPLEKATSHLDTYVGINSEELKQEKYKQKDA
        VIOKCLELMDKKLQHEGVRVTVIVDNSNTIAHLIEKKKMDGKDIDLTTDAKQK
        SIYNNKNDYSGQTAIHQGTGLALVSPSYDVVPMYGMKSNKEENKLTDEKPEL
        NKFOITTSPTSGTOKILITAMIGLNKTLDDKTSYKIDGKQMKSGKNVTVQYEVN
        GNIDLKQALSSNDIFARVALELGSKFEKCGKRLGVEDIPSDYFNAOISNKE
        DNEILLADSGYGGELLINPVOILISYSALENNGINAPHLIKDTKKNYKKNKIISKE
        NTNLNDGMOQVYNTKHKDIIYRSYANLICKSGTALMKKCGSGQIOIGFISYDKDN
        PNMMMAINVKDNDKMASYNAKISGVYDELIEYENKKTIDDE"
        complement(5524. .5952)
        /note="ORF142"
        /codon_start=-1
        /transl_table=-1
        /product="hypothetical protein"
        /protein_id="CA74377.1"
        /db_xref="GI:2791988"
        /db_xref="SPTREMBL:O54520"
        /translation="MKYDFIVGETFKTSLHITTEEIIIOFATTFDPQYMHIDKKA
        QSRFKGIASGMITLISIFKLVVEEGKEEYVAGTOMNNVFIKPVYPGNTLYIAE
        ITNKKSIKKENCILVTVSLSTYNNENIEIVFKEVETALINNS"
        complement(6049. .6183)
        /note="ORF44"
        /codon_start=-1
        /transl_table=-1
        /product="hypothetical protein"
        /protein_id="CA74378.1"
        /db_xref="GI:2791989"
        /db_xref="SPTREMBL:O54083"
        /translation="MYKAGYELNVTVKKPARANGLANWGVGIFTVDADKMHLSQ
        complement(6354. .6791)
        /note="ORF145"
        /codon_start=-1
        /transl_table=-1
        /product="hypothetical protein"
        /protein_id="CA74379.1"
        /db_xref="GI:2791990"
        /db_xref="SPTREMBL:O9387"
        /translation="MUTVYGRGLPSKAPDENTIASFKAASEVEGINMLELDAVAITKDE
        QLIILHDDYLERITNMSCEITELANYDEIKDASGWFGEKFKDEHLPTFDDVVKIANE
        YMMNLVELKGTGTGNGALSKSMVKOVEQQLNLNNOQEELI"
        8096. .8770
CDS

```

```

        /note="ORF224"
        /codon_start=-1
        /transl_table=-1
        /product="putative transposase"
        /protein_id="CA74380.1"
        /db_xref="GI:2791991"
        /translation="MNYFRYKQFNKQDVITVAGYLYRITLSYRDISIELRERGVNHH
        STYRBMVOEYAPILYOIMKKKKHKKAYKKRIDETIYIKIGKWSYLYRAIDAGHTLID
        WLRKQNSAFAFIRLLIKORCKPKQVITTDQASPTKVMAMVYKAFKIKPKCHCTSK
        YLKNLIEDQHRHKKVKKTRQSIINRAKNLTKGIECIYALFKNRSLOIGFSPCHEI
        SIMLAS"
BASE COUNT      3099 a      1469 c      1257 g      3222 t
ORIGIN
Query Match      100.0%; Score 28; DH 1; Length 9047;
Best Local Similarity 100.0%; Pred No. 0.01;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY      1      A A A T T G G T A C A G A T G A T A C C T T C G T T      28
Db      4079      A A A T T G C G T A C A G A T G A T A C C T T C G T T      4106

RESULT 14
AB063173
LOCUS      AB063173      21777 bp      DNA      linear      BCT 09-APR-2002
DEFINITION      Staphylococcus aureus DNA, type-IV staphylococcal cassette
ACCESSION      AB063173
VERSION      AB063173
KEYWORDS      chromosome mec, strain:JCS1978(8/6-3p).
SOURCE      AB063173.1 GI:17025993
ORGANISM      Staphylococcus aureus (strain:JCS1978(8/6-3p)) DNA.
REFERENCE      Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS      1
Hiramatsu, K., Cui, L., Kuroda, M. and Ito, T.
TITLE      The emergence and evolution of methicillin-resistant Staphylococcus
JOURNAL      aureus Microbiol. 9 (10), 486-493 (2001)
MEDLINE      21482917
AUTHORS      2
Ma, X.X., Ito, T., Tienasastorn, C., Jamklang, M., Chongtrakool, P.,
Boyle-Vavra, S., Damm, R.S. and Hiramatsu, K.
TITLE      Novel type of Staphylococcal Cassette Chromosome mec identified in
JOURNAL      Community-acquired methicillin-resistant Staphylococcus aureus
Strains
MEDLINE      Antimicrob. Agents Chemother. 46 (4), 1147-1152 (2002)
AUTHORS      3 (bases 1 to 21777)
JOURNAL      21895198
REFERENCE      3 (bases 1 to 21777)
AUTHORS      Xue, M.X., Ito, T., Hiramatsu, K. and Tienasastorn, C.
TITLE      Direct Submission
JOURNAL      Submitted (12-JUN-2001) Terryu Ito, Juntendo University, Department
of Bacteriology, Hongo 2-1-1, Bunkyo-ku, Tokyo 113-8421, Japan
(E-mail:teruyabac@med.juntendo.ac.jp, Tel:81-3-5802-1041,
Fax:81-3-5684-7830)
FEATURES
source      1. 21777
Location/Qualifiers
1. 21777
/organism="Staphylococcus aureus"
/strain="JCS1978(8/6-3p)"
/db_xref="taxon:1280"
/note="community-acquired MRSA strain isolated at the
University of Chicago children's hospital"
301. .21221
/note="302. .21222 or 303. .21223 or 304. .21224
type-IV SCCmec of JCS1978(8/6-3p)"
301. .326
/note="Inverted complementary repeat(IR-L) of SCCmec of
JCS1978"
repeat_region      JCS1978"
/ftl_type="inverted
complement(325. .1446)
/note="ORF No. CM001"
/codon_start=-1
/transl_table=-1
CDS

```

```

/product="hypothetical protein"
/protein_id="BAB72122.1"
/db_xref="GI:17025994"
/translation="MKMSYQIRIWMGPKSYLNEFLHOPYITLEDYIIKIDSLTRNLVE
KFTNNYEEILKDKIILAKTESYSGITSAALSNFIQIVNKSIEFGNGIILONPKRSVI
NOIKNSFDENQYAFCEVEYPKLDLAVLSNIKERSTEOLEGOVNAIKRIALSLYKTSK
SRKSIIVLMLVGPSCVGTKEMSKIISECIQGLKPKRMSKNTYMPDIPFNNGTSPS
LARDLIRRESNIVLLDFPDQKGVNELNSAFQLPDEGIPEDSQYKVTMNSIITICGNS
KGEQIIRRELSDPYIYRDEDFIEFALNDEKKKILITFIISEFPNKLSDNKSLLPRE
EILKQYMIKIQKQFTNRIHMKLVENDINLRISALMLNF"
complement(1424..2194)
/feature="ORF No. CM002"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72123.1"
/db_xref="GI:17025995"
/translation="MKLIYFDESTASDYLIKILIONGRESKQYIETKKNOKQTSIGCKFG
IGPMSEKVFESLPSIEGMGGINNTSSEKYEKLTJNALISDPKMLAENBELIKKFS
EYKLSYVENSIAHFQTIISPYLSMLDGNVLDOEVSININKHEFTLKIGKYEYILAKK
MENECIYRENNKAFVNNYNLTDLSDOMOLTYGKGIIDINQNLNPNAINSIGFQNKY
VTSISEEVNRSFNNQSIEMPTDIIAGVEYENELSN"
2311..3741
/feature="ORF No. M001"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72124.1"
/db_xref="GI:17025996"
/translation="MNFENYKFTGCKDLMKCNLSSEKMKSNMOKLEVVYIUDITTKYK
SNPSATNSGYSFNLFELELFIILNTIEDPPVPSAKFPDDIDLEELKKNNSHPIR
YITNITPDSIDNIKDALKAQIYASENSFTLEWLSAQSCSDALSSFPNNTNSIDLR
SSKILYKRIAHRIDEMETLMDNMTYDNEFNKQLYKHQYDKENNAETVYVYVNEH
PDDKSNSENHIDEMETLMDNMTYDNEFNKQLYKHQYDKENNAETVYVYVNEH
ITAYDIONGDESKIRBKIRKMEIYKYPNANGYELDEDLFTNQRITINDYKSN
TEPDIONPESRDINISNSKRLISNDKPNYIKDDYSLSKSNLPHIRQSYIHDGIN
SNOVDFLNDIYRIHLUDIKYSSNKDIEPLSKINTELTNAFQLEKELKSTQIKDEIV
SKKYNDSSWSIAALSETLNDLNF"
3861..5651
/feature="ORF No. M002"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72125.1"
/db_xref="GI:17025997"
/translation="MNNNIFKQYFYLNSNGEYEVIPKPSNNDEKIIQLSPIITEN
KFLDPSTGVEKLIITDGKNIRIEASDILTSFKLIGLIKIFNINERYIKLSYALQS
MROSLPISKIYTGAVLOSDEGWIISLDKPYFSKEILOSQANELICETHYDLOPKT
FKGMWEMYLKQVKNLLELAVIFGISALVNSPIBHKHATEPAGIIESFGQSSSTGKS
TASIAVAVACNPTKNGETLFRSNAPATRNALEGYLSNNYGIPIVDELSATPRDITC
LLYSITBEGQRORSNVEGVTPKMGTSVISTEYSLFNSQNDGLRVTIETNER
FTKDATNSDNLIKTVALLVYGLVPLVAVYLINREDEVIQWFEEDWENESLAKETNN
TGIRMFKRYAVITTSAKILGRVLSIDIDIANIRDEYFIDYHTHTVSERSLADKADIVII
QFVAQNRKGFSEDEGALKMFPENYGLISLKDHIIEVKMIANFKQMLNNHQRQDVANNV
NALRDKGFILADRCROTTKRSVNDGSKKOSLVFYLKLDVEFASIIGLTMDKSLQNL
WTPSNDNKAKEALKFSANEGIGPSGVHEDF"
5732..5797
/feature="ORF No. M003"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72126.1"
/db_xref="GI:17025998"
/translation="MDEIETLADLVIEINQTNQ"
5885..7234
/feature="ccrA"
/feature="ccrA"
5885..7234
/feature="ccrA"
/feature="ccrA"
/feature="ORF No. M004"
/codon_start=1
/transl_table=11
/product="cassette chromosome recombinase A"
/protein_id="BAB72127.1"

```

```

/db_xref="GI:17025999"
/translation="MKOYIGYLRQSTMKQOSIAQKQALIEAIAEKHHIOHINFSDKO
SGKRDNRSGYRQMTQOLIQQGQCDILICRRLNRLHNKLNALKILKICOTYVHILSVH
DGYEDMDQAFRLKLNITFISLAELSDICIGOVNNGLOEKAKQOLITTHAPFQYDIIH
NGTFLINQNSERTLVKAVENYITKIGHYKIKIGOLLEEDNTYINRQPYVRANIIMPNTC
GRIVINOQGFQNMFPSTIVSANVYDQAGRLRLOKQKOTSSONOLKOKIKCSCAVLT
MNTIRKKHKTIRRYVCPKPNMASRVCDFQKGINOTLEDVLYEVCBPDYONORIYTKI
KCAIDKRIKROBRIEKKHLLTOEOLIEKLAGCIIIDAEYFRQOTOSLNOOPORTYINC
HOIQTIONTIQKRFITNIIYLETIITHKOKNLIGTYFNEPLNLYNQMOSSIA"
7256..8884
/feature="ccrB"
/feature="ccrB"
7256..8884
/feature="ccrB"
/feature="ccrB"
/feature="ORF No. M005"
/codon_start=1
/transl_table=11
/product="cassette chromosome recombinase B"
/protein_id="BAB72128.1"
/db_xref="GI:17026000"
/translation="MGOIKTKRQVGIYVRVSTEMOSTEGSYIDQOINQIKKEYCDPHHPE
VKDIYADRGISGSKMNRPELORMILKDAEGNIDCYMITKTRKLARNSTDLEKTYEDLI
KONVEFSLSRMEVNTSSGKLMILQILASESEFERNITVENVEFGOTRRADGYTQGN
LPLGDIKIPDSKHELMINQHEANIVKTYIESYAGHGKRIANALNIRKGYTKKGRPF
SISITTYILANPYIGKIQPARKDMSEKRRKQINDKPVIAEGKHP1INODLMDKQV
MRKQVSGKPOVHGKTNLITGI1HCPCCGAPMAASTNTN1IKGTKKRIKYVYCSGN
RNKGSKVCANSVRADYIEDYVMKOILIEIVSDMYIOHVRVARNQENKVDGALHHD1
AYKQOQVDEQTKNNLIKTEEDPDLSVSIRPSIOREKOLNDITNOINOLKQONE
DKSLFDAQISIKLOIHFIHDIKHIEKSLKALYISVIDRIDIKKDGNNKQFYTTKL
NNEITIKOLENNKQDEVALHSTSLFPLQTLITI"
9406..9756
/feature="ORF No. M006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72129.1"
/db_xref="GI:17026001"
/translation="MKTITQELKQYITHLFQISNNAECCALIEAAENIIPERRIND
SPLVHLTLEYTYVYNDELHELISYFPFLVANNOLISVGYLIDHPMDPLLYLTDQNI11
DERHLKQGGQDHE"
9843..10154
/feature="ORF No. M007"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72130.1"
/db_xref="GI:17026002"
/translation="MKIRNYITRGINESIPLDQILMHVYKKNQNOPHTDYLHIFKL
QEDENILISTHEQGPYTKLEVHTNTYNEKQNALPKKYYVIREDDVAFYVMLLPEP
Y"
10166..10675
/feature="ORF No. M008"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72131.1"
/db_xref="GI:17026003"
/translation="MMNTIKSTIHTALISDEQHRLLKKTWDEKKAACVITMYTPH
LDGVSLDITLVLLINOLANSERGAVALVNFSTRPENLKHIKPDEHDIHLM
KAISESDVILAYGAYAKRPVYIDRVEDVEMMLPKHKKKVKKLINPVNTNEIMPLNPK
AROKWILKS"
10676..12334
/feature="ORF No. M009"
/pseudo
/codon_start=1
/transl_table=11
/complement(12557..13543)
/feature="mecR1"
/pseudo
/complement(12557..13543)
/feature="mecR1"
/feature="ORF No. CM003"
/pseudo
/codon_start=1

```

```

      gene               /product="signal transducer protein Mecr1"
                        /note="ORF No. 0001"
      CDS                /codon_start=1
                        /product="hypothetical protein"
                        /protein_id="BAB72102.1"
                        /db_xref="GI:17025973"
                        /translation="MIDP(CD)SSYIRVADESLITITAAETHIHANVSGIRDYAI
Query Match          100.0%; Score 28; DB 1; Length 21777;
Host Local Similarity 100.0%; Pred. No. 0.01;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAATGGGTACAGATGATACCTTCGTT 28
Db 14251 AAATGGGTACAGATGATACCTTCGTT 14278

RESULT 15
AB063172      26090 bp      DNA      linear      BCT 09-Apr-2002
LOCUS         AB063172
DEFINITION    Staphylococcus aureus DNA, type-IV staphylococcal cassette
KEYWORDS      Staphylococcus aureus
SOURCE        Staphylococcus aureus
ORGANISM      Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE     1
AUTHORS       Hiramatsu, K., Cui, L., Kuroda, M. and Ito, T.
TITLE         The emergence and evolution of methicillin-resistant Staphylococcus
JOURNAL       Trends Microbiol. 9 (10), 486-493 (2001)
MEDLINE       2
REFERENCE     2
AUTHORS       Ma, X. X., Ito, T., Tienasastorn, C., Jamklang, M., Chongtrakool, P.,
              Boyle-Vavra, S., Daum, R. S. and Hiramatsu, K.
TITLE         Novel type of Staphylococcal Cassette Chromosome mec identified in
              Community-Acquired Methicillin-Resistant Staphylococcus aureus
              Strains
JOURNAL       Antimicrob. Agents Chemother. 46 (4), 1147-1152 (2002)
MEDLINE       3
REFERENCE     3
AUTHORS       Xue, M. X., Ito, T., Hiramatsu, K. and Tienasastorn, C.
TITLE         Direct Submission
              Submitted (12-JUN-2001) Teruyo Ito, Juntendo University, Department
              of Bacteriology, Hongo 2-1-1, Bunkyo-ku, Tokyo 113-8421, Japan
              (E-mail: teruybac@med.juntendo.ac.jp, Tel: 81-3-5802-1041,
              Fax: 81-3-5684-7830)
              On Mar 11, 2002 this sequence version replaced gi:17025971.
              Location/Qualifiers
                1..26090
                /organism="Staphylococcus aureus"
                /strain="JSCC 1968 (CA05)"
                /db_xref="taxon:1280"
                /note="community-acquired MRSA strain isolated at the
                University of Chicago children's hospital"
                976..25224
                /note="977..25225 or 978..25226 or 979..25227
                type IV SCCmec of JSCC1968 (CA05)"
                976..1001
                /note="inverted complementary repeat(IR-L) of SCCmec of
                JSCC1968"
                /rpt_type="inverted
                complement(1280..1900)
                /note="ORF No. C0001"
                /codon_start=1
                /transl_table=11
                /product="hypothetical protein"
                /protein_id="BAB72101.1"
                /db_xref="GI:17025972"
                /translation="MKETEVEVIEHLVKAYEAGKPPYPHENLYRGNRNHSISGIGDL
                LGAYLISREGVOIFIDPILSMIDKSLSTRPOLLICEENIELEVKMDLCTYQKRD
                FIDYCKRKEEMISNIYKQCVLSRKREDKIPMIADIKFHVYIYSENNQPKRDEEI

```

```

      CDS                /codon_start=1
                        /product="hypothetical protein"
                        /protein_id="BAB72102.1"
                        /db_xref="GI:17025973"
                        /translation="MIDP(CD)SSYIRVADESLITITAAETHIHANVSGIRDYAI
                        KLASIVYSGESDMDLGYKNMPPHTEVQHNDDIYVGNIKAVLHTPGHTPSSISFL
                        TDEGAAQVPMGLPGSDFIPVGDIPGDDLEKAVKVGSLICAKQMPKSLISIKDLP
                        DYIOIPGHCAGSPGCSLGAIPSTLGYEKNMAFSENNEAETFDKILISDPAPPH
                        HFAQMKINQFQGNLQYPTVYVYATSTNRITFPLRSEKAVHGCHIEGTINPYDKNFI
                        NQIGWLANQEIINLIGDHYLVSKATHNLIYNLDMIMCLDISYHKLKRNHNLFIYKI
                        "
                        complement(4281..5771)
                        /note="ORF No. C0002"
                        /codon_start=1
                        /transl_table=11
                        /product="hypothetical protein"
                        /protein_id="BAB72103.1"
                        /db_xref="GI:17025974"
                        /translation="MHRBSKYIEYKSKRGLSNDIWSYSAVANTBEGTIIYLCIEKK
                        IEDKRVSVSGVEDPEKMLIEDFNALYGRKVSQNLISKKDKYVNIENKACIEIHVP
                        EAPYSKRPPIYDNKDKLVYKRVDDADRIFATEEYKFMIVNSODPIDTELDNDMSDL
                        NHEISINYRKLLIKTNDERYANMSOLDIMIDGAYRKDRSSKQKQKMTACLLEFG
                        KYNAIDRPPGFOLDYFKKTYNIDTQMKDITSSGDICNDILNVYSEFEVLIKLTQNI
                        ESEFSLNDGILTRONVARDKVALREALVNTIMAAVYDTGROSIKIVNCGDFIEFYNGCN
                        MRINKEDFIHGCHSKDRNSILSLFPRVCSSEAGSGRPIPIVYVNRHKLKPIEILT
                        DMQTNVYLMKQDLAKKEKIPEDLKKVYKTIIDYGSISKGALEKMEHETQPRNLIK
                        KLKDDNLIKKREGSPATKYVYLIESKADILRTKVIKLSSEFFRNK"
                        complement(6389..7438)
                        /note="ORF No. C0003"
                        /codon_start=1
                        /transl_table=11
                        /product="hypothetical protein"
                        /protein_id="BAB72104.1"
                        /db_xref="GI:17025975"
                        /translation="MIPLEELIDKYGNIVDYIAKPVYVYKEDLLILLSLSDLNHQ
                        KMDRVSPFIKKHLNSNDYLDDEFRSINKIYSLNLMIRHINSQNNKRNVPINIEQ
                        KLSLAIRKVDAMSYDNDITSKALAEINKTKORLIVTKIIDTIYNNQKKNKRVFCEK
                        ISYTKLENNHKYLYNFIQFYNLNNOLISYVALDOEYANAFNELFLIELLYLAKFRQ
                        KKTIDYERKKLNEFTIOSYIITLIDIRLPVRLITRIDVDTGEGKNQKKTITLIE
                        SIKIRYVADQIKREFRNGLESILNATLSIEQMLKVKIDYIKACFEPREKTHNIE
                        YNSLFEKALDALAK"
                        7577..7867
                        /note="ORF No. 0002"
                        /codon_start=1
                        /transl_table=11
                        /product="hypothetical protein"
                        /protein_id="BAB72105.1"
                        /db_xref="GI:17025976"
                        /translation="MNKSKQOEKLYNFIIAKSPQPVGSFTFYGLAKKYNVVCSTN
                        DQREVGRFPAFYKTYTPGLPFKIVGTKNKSLLYXKIGINPCNNSPIPLKGDC"
                        7867..9654
                        /note="ORF No. 0003"
                        /codon_start=1
                        /transl_table=11
                        /product="hypothetical protein"
                        /protein_id="BAB72106.1"
                        /db_xref="GI:17025977"
                        /translation="MSYTLPEIGPFDLDSFGWKMTIPPKQDSDSKVVMASPIIVNA
                        RSDPITGVKELITNNNGKKOIFESDILITTRNLSLKYCSINEXYIRSLSTALQ
                        MKDRPLPSELIEBVGILETPFGILSLDVLVLSIQPNSSPSYPIVDSAYVDLTPKGT
                        DNWFNMYIDEVGHLLELAVIFGISALVSPKRNHELEFAGILFSPFGOSSTGKST
                        AALAVSAGNPTKGNELTFRSMNATRNALLEGYLSNNVGIPYIPDELSTTLRDTG
                        LYSIAGQGRORSNVGHEVETPKMNGTSYISTSEYSIFNDSQNDGLRYRTIENEG
                        TTNATNADNIIKAVALLNGHYVLPLVAKYUINDEEDYIOWEYEVSMPEAKKIDEINNT
                        GIRMFRVAIVITTSAKILGRVISTOIIDIANIDEDYIDYVTFYVSRSLADRAIDYITIO
                        PVAONGKRSQCALKNMFEENGILSKDHIIEVKMIANVFQKMLNNHNOFQDVNNVVA
                        ALRDKCFIILADKQRTKRSVQNDNGSKOSLVYHLKLDVEFASITLGLTKDSKSLIQNW
                        TPANDNKAKELEKFSANEGIGPSGVHEDE"
                        9735..9800
      CDS

```

/note="ORF No. 0004"
/codon_start-1
/transl_table-11
/product="hypothetical protein"
/protein_id="BAB72107.1"
/db_xref="GI:17025978"
/translation="MDELIELADLVEINEQTND"
9888. 11237
/gene="ccrA"
9888. 11237
/gene="ccrA"
/note="ORF No. 0005"
/codon_start-1
/transl_table-11
/product="cassette chromosome recombinase A"
/protein_id="BAB72108.1"
/db_xref="GI:17025979"
/translation="MKQVIGYLRQSTMKQSLAAKQAIIEAIEKHIIQIHNIEYSDKQ
SGRKDRSGYRQMTOLIQGQCDILCCYRLNRLHRLNKLKILCQTYRVHILSVH
DGYEDMDQAFRLKLIIFISLALESNDIGEVRNGLOEKAKGRLITTHAFGYDYH
NGFTIINONESPTKAVPNVYIKGHYKKAQIILEEDNTYINROPYVANIINPNYC
GRVNNVCGPDNMPISIVSTSIYEOAORLQLOKOTSSDNLKOKIKCPCCNATLT
KMTIRKKHNTLRVYVCPKNNMASRPVCDKGINAQTLEDKYLEGCRDFYONORIYTKI
KGAIDRKIRKQRIKHHILITOEPIEKLAGSITDAETFREQTOSLRQOPORTTSING
HQIQHTIOTIKRFTLNLIPYIETIHITKDKNLIGYFKNEPLINVAQMOSSIA"
11259. 12887
/gene="ccrB"
11259. 12887
/gene="ccrB"
/note="ORF No. 0006"
/codon_start-1
/transl_table-11
/product="cassette chromosome recombinase B"
/protein_id="BAB72109.1"
/db_xref="GI:17025980"
/translation="MOOLKTRKVGIVYRVSTMOSTEGSIDQINQIKREYCDPFHFE
VKDIYADRGISQSMNRPEIORMLKDAKRGNTDCMYIKTNRLNATSLIKIYEDLH
KONVEFSLSERMEVNTSSGKLMLOILASFSEFERNINVENTFQOTRRAQGGITYGN
LPLGDKTIPDSKHELMINQHEANIVKIFESYAKGHGYRKIANALNHKGYVTKGKPE
SISITVYILANPFYIGKIQFAKYKDMSEKRRKGLNDKPVIAEGKSPILINDLMDKVQ
MKKQVYSQKPYQHYGKTNLTGCIHCPOGAPMAASNTTNLTLDGCKRKIRYSCSNF
RNKSGKVCANSVRADVIEDYVMAKQILEIVSKDYIORVAVRQENKNGAALHDDI
AYKQOQYDEVOTKLNLIKTIEDNPDLTVIRPSIOKEYEKOLNDITNOINOLKNOONE
DKSLFDARQISKLQIHODIKHMEKSKALYLSVIDRINIRKQGNHKQKYVYLKL
NNEITKQLPNKQLDDEVHLSLFLPOTLYLTYI"
13409. 13759
/note="ORF No. 0007"
/codon_start-1
/transl_table-11
/product="hypothetical protein"
/protein_id="BAB72110.1"
/db_xref="GI:17025981"
/translation="MKYITQELKQYITMIFQISNNEAMECEALEAENILPERFIND
SPLVHLTLEYTYVNDLHELSTIYPFLMYANNOLISVGLDHFMDFLYLTDTQNI
DERHLKQGGQDHE"
13846. 14157
/note="ORF No. 0008"
/codon_start-1
/transl_table-11
/product="hypothetical protein"
/protein_id="BAB72111.1"
/db_xref="GI:17025982"
/translation="MKINRYIRGINESIPLDLOILLMHMVEKRDNOPHTDYLAHFKL
QEDENILSTHQEQPTYKLEHYHTNYENKQNALPKKYVIFREDYVDAFYVYMLLPEE
V"
14169. 14678
/note="ORF No. 0009"
/codon_start-1
/transl_table-11
/product="hypothetical protein"
/protein_id="BAB72112.1"
/db_xref="GI:17025983"

Query Match 100.0%; Score 28; DB 1; Length 26090;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAGATGATACCTTCGTT 28
|||||
Db 18254 AAATTGGGTACAGATGATACCTTCGTT 18281

Search completed: December 10, 2002, 20:16:41
Job time : 619.209 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 433.631 Seconds

(without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-21

Perfect score: 20

Sequence: 1 gtagtgatgatalattgtgcc 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrl:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	20	100.0	20	6	AX306852	AX306852 Sequence
2	20	100.0	20	6	AX306862	AX306862 Sequence
3	20	100.0	39	6	AX306869	AX306869 Sequence
4	20	100.0	1789	6	E09772	E09772 The base se
5	20	100.0	2007	6	AR089410	AR089410 Sequence
6	20	100.0	2007	6	AR093610	AR093610 Sequence
7	20	100.0	2322	6	SABP	Y00688 Staphylococ
8	20	100.0	2322	6	E03736	E03736 DNA sequenc
9	20	100.0	2454	6	SEMECAPB	X52592 S. epidermi
10	20	100.0	2455	6	SEMECAPB	E09771 The base se
11	20	100.0	2456	6	AX110445	X52593 S. aureus m
12	20	100.0	2456	6	AX110445	AX110445 Sequence
13	20	100.0	5596	1	SSK8MECA	Y13096 S. sciuri me
14	20	100.0	6368	1	SSK3MECA2	Y13095 S. sciuri me
15	20	100.0	9047	1	SSK3MECA11	Y14051 Staphylococ
16	20	100.0	21777	1	AB063173	AB063173 Staphyloc
17	20	100.0	26090	1	AB063172	AB063172 Staphyloc
18	20	100.0	39332	1	AB033763	AB033763 Staphyloc
19	20	100.0	58237	1	D86934	D86934 Staphylococ
20	20	100.0	68256	1	AB037671	AB037671 Staphyloc
21	20	100.0	290250	1	AP004822	AP004822 Staphyloc
22	20	100.0	298050	1	AP003129	AP003129 Staphyloc
23	20	100.0	349999	1	AP003358	AP003358 Staphyloc
24	18.4	92.0	72988	2	AC101581	AC101581 Mus muscu
25	17.4	87.0	1335	8	AY128359	AY128359 Arabidops
26	17.4	87.0	3000	8	AF064515	AF064515 Schizosac
27	17.4	87.0	7410	14	AF177911	AF177911 Coxsackie
28	17.4	87.0	30953	8	SPAC4D7	Z96802 S. pombe chr
29	17.4	87.0	43387	8	ATK10A8	AL191151 Arabidops
30	17.4	87.0	54982	2	AC100814	AC100814 Homo sapi
31	17.4	87.0	88947	2	AP005463	AP005463 Oryza sat
32	17.4	87.0	120427	2	AC094308	AC094308 Rattus no
33	17.4	87.0	124225	8	IG002M01	AP007269 Arabidops
34	17.4	87.0	125346	2	AP004329	AP004329 Oryza sat
35	17.4	87.0	144017	2	AF233106	AF233106 Homo sapi
36	17.4	87.0	159387	9	HS455H14	AL023280 Homo sapi
37	17.4	87.0	177519	9	AC068702	AC068702 Homo sapi
38	17.4	87.0	181907	2	AC108731	AC108731 Homo sapi
39	17.4	87.0	182391	2	AC110860	AC110860 Rattus no
40	17.4	87.0	185672	2	AC107276	AC107276 Rattus no
41	17.4	87.0	186896	9	AC019057	AC019057 Homo sapi
42	17.4	87.0	196149	8	ATCHRIV3	AL161491 Arabidops
43	17	85.0	103353	8	AC010704	AC010704 Arabidops
44	17	85.0	196319	2	AC115268	AC115268 Rattus no
45	17	85.0	237221	1	AP003599	AP003599 Nostoc sp

ALIGNMENTS

RESULT 1
AX306852
LOCUS AX306852
DEFINITION Sequence 11 from Patent EP1160333.
ACCESSION AX306852
VERSION AX306852.1 GI:17894674
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
AUTHORS Taya, T., Ishiguro, T. and Saito, J.
TITLE Oligonucleotides and method for detection of meca gene of methicillin-resistant Staphylococcus aureus
JOURNAL Patent: EP 1160333-A 11 05-DEC-2001

Pred. No. is the number of results predicted by chance to have a

FEATURES Tosoh Corporation (JP)
Source Location/Qualifiers
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide capable of binding specifically to
meca gene or RNA derived from said gene"

BASE COUNT 4 a 3 c 4 g 9 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTAGTTGAATATCTTGGC 20
|||||

Db 1 GTAGTTGAATATCTTGGC 20

RESULT 2
X306862

LOCUS AX306862 20 bp DNA Linear PAT 14-DEC-2001

DEFINITION Sequence 21 from Patent EP1160333.

ACCESSION AX306862

VERSION AX306862.1 GI:17894684

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS Taya,T., Ishiguro,T. and Saito,J.

TITLE Oligonucleotides and method for detection of meca gene of methicillin-resistant Staphylococcus aureus

JOURNAL Patent: BP 1160333-A 21 05-DEC-2001;
Tosoh Corporation (JP)

FEATURES
Source Location/Qualifiers
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 4 a 3 c 4 g 9 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTAGTTGAATATCTTGGC 20
|||||

1 GTAGTTGAATATCTTGGC 20

RESULT 3
AX306869

LOCUS AX306869 39 bp DNA Linear PAT 14-DEC-2001

DEFINITION Sequence 28 from Patent EP1160333.

ACCESSION AX306869

VERSION AX306869.1 GI:17894691

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS Taya,T., Ishiguro,T. and Saito,J.

TITLE Oligonucleotides and method for detection of meca gene of methicillin-resistant Staphylococcus aureus

JOURNAL Patent: BP 1160333-A 28 05-DEC-2001;
Tosoh Corporation (JP)

FEATURES
Source Location/Qualifiers
1..39
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Probe"

BASE COUNT 5 a 7 c 4 g 23 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTAGTTGAATATCTTGGC 20
|||||

Db 1 GTAGTTGAATATCTTGGC 20

RESULT 4
E09772/c

LOCUS E09772 1789 bp RNA Linear PAT 29-SEP-1997

DEFINITION The base sequence of modified meca DNA.

ACCESSION E09772

VERSION E09772.1 GI:22026401

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.

TITLE NOVEL 'MECA PROTEIN' CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS

JOURNAL Patent: JP 1995209294-A 2 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA
PI SUGURO KAZUYA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC C12N1:19)
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH key Location/Qualifiers
FT source 1..1789
FT 1..1608 /organism='Staphylococcus aureus' FT CDS
1..1789 /product='modified meca'.
FT Location/Qualifiers
1..1789
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

BASE COUNT 735 a 263 c 302 g 489 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1789;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTAGTTGAATATCTTGGC 20
|||||

Db 581 GTAGTTGAATATCTTGGC 562

RESULT 5
AR089410/c

LOCUS AR089410 2007 bp DNA Linear PAT 07-SEP-2000

DEFINITION Sequence 169 from patent US 5994066.

ACCESSION AR089410

VERSION AR089410.1 GI:10016167

KEYWORDS

SOURCE

ORGANISM

REFERENCE

Unknown.
Unclassified.
1 (bases 1 to 2007)

AUTHORS Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
 TITLE Species-specific and universal DNA probes and amplification primers
 to rapidly detect and identify common bacterial pathogens and
 associated antibiotic resistance genes from clinical specimens for
 routine diagnosis in microbiology laboratories
 JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..2007
 BASE COUNT 855 a 270 c 341 g 541 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACTGGAATATCTTTGCC 20
 Db 980 GTTACTGGAATATCTTTGCC 961

RESULT 6
 LOCUS AR093610 2007 bp DNA linear PAT 08-SEP-2000
 DEFINITION Sequence 169 from patent US 6001564.
 ACCESSION AR093610
 VERSION AR093610.1 GI:10020359
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 2007)
 AUTHORS Bergeron,M.G., Ouellette,M. and Roy,P.H.
 TITLE Species specific and universal DNA probes and amplification primers
 to rapidly detect and identify common bacterial pathogens and
 associated antibiotic resistance genes from clinical specimens for
 routine diagnosis in microbiology laboratories
 JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
 FEATURES Location/Qualifiers
 source 1..2007
 BASE COUNT 855 a 270 c 341 g 541 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GTTACTGGAATATCTTTGCC 20
 Db 980 GTTACTGGAATATCTTTGCC 961

RESULT 7
 SABP/c 2322 bp DNA linear BCT 12-SEP-1993
 LOCUS Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible
 penicillin-binding protein.
 ACCESSION Y00688
 VERSION Y00688.1 GI:46628
 KEYWORDS penicillin-binding protein.
 SOURCE Staphylococcus aureus.
 ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
 REFERENCE 1 (bases 1 to 2322)
 AUTHORS Song,M.D., Wachi,M., Doi,M., Ishino,F. and Matsushashi,M.
 TITLE Evolution of an inducible penicillin-target protein in
 methicillin-resistant Staphylococcus aureus by gene fusion
 JOURNAL FEBS Lett. 221 (1), 167-171 (1987)
 MEDLINE 87304805
 PUBMED 3305073
 REFERENCE 2 (bases 1 to 2322)
 AUTHORS Kyffel,C., Meschn,W., Birch-Machin,I., Reynolds,P.E.,

TITLE Barberis-Maino,L., Kayser,F.H. and Berger-Bachhi,B.
 Sequence comparison of mecA genes isolated from
 methicillin-resistant Staphylococcus aureus and Staphylococcus
 epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT Data kindly reviewed (13.1.88) by Matsushashi.
 FEATURES Location/Qualifiers
 source 1..2322
 /organism="Staphylococcus aureus"
 /db_xref="taxon:1280"
 1..2013
 /note="penicillin-binding protein (PA 1-670)"
 /codon_start=1
 /protein_id="CA68684.1"
 /db_xref="GI:46629"
 /db_xref="SWISS-PROT:P07944"
 /translation="MKKIKIVPLILIVVVGFCIFYASKDKEINNIDAIEDKNFKQ
 VYKDSYISKSDNGEVEETERPRIKIVNSLGVKDINIDRRIRKVSNNKRVDAQYKIK
 TVNGNIDRVVOENFEKEDGMKIDMDHSYIIPGMQDOSIIIEENLSEKSGIIDRVN
 ELANTGTHMRIGIVPKNVSKDKYAKELISEDIINNKKMIRIGKMIIPSEHETVYK
 KMDEVLSDFAKKPEHLTNETESANVPLGKATSHLGYVGPINSEFLKOKEYGYKQDA
 VIGKGLLEKLYDKLOHEDCYRYVTVRVDDNSWTIAHTLIIEKKKKRQDIQLTIDAKV
 OKSIYNNKNDYGSCTAIHPOTCELLAIYSTSYDVPYPTGASNPEVNLTEDEKREP
 LNKFEITTSPESTOKILTPAMIGLNKTLDDKTSYIDKGMQKDSWKGYNVTRREV
 VNGNIDLKQAISSDNIFFARVALDELSKRFEGKMGILGVEDISDYPFYNAQISNS
 NLDNEILLADSGGGEILINPVQILSIYSALENNGININAPILLKDTKRWVKNNIIS
 KENINLINDGMQOVYNNKTHKEDIYRSYANLJGKSCFAELKKMGCEGRQIGWVLSYDK
 DNPMMMAINVDVQDKMGASVNAKISCAVYVDLDELNGKKKKDIDPE"

BASE COUNT 940 a 324 c 389 g 669 t
 ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACTGGAATATCTTTGCC 20
 Db 986 GTTACTGGAATATCTTTGCC 967

RESULT 8
 LOCUS E03736 2322 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA sequence of PBP2' gene for determination of methicillin
 resistance.
 ACCESSION E03736
 VERSION E03736.1 GI:2171951
 KEYWORDS JP 1992169200-A/9.
 SOURCE unidentified.
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 2322)
 AUTHORS Watanabe,Y., Nakamura,E., Teraoka,H., Wada,K., Minamide,W. and
 Murakami,K.
 TITLE DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
 JOURNAL SHIONOGI & CO LTD
 OS (methicillin resistant)staphylococcus aureus
 PN JP 1992169200-A/9
 PD 17-JUN-1992
 PF 31-OCT-1990 JP 1990296708
 PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI,
 MI MINAMIDE MAKIO, MURAKAMI KAZUHISA
 PC C1201/68, C12M15/11;
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH key Location/Qualifiers

```

FT      misc.feature 1..2322
FT      /note="PBP2' gene for determination of FT
FT      methicillin
FT      resistance'
FEATURES
source      1..2322
             /organism="unidentified"
             /db_xref="taxon:32644"
BASE COUNT  939 a 324 c 390 g 669 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 2322;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTTACTGCAATATCTTTGCC 20
Db      986 GTTACTGCAATATCTTTGCC 967

350UT 9
3MECAPB/C
LOCUS      SEMECAPB 2454 bp DNA linear BCT 12-SEP-1993
DEFINITION S. epidermidis meca gene for PBP2' (penicillin binding protein 2').
ACCESSION  X52592
VERSION     X52592.1 GI:46993
KEYWORDS   meca gene; methicillin resistance; penicillin-binding protein;
            penicillin-binding protein 2'.
SOURCE      Staphylococcus epidermidis
            Bacillus; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1 (bases 1 to 2448)
AUTHORS     Ryffel,C.
TITLE        Direct Submission
JOURNAL     Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
REFERENCE   2 (bases 1 to 2454)
AUTHORS     Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
TITLE        Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
            Barberis-Maino,L., Kayser,F.H. and Berger-Baechli,B.
            Sequence comparison of meca genes from methicillin-resistant
            Staphylococcus aureus and Staphylococcus epidermidis
            Gene (1990) In press
            3 (bases 1 to 2454)
            Ryffel,C.
            Direct Submission
            Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
            Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
            4 (bases 1 to 2454)
            Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
            Barberis-Maino,L., Kayser,F.H. and Berger-Baechli,B.
            Sequence comparison of meca genes isolated from
            methicillin-resistant Staphylococcus aureus and Staphylococcus
            epidermidis
            Gene 94 (1), 137-138 (1990)
JOURNAL     MEDLINE 91033056
PUBMED      2227446
COMMENT     See also <X52593-4> and <Y00688>.
            Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source      1..2454
             /organism="Staphylococcus epidermidis"
             /strain="WT55"
             /db_xref="taxon:1282"
             /clone="WT80/WT79"
             80..85
             /note="-35 region"
             101..105
             /note="-10 region"
             130..134
             /note="ribosome binding site"
             141..2159
             /note="primary transcript"
             141..2147
CDS

```

```

/note="PBP2' (AA 1 - 668)"
/codon_start=1
/transl_table=11
/protein_id="CAA36828.1"
/db_xref="GI:46994"
/db_xref="SPTREMBL:054113"
/translation="MKKIKIYIPILIIYVNGEGYFVASKKEINNTIDAIEDKFKO
YKDSYISKDNGCEVENTERPIKITYNSLGVKDINIDIRKIKVSKKKRYDAOTKIK
TNYGNIDRNVQFNFVEKEDGMKLMDSVITIPGQKDDSIHLENLKSERKILDRNNV
ELANTGATVAEIGIYPRKNVSKKDYKAIKELISEDYIKQMDQMVVODPTFVPLKTVK
KMDXYLSDPAKKFLLTNTETESRNPGLKATSHLIGVGPINSEIKOKERYKGYDKA
VIGKGLKELYDKRLOHEDGYRVTIVDNSNTIAHTLEKKKDGKDIOLIDAKVOK
SYNNKNDYDGSRTAIHPQTELLALVSTPGVDYPFMYGSKSNEEYNTLTDDKPEPL
MKFOITTPSGSTOKILTMIGLNLNKTITLDDKTSYKIDGKMGKDKSMGCTNTRREYVH
GNIDKQATIESDNIFFARVALELGSKFEGMKRIGVGDIPSDYPPYNAOISKNL
DNEITLADSGYGQCEIILINPOVILISYALENNCNIAPPHILLKPTKKNVWKNIISKE
NINILTDQMOOVNKTAKEDIYRSYANLIGKSGTAEILMKMGCTFGROIQWPISYDKDN
PNMMMAINVKRVQDQGMASYNAKISGVYDELYENGKRYDIDE"
441..448
/note="altaaac was ac in [1]"
/citation=[1]
old_sequence
641..643
/note="agc was ac in [1]"
/citation=[1]
old_sequence
652..653
/note="ta was tta in [1]"
/citation=[1]
731..733
/note="caa was ca in [1]"
/citation=[1]
780..781
/note="ct was ctt in [1]"
/citation=[1]
BASE COUNT  997 a 345 c 398 g 714 t
ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 2454;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTTACTGCAATATCTTTGCC 20
Db      1120 GTTACTGCAATATCTTTGCC 1101

RESULT 10
LOCUS      E09771/c 2455 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of meca DNA.
ACCESSION  E09771
VERSION     E09771.1 GI:22026400
KEYWORDS   staphylococcus aureus.
SOURCE      Staphylococcus aureus
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1 (bases 1 to 2455)
AUTHORS     Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
TITLE        NOVEL 'MECA PROTEIN', CODING DNA THEREFOR, AND DETECTION METHOD FOR
            METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
            Patent: JP 1995209294-A 1 11-AUG-1995;
            KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
            OS Staphylococcus aureus
            PN JP 1995209294-A/1
            PD 11-AUG-1995
            PF 10-JAN-1994 JP 1994012226
            PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
            MASAHISA,
            SUUGURO KAZUYA
            PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21,PC
            C12R1:19)
            PC (C12P21/02,C12N1:19);
            CC strandedness: Double;
            CC topology: Linear;

```

FEATURES

Key	Location/Qualifiers
FT	1..2455
FT	/organism="Staphylococcus aureus" FT
FT	134..2146
FT	/product="meca protein".
FEATURES	1..2455
source	/organism="Staphylococcus aureus"
source	/db_xref="taxon:1280"
HASH COUNT	997 a 344 c 401 g 713 t
ORIGIN	

Query Match 100.0%; Score 20; DB 6; Length 2455;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTGAATATCTTCC 20
|||||

b 1119 GTTAGTGAATATCTTCC 1100

RESULT 11
SAMECAPB/c 2456 bp DNA linear BCT 12-SEP-1993
LOCUS S. aureus meca gene for PBP2' (penicillin binding protein 2').
DEFINITION X52593.1 GI:46610
ACCESSION X52593.1
VERSION X52593.1
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2.
SOURCE Staphylococcus aureus
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2456)
AUTHORS Ryffel, C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zurich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zurich, Switzerland
REFERENCE 2 (bases 1 to 2456)
AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
Barberis-Maino, L., Kayser, F. H. and Berger-Bachli, B.
TITLE Sequence comparison of meca genes isolated from
methicillin-resistant staphylococcus aureus and staphylococcus
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52592>, <X52594> and <Y00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.

FEATURES

source	Location/Qualifiers
1..2456	
/organism="Staphylococcus aureus"	
/strain="NCTC8325, isolate-BB270"	
/db_xref="taxon:1280"	
/clone_lib="EMBL-3"	
80..85	
/note="35 region"	
101..105	
/note="10 region"	
130..134	
/note="ribosome binding site"	
141..2153	
/note="primary transcript"	
141..2147	
/note="PBP2' (AA 1-668)"	
/codon_start=1	
/transl_table=11	
/protein_id="CAA36829.1"	
/db_xref="GI:46611"	
/db_xref="SPTREMBL:053707"	
/translation="MKKIKIVPLILIVVVGPGITYYASKDKRINNTIDAIEQKPKO VKDSSYISKSDNGEYEMTERPKITNSLGVKIDINIDRKIKVSKKKKVDQVYKIK TNGNIDRNQENFEKEDGMKLDWDHSVILIPGKQDSIHENLSEKILIDRNRY	

ELANTGTHMLGTYPRKNSKKDYAKAKELSISFDYINNNKIKIGYKMFSPFKTYK
KMEYTLSEFAKFLHTNETESRNPLEKATSHLGVGPIINSELKQKKGKDDA
VTCRGLGKLYDKKLOHEDGYRVT1VDDNSNT1AHTL1EKKKKGND1Q1T1DAKKVOK
SIYNNMNDYSGTALHPOTCELLALSTPSYDYVPRYGMSENEYKNL1EDKKEPLI
NKROITTSPCSTOK11PAMIGLNKNTLDDKTSYK1DCKGMOKDSMGCVNTRYEVAN
GNIDLKQATSSSDNIFEFARVALESGKKFEKGMKLGVDIPSDYFEYNAOISNNKL
DNEILLADSSGSGOELLINPYOITISYSALENKNNTANPILKDTKRYKKN1ISKE
NINLNDGMQDVNKTREDEYRSYANLIGSGTAEKMKOGESGROIGMFTSYDKDN
PNMMMAINVDYDOKMASYNNAK1SGKVVDELYENKRYKVIDE"

BASE COUNT 1001 a 344 c 396 g 715 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 2456;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTA:TTGAAATATCTTCC 20
|||||

Db 1120 GTTAGTGAATATCTTCC 1101

RESULT 12
AX110445/c 2456 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 1178 from Patent WO0123604.
DEFINITION AX110445
ACCESSION AX110445
VERSION AX110445.1 GI:13926737
KEYWORDS
SOURCE
ORGANISM Staphylococcus aureus subsp. aureus NCTC 8325.
Staphylococcus aureus subsp. aureus NCTC 8325.
REFERENCE 1 (bases 1 to 2456)
AUTHORS Bergeron, M. G., Boissinot, M., Huilet, A., m Nard, C., Ouellette, M.,
Picard, F. J. and Roy, P. H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1178 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES

source	Location/Qualifiers
1..2456	
/organism="Staphylococcus aureus subsp. aureus NCTC 8325"	
/db_xref="taxon:93061"	

BASE COUNT 1001 a 344 c 396 g 715 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2456;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTGAATATCTTCC 20
|||||

Db 1120 GTTAGTGAATATCTTCC 1101

RESULT 13
SSK8MECA 5596 bp DNA linear BCT 16-JAN-1998
LOCUS S. sciuri meca gene, strain K8 (ATCC700663).
DEFINITION Y13096
ACCESSION Y13096.1 GI:2791919
VERSION Y13096.1
KEYWORDS meca gene; mecI gene; mecrI gene; NTORF101; NTORF78; ORF142.
SOURCE Staphylococcus sciuri.
ORGANISM Staphylococcus sciuri.
REFERENCE 1 (bases 1 to 5596)
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic organization of the meca region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 98101461
PUBMED 9440511
REFERENCE 2 (bases 1 to 5596)
AUTHORS Wu, S.

TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences X53818, X54660, L14020, X52593, Y09223.
FEATURES
source
1..5596
/organism="Staphylococcus sciuri"
/strain="K8 (ATCC70063)"
/sub_species="rodentius"
/db_xref="taxon:1296"
1..236
/gene="NTORF78"
<1..236
/gene="NTORF78"
/codon_start=3
/transl_table=11
/protein_id="CAA73550.1"
/db_xref="GI:2791920"
/db_xref="SPTREMBL:O54284"
/translation="AFKLKPCDCHTSKYLNLLEODHRIKVKRTYOSINTAKNTLK
GTECIYALKKRBSLOJYGFSPCHEISIMLAS"
complement(485..856)
gene
/gene="mecI"
complement(485..856)
CDS
/gene="mecI"
complement(485..856)
/codon_start=1
/transl_table=11
/product="MecI protein"
/protein_id="CAA73545.1"
/db_xref="GI:2791921"
/db_xref="SPTREMBL:O54285"
/translation="MDNKTYEISSAEWEYMNITMKKVASANYMIELOMQDKWSPT
ITLTILYKKGFIIDRKDKNLFQYYSLEESDIKYKTSKNFKNKYKGGFNSLVNF
VKEKLDSODEIEELNLNKK"
complement(101n(856..2613,2620..2626,2638..2643))
gene
/gene="mecr1"
complement(856..2613)
CDS
/gene="mecr1"
complement(856..2613)
/codon_start=1
/transl_table=11
/product="Mecr1 protein"
/protein_id="CAA73546.1"
/db_xref="GI:2791922"
/translation="MUSSLIMSLISSLITICVIFLVKMLYKTYONIMSHKILWLLV
VSTLPLIEYKISNFTSKDMKNRVSPTSSVSHMLDGOSSVTKDLAINVQFET
SNITWILLIWEFGSLCLEYMIKAFRQIDVETKSSLESSYINERLAKVQSKMQPKK
HTISYSSNIDPMWFGVKSQIVLPTVVETMNDKEIEYIILHELSHKSHDLIFNQ
LYVFKMIFWFPALYISKTMNDCEKVCDRNLKILNRHEIRYGESILKCSILKS
OHINVAOYLIGFNSNIKERVYIALYDSMPKPNRKRIVAYICISILLOAPLIS
AHVODKYETNYSYKKNLOLAPYFKGDSQSPVLYNDRQAVSIYNEPESKORYSPST
KYTIYLAIAFDONLISLNTIEQMDKHQIPREKNODONLNSMKYSVMYIENLNKH
LNODEKSTLDLIEGENEISGENENWNSSSLKISALIEVNLKNNKOHNMFDNKAI
EKVENSMTLKQDKTYKRYGKTGTGIVNKRKANGWVGVEYETKDNYYFATHLKGEDNA
NGEKAQOISERTILKEMELI"
complement(865..869)
gene
/gene="mecI"
complement(865..869)
RBS
/gene="mecI"
complement(865..869)
RBS
/gene="mecr1"
complement(2620..2626)
-10_signal
/gene="mecr1"
complement(2638..2643)
gene
/gene="mecr1"
2652..2657
/gene="meccA"
2652..2657
/gene="meccA"
-35_signal
/gene="meccA"
complement(2663..2668)
-35_signal
/gene="mecr1"
complement(2668)
gene
/gene="mecr1"
2676..4719
/gene="meccA"
2676..2681
-10_signal

RBS
/gene="meccA"
2702..2707
/gene="meccA"
2713..4719
CDS
/gene="meccA"
/codon_start=1
/transl_table=11
/product="MeccA protein"
/protein_id="CAA73547.1"
/db_xref="GI:2791923"
/db_xref="SPTREMBL:O54286"
/translation="MKKIKIVPLILIVVVGCGIYFVASKDEIINNITDAIEDKNFKO
VYKSSYISKSDNGEYEMTERPIKLIYNSIGVDIINLODKIKKSKNKRVAOYKIK
TNVGNIDRWQVDFNPKEDMKMLDMDHSYIIPGMOKDOSIHEINIKSERCKLIDNNY
ELANTGATEIGIVPRKNVSKDYKAIARELSIEDYIKQMDQNNVQDDTPYPLTKV
KMEYLSDFARKFHLTNTETESRNPLEKATSHLIGVGPINSEELKOEKGYKDDA
VIGKRGLEKLYDKKLQHEDEYRVTIVDQNSNTIAHTLEKKRKDKDIQITDAKVOK
SIYNNMKNDYGSCTA1HPQTELLALVSTSYDYVPFMGMSNEYNNLTEDKKEPL
NKFOITTSFGSTOKILITAMI GLNNKTLDKDTSYKIDGKQMKOSMGVNVTRYEVN
GNIDLKQATESSDNIIPFARVALLGSKFKKMGKIKIGVEDIIPSDYPPYNAQISKNL
DMEILLADSGYCGEGLINPVOLISYSLKENGNNINAPHILLKDTKKNVYKKNITISKE
NINLITDGMQVYVNTKTHKEDIYRSTANLIGKSGTALMKKQSEGTGROIGWFIYDKDN
PMMMAINVKYDVQDKMASYNAKISGKVIDELVGNKKYDIDE"
complement(4765..5266)
gene
/gene="ORF142"
complement(4765..5193)
CDS
/gene="ORF142"
complement(4765..5193)
/codon_start=1
/transl_table=11
/protein_id="CAA73548.1"
/db_xref="GI:2791924"
/db_xref="SPTREMBL:O54520"
/translation="MKYDEIYGETFEFKRSLHITPEEIIQFATFEDPOYMHIDKEAE
GSRFKGIASGMHTLISFKLIVEEGKGYGEVAVGTOMNNVFIRPYVPGNLYIAE
ITNKSIRKENELVYVSLSTVNEDEIYFKGCVTALINNS"
complement(5200..5205)
RBS
/gene="ORF142"
complement(5238..5243)
-10_signal
/gene="ORF142"
complement(5261..5266)
-35_signal
/gene="ORF142"
complement(5290..5596)
gene
/gene="NTORF101"
complement(5290..>5596)
CDS
/gene="NTORF101"
/codon_start=2
/transl_table=11
/protein_id="CAA73549.1"
/db_xref="SPTREMBL:O54616"
/translation="SFNVVLVLAELIIMPQYRAVIFHTTSFREDWRTLLDYCNKIV
NTEDAKLTAKKAKWKEAGVYELNVTNNKPARANOLANMGVDGIFTDNADKNVHLSQ"
BASE COUNT 1991 a 856 c 821 g 1928 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 5596;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 3692 GTTAGTTGAATATCTTTGCC 3673
RESULT 14
SSK3MECA2/C 6368 bp DNA linear BCT 16-JAN-1998
LOCUS SSK3MECA2
DEFINITION S.sciuri meca2 gene, strain K3 (HM2).
ACCESSION Y13095
VERSION Y13095.1 GI:2791912
KEYWORDS CTORF261 gene; meca2 gene; mecI gene; mecr1 gene; NTORF101; ORF142.
SOURCE Staphylococcus sciuri.
ORGANISM Staphylococcus sciuri

REFERENCE 1 Bacteria: Firmicutes: Bacillales: Staphylococcus.
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic organization of the mecA region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 98101461
PUBMED 9440511
REFERENCE 2 (bases 1 to 6368)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences U4020, X52593, Y09223.
FEATURES
source location/Qualifiers
1..6368
/organism="Staphylococcus sciuri"
/strain="K3 (MM2)"
/sub_species="rodentius"
/db_xref="taxon:1296"
/complement(1..883)
/gene="CTORF261"
/complement(<1..784)
/gene="CTORF261"
/codon_start=1
/transl_table=11
/protein_id="CAA73539.1"
/db_xref="GI:2791913"
/db_xref="SPTREMBL:O54280"
/translation="MKNLINDNEKRYIREYNNHNISKIQISKNLELNKATISSII
NKLKYSIVNEVEGDSYKSGGRPIILKVNHLVGFISLIDITVSSVEKMYVPGNV
IKHESYDLPDEKVSILSITKKHIDIQERLADYNGLGVSVISHCVDNEQAVLP
HETEGISIAKKIKETITNPVYVNEANLSALYERNNILSYNNILALSIHGIGAGL
IINNOLYRGANEGEIGKTLVSKVSDNVEIFHKIEDIFSQA"
complement(791..797)
RBS
/gene="CTORF261"
complement(855..860)
/gene="CTORF261"
complement(878..883)
/gene="CTORF261"
complement(1257..1628)
/gene="mecI"
complement(1257..1628)
CDS
/gene="mecI"
/codon_start=1
/transl_table=11
/product="MecI protein"
/protein_id="CAA73540.1"
/db_xref="GI:2791914"
/db_xref="SPTREMBL:O54281"
/translation="NDNKTYEISSAEVEYNNIIMKKYASANNIIEITOMQDMSPT
IRTLITRLYKGFIDRRKDNKIFQYISLVEESDITKTSKNTINNYKGFNSLVNF
VEREDLSODEIEELRNILNK"
complement(1628..3385,3392..3398,3410..3415))
gene
/gene="mecr1"
complement(1628..3385)
/gene="mecr1"
/codon_start=1
/transl_table=11
/product="Mecr1 protein"
/protein_id="CAA73541.1"
/db_xref="GI:2791915"
/db_xref="SPTREMBL:O54282"
/translation="MSSRFIMCITSSLTTCVITFLVRLYIKYTONIMSHKIMLILY
VSTLPLIPFKYISNFTPSKDMNRNVSSTTSVSHMDGOOSVTKDLATVNOEET
SNITVMIILWFGSLCLFYIKAFRODIVKSSSLESSYLNERLKYCQSMQYQET
HITISYSSNIDPMVFGLVKSOIVLPVVEETMDKELEYIILHELSHVSKSHDLFPQ
LYVFKMILFMFNPALYISKTMNDCEKVDNRNVLKILNRHEIRGESILCSILKS
OHINNAVOYLGFNSNIKERVYIALDSMPKPNRKRIVAYICSSILDSILS
AHVODKDYNSYKSLNOLAPYFKGPDGSEFVLVNRQGVASITNPESEKQSPNST
KYIYIALAFDNLSTLNITEQMDKHQYPERENNODNLNSMKYSVMYIENLNKH
LRQDEVKSTLIDLETGNEIRISGENEYNNWSSSLKISALIDOVNLKDKKONHFDNKAI
EKVNSMTLKQKDIKYVKGKTGTGLVNHKANGWFGVYETKDNITYYFATHLKGDNA

NGEKAQOISERLKEPMLI"
complement(1636..1640)
/gene="mecI"
complement(1636..1640)
/gene="mecI"
complement(3392..3398)
/gene="mecr1"
complement(3410..3415)
/gene="mecr1"
3429..3429
/gene="mecA2"
3424..3429
/gene="mecA2"
complement(3433..3438)
/gene="mecr1"
complement(3433..3438)
/gene="mecr1"
3448..3491
/gene="mecA2"
3448..3453
/gene="mecA2"
3474..3479
/gene="mecA2"
3485..3491
/gene="mecA2"
/codon_start=1
/transl_table=11
/product="MecA2 protein"
/protein_id="CAA73542.1"
/db_xref="GI:2791916"
/db_xref="SPTREMBL:O54283"
/translation="MKKIKIVPLILIVVVGHGIVYVASKQKEINNTIDAIQDKNFKQ
VYKDSIYSKSDNGEVEEMTERPIKITSNIGYKIDIMIDQRIKYSKNNKRVDAQYKIK
TNVGNIDRNVOFNPEFKEDGMKLDMDHSYIIPGQKQDSIHENLKSERKLLDNRNV
ELANTGTAIEIGIVPRKNVSKKRYKAIKELSTSEDTYKQMDQNMVDDTEFVPLTKV
KMDVLSYDPKAKFPLFTNPEESNYPILKATSHLIGYCPILNSHELKQEVGYCTDA
VIGKKGLEKTRKLLQHEDEGTVTTIVDSSNTIAHTLIRKKRDKDQIQLTIDAKYQK
SLYNNMKNDSYGSTAIPHQTGELALVSTPSYDVLPYMGMSNEEYNALTEKKREPL
NKFQITSPGSTOKILITAMIGLNKTLDDKTSYKIDGKGMQDKSMGQGNVRYEVN
GNIDKQALIESSDNIEFFARVALSLGSKREKQKMLGVEDIPSDYPPYNAQISKNL
DNEILLADSGYGOGEILINPVOILISYSALENNGNINPILLDKTRNNKKNYISKE
NINLITDGMQGVNKTAKEDUIRSYANLIGKSCPAELMKKQGETGTRPIQWPISTYQDN
PILMAINVKDVPDKQMASYNKISGKYIDELYENGKKYIDIE"
complement(3537..6038)
/gene="ORF142"
complement(5337..5965)
/gene="ORF142"
/codon_start=1
/transl_table=11
/protein_id="CAA73543.1"
/db_xref="GI:2791917"
/db_xref="SPTREMBL:O54520"
/translation="MKYDPEIVGETGFKRSLNITTEEIIIOFATTEDPQYMIIDKEKAE
OSRFKGIILASGMHTTISIPIKLVVEEGKGEVEVACTOMNNVFIKPYVGNILYVIAE
ITNKKSIGIKENGLVITSLSYENNEEIVKGEVVALINNS"
complement(5972..5977)
RBS
/gene="ORF142"
complement(6010..6015)
/gene="ORF142"
complement(6033..6038)
/gene="ORF142"
complement(6062..6368)
/gene="NTORF101"
complement(6062..6368)
/gene="NTORF101"
/codon_start=2
/transl_table=11
/protein_id="CAA73544.1"
/db_xref="GI:2791918"
/db_xref="SPTREMBL:O54616"
/translation="SFNVYVLAIEIPIQYIRAVIEFHTTSREDWRLLDYCNKIV
NTEDAKLTAKKMYKKEGELYELVTVNKPANANQLANMGVYDGIPTDNADKKVHLISO"

BASE COUNT 2230 a 998 c 884 g 2256 t

```
ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 6368;
Best local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTAGTGAATATCTTCC 20
        |||
Db      4464 GTTACTGCAATATCTTCC 4445

RESULT 15
SAMECAR11/c      9047 bp      DNA      linear      BCT 16-JAN-1998
LOCUS      Staphylococcus aureus meca, mecr1, mecl genes and ORF168, ORF142,
DEFINITION      ORF44, ORF145 and ORF224.
VERSION      Y14051.1 GI:2791983
KEYWORDS      meca gene; mecl gene; mecr1 gene; ORF142; ORF145; ORF224; ORF44;
              PBP2A; repressor protein; transposase.
JURCE      Staphylococcus aureus.
ORGANISM      Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE      1 (bases 1 to 9047)
AUTHORS      Wu, S..
JOURNAL      Direct Submission
TITLE      Submitted (27-JUN-1997) S. Wu, Laboratory of Microbiology, The
            Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
            2 (bases 1 to 9047)
            genetic organization of the meca region in methicillin-susceptible
            and methicillin-resistant strains of Staphylococcus sciuri
            J. Bacteriol. 180 (2), 236-242 (1998)
JOURNAL      MDLINE
PUBMED      98101461
FEATURES
source      Location/Qualifiers
            1..9047
            /organism="Staphylococcus aureus"
            /strain="BMS-1"
            /db_xref="taxon:1280"
            /note="ORF168"
            /codon_start=1
            /transl_table=11
            /product="putative repressor"
            /protein_id="CAA74373.1"
            /db_xref="GI:2791984"
            /translation="MYNYFDGNVYIKHESYDLPDEKYSITLIIKKIHIDIOEKIDTYNG
            LGVSVSHGVNDEQHVYILPHEHTGSIKAKIKITVPPVVEANLSAITYEN
            PNINISYNNIALSIRKIGIAGLIINNQLKRCANGCEIGKTLVSKVSDNVNIFPKI
            EDLPSQEA"
            complement(1244..1615)
            /gene="mecI"
            /complement(1244..1615)
            /gene="mecI"
            /codon_start=1
            /transl_table=11
            /product="MecI protein"
            /protein_id="CAA74374.1"
            /db_xref="GI:2791985"
            /translation="MDNKTYEISSAEWEVNNIIMKKYASANNIIIEIOMQIDMSPT
            IRTLRLRYLKKGFIDRRKDKKIFQYSLVESDILKKTSKNFINKYKGGFNSLVNLF
            VEKEDLSODIELELNILNK"
            complement(1615..3372)
            /gene="mecR1"
            /complement(1615..3372)
            /gene="mecR1"
            /codon_start=1
            /transl_table=11
            /product="MecR1 protein"
            /protein_id="CAA74375.1"
            /db_xref="GI:2791991"

gene
CDS
            /db_xref="GI:2791986"
            /translation="MLSSFLMLSTISLLTICVILFVRLMYIKYTONIKSHIWLVLV
            VSTLIPILPTKISNFPKDMKMRNSDITSSVSHLIDQSSVTKDLINVOEFT
            SNTYMLLILWFGSLICLFYMIKAPRIDIVIKSSLESSYLNEKIKVCSKQNPYK
            HITISYSDINPNVGLVKSQILPVPVVEVNDKILVYILHLSHVSHDILNQ
            LYVFKMIENPNVGLVKSQILPVPVVEVNDKILVYILHLSHVSHDILNQ
            OHINNVAAQYLLGFSNIRKERVYIALYDSMPKRNKRIVAYVCSISLLQAPLS
            AHVQDQKYEFTNVSVKLNOLAPYFKGDSGFVLVNERQAVSYINDESKQRYSPNST
            KYLYLMAFDONLILNHTQODMKHQVPRKMNODONINSSMKYSVNNTYINLKH
            LRQDEKASYLDLIEYGNELSGENLWNSSILSAIYQVNLKNNKHMMHMDNNA
            EKVNSMTYLRQKQDTYKRVCKTGTGVNKKPANCMPVGVYETKNTYYPATVLRQENNA
            NGEKAOQISERILKEMELI"
            3472..5478
            /gene="meca"
            3472..5478
            /gene="meca"
            /codon_start=1
            /transl_table=11
            /product="PBP2A"
            /protein_id="CAA74376.1"
            /db_xref="GI:2791987"
            /db_xref="SPTREMBL:053707"
            /translation="MKKIKIVPLILIVVVGFCIYYPASKDKKINNTIDAIDKKNKQ
            VYDSSYISKSDNGEVEEMTERPIKINSLGVKQINIDRRIKRVSNKKRVDAQYKIK
            TNYGNDIRNVQENFVEKEDGMKLDMDHSVILPMQDQDSIHINKLSERKQIDRRNVY
            ELANTGTHMRGLGVPRKVSKKDYKALAKELISIEDYINNMKIKIGYKMLPSHFETVK
            KMDVEYLSDFAKKPHLTTPESNNVPLEKTSHLGVGQINSEELKQKPYKGYKQDA
            VIKKGLKELVDKRLQHDGVRVTVDDNSNTLAHTLIEKKKKQKQDLOLTIDAKQK
            SIYNNKNDYSGCTAJHPQGEILAYSTPSYVYPPMYSKSEYKDKLTEDKREPLL
            NKQITTSPEGSTOKILTAMTGLNKKITLDDKTSYKIDGKQKQKSMGQVNTYEVN
            GNLIDQALDESSDNIFEFA"ALELGSKKFEKGGKKLGVGEDIPSDYFVNAQISNKL
            DNELIADSGYGGQELILIVQILSYSALENNGNINAPILLDQTNKVKKKNIISKE
            NINLNDGQQVNVNTHKEDIYRSYALJCKSGTAEIKMGCSGQJGWFISYDQDN
            PNMMMAINVKDQDGMASYNAKISGVYDELEVNGKKRYDIDE"
            complement(5524..5952)
            /note="ORF142"
            /codon_start=1
            /transl_table=11
            /product="hypothetical protein"
            /protein_id="CAA74377.1"
            /db_xref="GI:2791988"
            /db_xref="SPTREMBL:054520"
            /translation="MKYDPRIVGTEETKTSLSHTEETIIQFATTPDPOYHIDKEKAE
            QSRPKGIASGHTLISFKLWBEKGYGGEVYAGTOMNNAFKIKFYVQNTLYIAE
            ITNKKSIKKEGVLVSLSTYNNENELVFGVYALINNS"
            complement(6049..6183)
            /note="ORF44"
            /codon_start=1
            /transl_table=11
            /product="hypothetical protein"
            /protein_id="CAA74378.1"
            /db_xref="GI:2791989"
            /db_xref="SPTREMBL:054083"
            /translation="WVEAGYELNVTVNKPARANQLANMGVYDGIPTDNADKKVHLSQ
            "
            complement(6354..6791)
            /note="ORF145"
            /codon_start=1
            /transl_table=11
            /product="hypothetical protein"
            /protein_id="CAA74379.1"
            /db_xref="GI:2791990"
            /db_xref="SPTREMBL:099387"
            /translation="MLTVYGRGLPSKAPENITASFKAASVYECIMWLELDVAITKDE
            QLIITHDDYLERKTNMSEITTELVDYELIDASAGSWFGKFPDEHLPTPDVYKIANE
            YNNLNVLELKGITGPNGLASKSMVQVEQLTNLQNOBELI"
            8096..8770
            /note="ORF224"
            /codon_start=1
            /transl_table=11
            /product="putative transposase"
            /protein_id="CAA74380.1"
            /db_xref="GI:2791991"
```

/translation="MNYFHYKOFNKDVITVAVGYLRYTLSTYRDLSPELLREGCNVVH
STVYRVQETAPILYOLWKKKKKKAYKKRIRIDETTYIKIKGKMSYLYRAIDAECHTLDI
WLRKORDNHSAYAFIKRLIKQFGKPOKVTIDQAPSTKVAMAKVIAFKLKPDCCHTSK
YLMNLIEODHRHAKVRKTRYQISINTAKNTLKGIECIYALYKKNRRSLQIYGFSPCHEI
SIMLAS"

BASE COUNT 3099 a 1469 c 1257 g 3222 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 9047;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTAGTTGAATATCTTGCC 20

|||||

Db 4451 GTTAGTTGAATATCTTGCC 4432

Search completed: December 10, 2002, 20:16:52
Job time : 436.756 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 ; Search time 136.911 Seconds
(without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579a-20

Perfect score: 21
Sequence: 1 ttctcttctctataatg 21

Scoring table: IDENTITY_MUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq.101002:*
1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	21	24	ABK85910	Methicillin resist
2	21	100.0	21	24	ABK85920	Methicillin resist
3	21	100.0	36	20	AAK15488	Probe meca938-36 f
4	21	100.0	36	20	AAK15489	Probe meca938-36 f
5	21	100.0	39	24	ABK85927	Methicillin resist
6	21	100.0	59	20	AAK05905	Oligonucleotide pro
7	21	100.0	59	20	AAK15477	Probe meca932-59r
8	21	100.0	89	20	AAK05906	Oligonucleotide pro
9	21	100.0	89	20	AAK15478	Probe meca945-89

C 10	21	100.0	108	20	AAK15487	Probe meca913-1020
C 11	21	100.0	1789	16	AAK04536	Staphylococcus aur
C 12	21	100.0	2007	13	AAK028599	Encodes penicillin
C 13	21	100.0	2007	17	AAK288568	Bacterial antibiotic
C 14	21	100.0	2007	19	AAK68337	Antibiotic binding
C 15	21	100.0	2007	22	ABK76993	Antibiotic resista
C 16	21	100.0	2028	24	ABN92247	Staphylococcus epi
C 17	21	100.0	2110	14	AAQ35213	Sequence of the me
C 18	21	100.0	2322	13	AAQ25905	pp2', Synthetic.
C 19	21	100.0	2455	16	AAK04538	Staphylococcus aur
C 20	21	100.0	2456	22	AAH01187	Staphylococcus aur
C 21	20	95.2	1467	21	AAK95348	B. subtilis surfac
C 22	19.4	92.4	699	23	AAK51923	Staphylococcus aur
C 23	19.4	92.4	69	23	AAK54834	Staphylococcus aur
C 24	19.4	92.4	781	20	AAK16552	Human gene express
C 25	19.4	92.4	6254	18	AAK74715	Staphylococcus aur
C 26	19.4	92.4	41488	22	AAK87512	Human immunohaema
C 27	18.4	87.6	530	23	ABK52716	Human prostate exp
C 28	18.4	87.6	3650	22	AAK54392	S. epidermidis gen
C 29	18.4	87.6	6888	21	AAK70114	Plasmodium falcipa
C 30	18.4	87.6	32476	22	AAK85314	Human immune/haema
C 31	18.4	87.6	33353	22	AAK70003	Human adenocarcino
C 32	17.8	84.8	345	24	ABK62597	Human nervous syst
C 33	17.8	84.8	357	22	ABK17965	Human polynucleoti
C 34	17.8	84.8	388	22	AAK191865	Human ovarian tumo
C 35	17.8	84.8	395	22	AAK23887	Human ovarian PCR-
C 36	17.8	84.8	395	22	AAK82444	Human CDNA for an
C 37	17.8	84.8	548	22	AAK56500	Human ovarian PCR-
C 38	17.8	84.8	670	22	AAK824179	Human ovarian PCR-
C 39	17.8	84.8	670	22	AAK82754	Human ovarian tumo
C 40	17.8	84.8	798	21	AAK02444	Human colon cancer
C 41	17.8	84.8	1245	22	AAK33101	Human colon cancer
C 42	17.8	84.8	1301	22	AAK48657	Aspartate/ornithin
C 43	17.8	84.8	1305	21	AAK51562	Arabidopsis thailia
C 44	17.8	84.8	1341	20	AAK61756	B. burgdorferi ant
C 45	17.8	84.8	1350	14	AAQ43202	Sequence encoding

ALIGNMENTS

ABK85910	ABK85910 standard; DNA; 21 Bp.
AC	ABK85910:
AC	16-AUG-2002 (first entry)
DE	Methicillin resistant Staphylococcus aureus detection primer #10.
XX	
KW	Methicillin resistant Staphylococcus Aureus; MRSA; primer; ss:
OS	mechA probe.
XX	
OS	Staphylococcus aureus.
XX	
PN	EP1160333-AZ.
XX	
PD	05-DEC-2001.
XX	
PF	29-MAY-2001; 2001EP-0112100.
XX	
PR	29-MAY-2000; 2000UP-0163149.
XX	
PR	09-JUN-2000; 2000UP-0179394.
XX	
PA	(TOYJ) TOSOH CORP.
XX	
PI	Taya T, Ishiguro T, Saito J;
XX	
DR	WPI; 2002-395832/43.
XX	
PT	New oligonucleotide specific for the mecA methicillin-resistance gene, useful for cleavage, detection and amplification of the gene or related

PT mRNA -
 XX
 PS Claim 1; Page 16; 28pp; English.
 CC
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the meca gene (associated with methicillin resistance in
 CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
 CC a detection method employing an RNA amplification process, using RNA
 CC derived from the meca gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a
 CC change in the fluorescent property relative to that of a situation where
 CC a complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant *S. aureus* in
 CC clinical samples. They may also be used therapeutically to inhibit RNA
 CC reverse transcription or translation. These oligonucleotides permit
 CC rapid and very sensitive detection/identification of the meca gene, at a
 CC relatively low temperature without the need for heat denaturation of
 CC target RNA. The present sequence represents a methicillin resistant
 CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
 CC
 SO Sequence 21 BP; 3 A; 3 C; 1 G; 14 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 21;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TTTCTTTTCTCTATTATG 21
 Db 1 TTTCTTTTCTCTATTATG 21
 RESULT 2
 ABRK85920
 ID ABRK85920 standard; DNA: 21 BP.
 AC ABRK85920;
 DT 16-AUG-2002 (first entry)
 DE Methicillin resistant *Staphylococcus aureus* detection primer #20.
 XX
 KM Methicillin resistant *Staphylococcus aureus*; MRSA; primer; ss;
 KM meca; probe.
 XX
 Staphylococcus aureus.
 EP1160333-A2.
 PD 05-DEC-2001.
 PF 29-MAY-2001; 2001EP-0112100.
 PR 29-MAY-2000; 2000JP-0163149.
 PR 09-JUN-2000; 2000JP-0179394.
 XX
 PA (TOYU) TOSOH CORP.
 XX
 PI Taya T, Ishiguro T, Saito J;
 DR WPI: 2002-395832/43.
 XX
 PT New oligonucleotide specific for the meca methicillin-resistance gene,
 PT useful for cleavage, detection and amplification of the gene or related
 PT mRNA -
 XX
 PS Claim 5; Page 19; 28pp; English.
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the meca gene (associated with methicillin resistance in

CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
 CC a detection method employing an RNA amplification process, using RNA
 CC derived from the meca gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a
 CC change in the fluorescent property relative to that of a situation where
 CC a complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant *S. aureus* in
 CC clinical samples. They may also be used therapeutically to inhibit RNA
 CC reverse transcription or translation. These oligonucleotides permit
 CC rapid and very sensitive detection/identification of the meca gene, at a
 CC relatively low temperature without the need for heat denaturation of
 CC target RNA. The present sequence represents a methicillin resistant
 CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
 CC
 SO Sequence 21 BP; 3 A; 3 C; 1 G; 14 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 21;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TTTCTTTTCTCTATTATG 21
 Db 1 TTTCTTTTCTCTATTATG 21
 RESULT 3
 AAX15488/C
 ID AAX15488 standard; DNA: 36 BP.
 AC AAX15488;
 DT 07-MAY-1999 (first entry)
 DE Probe meca938-36 for detecting an antibiotic resistant meca gene.
 XX
 KM Antibiotic resistant meca gene; transmission; treatment;
 KM methicillin resistant; *Staphylococcus*; probe; ss.
 OS Synthetic.
 OS *Staphylococcus* sp.
 XX
 PN W09901572-A2.
 PD 14-JAN-1999.
 PF 03-JUL-1998; 98WO-CA00633.
 PR 22-JUN-1998; 98US-0090276.
 PR 03-JUL-1997; 97US-0051643.
 PR 18-MAY-1998; 98US-0086020.
 XX
 PA (IDBI-) ID BIOMEDICAL CORP.
 XX
 PI Bekkaoui F, Cloney LP;
 DR WPI: 1999-106072/09.
 XX
 PT Method for determining the presence of an antibiotic resistant meca
 PT gene in a sample - using a scissile link containing nucleic acid
 PT probe for antibiotic resistant meca gene
 XX
 PS Example 1; Page 17; 59pp; English.
 CC The present sequence represents a probe used for determining the
 CC presence of an antibiotic resistant meca gene in a biological sample.
 CC The method provides a means for the rapid detection, for both
 CC the prevention of transmission and treatment of, methicillin resistant
 CC *Staphylococcus* species.

```
SQ Sequence 36 BP; 22 A; 2 C; 7 G; 5 T; 0 other;
Query Match 100.0%; Score 21; DB 20; Length 36;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
   |||||
DB 24 TTTTCTTTTCTCTATTATG 4

RESULT 4
AAK15489/C
ID AAK15489 standard; DNA; 36 BP.
AC AAK15489;
XX
XX 07-MAY-1999 (first entry)
DT
XX Probe mecA938-36 for detecting an antibiotic resistant mecA gene.
XX
XX Antibiotic resistant mecA gene; transmission; treatment;
XX methicillin resistant; Staphylococcus; DNA/RNA hybrid; probe; ss.
XX Synthetic.
OS Staphylococcus sp.
XX
XX Key Location/Qualifiers
FH misc_RNA 15..18
FT /*tag= a
FT
XX
XX MO9901572-A2.
XX
XX 14-JAN-1999.
XX
XX 03-JUL-1998; 98WO-CA00633.
XX
XX 22-JUN-1998; 98US-0090276.
XX 03-JUL-1997; 97US-0051643.
XX 18-MAY-1998; 98US-0086020.
XX
XX (IDBI-) ID BIOMEDICAL CORP.
XX
XX Bekkaoui F, Cloney LP;
XX
XX WPI: 1999-106072/09.
XX
XX Method for determining the presence of an antibiotic resistant mecA
XX gene in a sample - using a scissile link containing nucleic acid
XX probe for antibiotic resistant mecA gene
XX
XX Example 1; Page 18; 59pp; English.
XX
XX The present sequence represents a probe used for determining the
XX presence of an antibiotic resistant mecA gene in a biological sample.
XX The method provides a means for the rapid detection, for both
XX the prevention of transmission and treatment of, methicillin resistant
XX Staphylococcus species.
XX
XX Sequence 36 BP; 22 A; 2 C; 7 G; 5 T; 0 other;
SQ
Query Match 100.0%; Score 21; DB 20; Length 36;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
   |||||
DB 24 TTTTCTTTTCTCTATTATG 4

RESULT 5
ABK85927
ID ABK85927 standard; DNA; 39 BP.

XX
XX ABK85927;
XX
XX 16-AUG-2002 (first entry)
XX
XX Methicillin resistant Staphylococcus aureus cleavage probe #2.
XX
XX Methicillin resistant Staphylococcus Aureus; MRSA; primer; ss;
XX mecA; probe.
XX
XX Staphylococcus aureus.
XX
XX Key Location/Qualifiers
FH modified_base 39
FT /*tag= a
FT /*note= "Amidated"
XX
XX EP1160333-A2.
XX
XX 05-DEC-2001.
XX
XX 29-MAY-2001; 2001EP-0112100.
XX
XX 29-MAY-2000; 2000JP-0163149.
XX 09-JUN-2000; 2000JP-0179394.
XX
XX (TOYJ ) TOSOH CORP.
XX
XX Taya T, Ishiguro T, Saito J;
XX
XX WPI: 2002-395832/43.
XX
XX New oligonucleotide specific for the mecA methicillin-resistance gene,
XX useful for cleavage, detection and amplification of the gene or related
XX mRNA
XX
XX Example 2; Page 21; 28pp; English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
XX and amplifying the mecA gene (associated with methicillin resistance in
XX Staphylococcus aureus) or its derived RNA. The invention also comprises
XX a detection method employing an RNA amplification process, using RNA
XX derived from the mecA gene as template. Also disclosed is a detection
XX method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
XX amplification process in the presence of a complementary oligonucleotide
XX probe labelled with an intercalated fluorescent dye, where complementary
XX binding of the probe to the RNA transcription product results in a
XX change in the fluorescent property relative to that of a situation where
XX a complex formation is absent, and then measuring the fluorescence
XX intensity of the reaction solution. The oligonucleotides may be used as
XX primers or probes, for detecting methicillin-resistant S. aureus in
XX clinical samples. They may also be used therapeutically to inhibit RNA
XX reverse transcription or translation. These oligonucleotides permit
XX rapid and very sensitive detection/identification of the mecA gene, at a
XX relatively low temperature without the need for heat denaturation of
XX target RNA. The present sequence represents a methicillin resistant
XX Staphylococcus aureus (MRSA) cleaving probe used in the detection
XX method of the invention.
XX
XX Sequence 39 BP; 6 A; 5 C; 6 G; 22 T; 0 other;
SQ
Query Match 100.0%; Score 21; DB 24; Length 39;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
   |||||
DB 1 TTTTCTTTTCTCTATTATG 21

RESULT 6
AAK05905/C
ID AAK05905 standard; RNA; 59 BP.
```

```

DT 11-APR-1996 (first entry)
XX
XX Staphylococcus aureus 'meca' protein coding sequence.
DE
XX methicillin-resistant Staphylococcus aureus; MRSA; 'meca' protein;
KM antibiotic resistance; ds.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH 1.1608
FT CDS /tag= a
FT /product= 'mecA' protein
PN JP07209294-A.
XX
XX 11-AUG-1995.
PD
XX 10-JAN-1994: 94JP-0012226.
PF
XX 10-JAN-1994: 94JP-0012226.
PX
XX 10-JAN-1994: 94JP-0012226.
PY
XX (DENK-) DENKA SEIKEN KK.
PA (KAWA/) KAWANO M.
PA (MITU) MITSUBISHI CHEM CORP.
XX
XX WPI, 1995-313917/41.
DR P-PSDB; AAR80035.
XX
XX New 'mecA' protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
XX
XX Claim 5; Page 11-13; 15pp; Japanese.
PS
XX The present sequence codes for the 'mecA' protein which controls
CC methicillin resistance in methicillin-resistant Staph. aureus. The
CC 'mecA' protein (mol. wt. 40000) is useful for preparation of
CC an antiserum specific for MRSA, thereby allowing methicillin-resistant
CC and methicillin-sensitive strains to be distinguished. The coding
CC sequence was obtained by PCR amplification of the 'mecA' sequence
CC (see AAT04538) using primers AAT04537 and AAT04539.
CC N.B. In the sequence listing of the patent specification, the
CC sequence length is stated to be 1785 bp.
XX
XX Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;
SQ
Query Match 100.0%; Score 21; DB 16; Length 1789;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTTTCTTTTCTCTATTATG 21
XX |
XX 556 TTTTCTTTTCTCTATTATG 536
DB
RESULT 12
AAQ28599/c
ID AAQ28599 standard; DNA: 2007 BP.
XX
XX AAQ28599:
AC
XX 19-FEB-1993 (first entry)
DT
XX
XX Encodes penicillin binding protein PBP2A-27R.
DE
XX
XX Penicillin; antibiotic; bacteria; methicillin; staphylococci;
KM soluble; chelating peptide; MRS infection; methicillin resistant;
KM strain.
XX
XX Staphylococcus aureus strain 27R.
OS
XX
XX Key Location/Qualifiers
FH 1.2007
FT CDS

```

```

FT
XX
XX /tag= a
PN EP505151-A.
XX
XX 23-SEP-1992.
PD
XX
XX 18-MAR-1992: 92EP-0302298.
PF
XX
XX 19-MAR-1991: 91US-0672704.
PR
XX
XX (ELL) LILLY & CO ELL.
PA
XX Blaszcak LC, Skatrud PL, Smith MC, Wu CYE;
XX WPI, 1992-318034/39.
DR
XX
XX Polynucleotide cdp. encoding PBP 2A-27R protein or its deriv. -
PT contains PBP isolated from Staphylococcus aureus and is used to
PT treat methicillin resistant staphylococci
XX
XX Disclosure; Page 14; 101pp; English.
PS
XX
XX This sequence encodes a PBP2A penicillin binding protein isolated
CC from S. aureus strain 27R. A cDNA library was constructed from
CC S. aureus DNA in lambda phage EMB3. Packaging extracts from this were
CC then used to infect E. coli Cj236. Plaques were screened for the
CC presence of the 'meca-27R' gene by a probe produced by PCR amplification
CC of the 'meca' gene using primers Q28600.1. Positive plaques were purified
CC and digested with HindIII, and this fragment digested with XbaI and
CC cloned into M13mp18 and M13mp19 for sequencing.
XX
XX Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
SQ
Query Match 100.0%; Score 21; DB 13; Length 2007;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTTTCTTTTCTCTATTATG 21
XX |
XX 955 TTTTCTTTTCTCTATTATG 935
DB
RESULT 13
AAT28568/c
ID AAT28568 standard; DNA: 2007 BP.
XX
XX AAT28568:
AC
XX 01-APR-1997 (first entry)
DT
XX
XX Bacterial antibiotic resistance gene, 'meca', probc.
DE
XX
XX Detection; probe; amplification primer; bacterial pathogen; pneumonia;
KM Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
KM Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
KM Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
KM Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
KM Haemophilus influenzae; Moraxella catarrhalis; septicemia; meningitis;
KM infection; intra-abdominal infection; skin infection;
KM bacterial resistance; beta-lactam antibiotic; ds.
XX
XX Synthetic.
XX
XX WO9608582-A2.
PN
XX
XX 21-MAR-1996.
PD
XX
XX 12-SEP-1995: 95WO-CA00528.
PF
XX
XX 12-SEP-1994: 94US-0304732.
PR
XX
XX (BERG/) BERGERON M G.
PA (OUEL/) OUELLETTE M.

```


XX Method for detecting target bacterial species in a sample, comprises
 PT detecting the presence or amount of bacterial nucleic acid amplified by
 PT a primer derived from bacterial DNA, specific for the target bacterial
 PT species

XX PS Claim 16; Page 159-160; 168pp; English.

XX The invention relates to detecting target bacterial species suspected to
 CC be present in a sample, comprising contacting nucleic acids of target
 CC bacterial species with an amplification primer pair derived from a
 CC bacterial DNA fragment (ABA/6825-ABA/6861) specific for the target
 CC bacterial species but ubiquitous for different strains, amplifying the
 CC nucleic acid and detecting the presence or amount of an amplified
 CC sequence as an indication of the presence or amount of the target
 CC bacterial species. The invention includes primers and probes
 CC (ABA/6862-ABA/6984) against the target bacterial species, especially
 CC *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *P. mirabilis*, *S. pneumoniae*,
 CC *S. aureus*, *S. epidermidis*, *E. faecalis*, *S. saprophyticus*, *S. pyogenes*,
 CC *H. influenzae*, *M. catarrhalis* and/or group A *Streptococci* producing
 CC exotoxin A gene spe A, suspected to be present in a sample which is
 CC obtained from human patients, animals, environment or food, and which
 CC consists of one or more bacterial colonies. Oligonucleotide
 CC probes and primers complementary to the bacterial genes encoding
 CC resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aacB,
 CC aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanH, vanX, satA, aacA-apbD, vat,
 CC vga, msrA, sul and/or int (ABA/6985-ABA/7001) are also useful to identify
 CC commonly encountered and clinically important resistance genes. The
 CC invention provides a rapid method of bacterial identification that can be
 CC achieved, which reduces the time currently required for the
 CC identification of pathogens in the clinical laboratory.

XX SQ Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other:

Query Match 100.0%; Score 21; DB 22; Length 2007;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATG 21
 ||||||||||||||||

Db 955 TTTCTTTTCTCTATTATG 935

Search completed: December 10, 2002, 17:32:32
 Job time : 138.911 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 ; Search time 28.6257 Seconds
(without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579A-20

Perfect score: 21
Sequence: 1 tttctttctctatcaatg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2.6/prodata1/1na/5A_COMB.seq: *
2: /cgn2.6/prodata1/1na/5B_COMB.seq: *
3: /cgn2.6/prodata1/1na/6A_COMB.seq: *
4: /cgn2.6/prodata1/1na/6B_COMB.seq: *
5: /cgn2.6/prodata1/1na/PCTUS_COMB.seq: *
6: /cgn2.6/prodata1/1na/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	100.0	2007	2	US-08-743-637B-169 Sequence 169, App
C 2	21	100.0	2007	3	US-08-526-840B-169 Sequence 169, App
C 3	17.8	100.0	2028	4	US-09-134-001C-1710 Sequence 1710, Ap
C 4	17.8	84.8	1350	2	US-08-244-205-1 Sequence 1, App11
C 5	17.8	84.8	1350	5	PCT-US92-10284-1 Sequence 1, App11
C 6	17.4	82.9	2162	2	US-08-870-518-5 Sequence 5, App11
C 7	17	81.0	29	3	US-09-109-857-4 Sequence 4, App11
C 8	17	81.0	29	3	US-09-109-857-5 Sequence 5, App11
C 9	17	81.0	1665	4	US-09-221-017B-1017 Sequence 1017, Ap
C 10	16.8	80.0	432	4	US-09-134-001C-104 Sequence 104, App
C 11	16.8	80.0	583	4	US-09-385-982-86 Sequence 760, App
C 12	16.8	80.0	666	4	US-09-134-001C-760 Sequence 760, App
C 13	16.8	80.0	1143	4	US-09-134-001C-993 Sequence 993, App
C 14	16.8	80.0	1875	1	US-08-286-325A-1 Sequence 1, App11
C 15	16.8	80.0	2667	1	US-09-134-001C-195 Sequence 195, App
C 16	16.8	80.0	3234	4	US-08-286-325A-7 Sequence 7, App11
C 17	16.8	80.0	9713	4	US-08-961-527-43 Sequence 43, App1
C 18	16.4	78.1	2770	4	US-08-426-509A-5 Sequence 5, App11
C 19	16.4	78.1	2770	5	PCT-US95-0500A-5 Sequence 5, App11
C 20	16.4	78.1	7607	1	US-08-222-616-19 Sequence 19, App1
C 21	16.4	78.1	7607	4	US-08-446-648-19 Sequence 19, App1
C 22	16.4	78.1	7607	5	PCT-US95-04228-19 Sequence 19, App1
C 23	16.4	78.1	84495	4	US-09-797-906-3 Sequence 3, App11
C 24	16.2	77.1	474	1	US-08-412-614-93 Sequence 93, App1
C 25	16.2	77.1	474	2	US-08-635-761-93 Sequence 93, App1
C 26	16.2	77.1	474	4	US-09-312-520-93 Sequence 93, App1
C 27	16.2	77.1	476	1	US-08-412-614-94 Sequence 94, App1

C 28	16.2	77.1	476	2	US-08-635-761-94 Sequence 94, App1
C 29	16.2	77.1	476	4	US-09-312-520-94 Sequence 94, App1
C 30	16.2	77.1	547	3	US-09-188-930-14 Sequence 14, App1
C 31	16.2	77.1	699	4	US-09-328-111-190 Sequence 190, App
C 32	16.2	77.1	759	4	US-09-134-001C-2807 Sequence 2807, Ap
C 33	16.2	77.1	1051	4	US-09-063-743-4 Sequence 4, App11
C 34	16.2	77.1	1051	4	US-09-590-540-4 Sequence 4, App11
C 35	16.2	77.1	1056	2	US-08-929-417-1 Sequence 1, App11
C 36	16.2	77.1	2173	6	5168051-10 Patent No. 5168051
C 37	16.2	77.1	2338	3	US-09-058-489-37 Sequence 37, App1
C 38	16.2	77.1	4235	4	US-09-342-681C-18 Sequence 18, App1
C 39	16.2	77.1	4792	4	US-09-189-462-5 Sequence 5, App11
C 40	16.2	77.1	5113	3	US-08-973-273-2 Sequence 2, App11
C 41	16.2	77.1	5715	3	US-09-107-847-1 Sequence 1, App11
C 42	16.2	77.1	6755	3	US-08-931-999-4 Sequence 4, App11
C 43	16	76.2	35828	4	US-09-449-218D-17 Sequence 17, App1
C 44	15.8	75.2	420	4	US-09-641-638-331 Sequence 331, App
C 45	15.8	75.2	672	4	US-09-134-001C-1570 Sequence 1570, Ap

ALIGNMENTS

RESULT 1
US-08-743-637B-169/C
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: OUELLETTE & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586, 90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0% Score 21: DB 2: Length 2007:

Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTCTTTTCTCTATTATG 21
|||||
DB 955 TTTCTTTTCTCTATTATG 935

RESULT 2
US-08-526-840B-169/C
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 21; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTATG 21
|||||
DB 955 TTTCTTTTCTCTATTATG 935

RESULT 3
US-09-134-001C-1710/C
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucellette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 21; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTCTTTTCTCTATTATG 21
|||||
DB 976 TTTCTTTTCTCTATTATG 956

RESULT 4
US-08-244-205-1
; Sequence 1, Application US/08244205
; Patent No. 5952544
; GENERAL INFORMATION:
; APPLICANT: Browse, John, Kinney, Anthony J.,
; APPLICANT: Pierce, John, Wierzbicki, Anna M.,
; APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
; TITLE OF INVENTION: Fatty Acid Desaturase Genes
; TITLE OF INVENTION: from Plants
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,205
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/804,259
FILING DATE: 4 DECEMBER 1991
ATTORNEY/AGENT INFORMATION:
NAME: Floyd, Linda A.
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1036-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO

ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: PCF3
FEATURE:
NAME/KEY: CDS
LOCATION: 46..1206
US-08-244-205-1

Query Match 84.8%; Score 17.8; DB 2; Length 1350;
Best Local Similarity 90.5%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTATG 21
|||||
DB 1308 TTTCTTTTCTTTATTATG 1328

RESULT 5
PCT-US92-10284-1

Sequence 1, Application PC/TUS9210284

GENERAL INFORMATION:

APPLICANT: Browse, John, Kinney, Anthony J.,
APPLICANT: Pierce, John, Wierzbicki, Anna M.,
APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
TITLE OF INVENTION: Fatty Acid Desaturase Genes
TITLE OF INVENTION: from Plants
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: Macintosh System, 6.0

SOFTWARE: Microsoft Word, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10284

FILING DATE: 19921203

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/804,259

FILING DATE: 4 DECEMBER 1991

ATTORNEY/AGENT INFORMATION:

NAME: Floyd, Linda A.

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: BB-1036-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 992-4929

TELEFAX: (302) 892-7949

TELEFX: 835420

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1350 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Arabidopsis thaliana IMMEDIATE SOURCE:

IMMEDIATE SOURCE:

CLONE: PCF3

FEATURE:

NAME/KEY: CDS

LOCATION: 46..1206

PCT-US92-10284-1

Query Match 84.8%; Score 17.8; DB 5; Length 1350;

Best Local Similarity 90.5%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTATG 21
|||||
DB 1308 TTTCTTTTCTTTATTATG 1328

RESULT 6

US-08-870-518-5/C

Sequence 5, Application US/08870518

Patent No. 5925366

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.

APPLICANT: Galcheva-Gargova, Zoya

TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX

TITLE OF INVENTION: PROTEINS AND USES THEREOF

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSER: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/870,518

FILING DATE: 06-JUN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/019,219

FILING DATE: 06-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Passe, Peter J.

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 04020/102001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEFX: 200154

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2162 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 89...1465

US-08-870-518-5

Query Match 82.9%; Score 17.4; DB 2; Length 2162;

Best Local Similarity 94.7%; Pred. No. 1.8e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTATG 19
|||||
DB 1978 TTTCTTTTCTTTATTATG 1960

RESULT 7

US-09-109-957-4/C

Sequence 4, Application US/09109957

Patent No. 6136533

GENERAL INFORMATION:

APPLICANT: Bekkaoui, Faouzi

APPLICANT: Modrusan, Zora D.

APPLICANT: Pische, Isabelle A.

APPLICANT: Duck, Peter D.

```

; APPLICANT: Cloney, Lynn P.
; APPLICANT: Wong, Alfred C.K.
; TITLE OF INVENTION: ADDITIVES FOR USE IN CYCLING PROBE REACTIONS
; FILE REFERENCE: 480094.419
; CURRENT APPLICATION NUMBER: US/09/109,957
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Solid Phase Synthesis
US-09-109-957-4

Query Match          81.0%: Score 17; DB 3; Length 29;
Best Local Similarity 100.0%: Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

f 1 TTTTCTTTTCTCTATT 17
   |||||||
Db 17 TTTCTTTTCTCTATT 1

RESULT 8
US-09-109-957-5
; Sequence 5, Application US/09109957
; Patent No. 6136533
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Modrusan, Zora D.
; APPLICANT: Pische, Isabelle A.
; APPLICANT: Duck, Peter D.
; APPLICANT: Cloney, Lynn P.
; APPLICANT: Wong, Alfred C.K.
; TITLE OF INVENTION: ADDITIVES FOR USE IN CYCLING PROBE REACTIONS
; FILE REFERENCE: 480094.419
; CURRENT APPLICATION NUMBER: US/09/109,957
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Solid Phase Synthesis
US-09-109-957-5

Query Match          81.0%: Score 17; DB 3; Length 29;
Best Local Similarity 100.0%: Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTTCTTTTCTCTATT 17
   |||||||
Db 13 TTTCTTTTCTCTATT 29

RESULT 9
US-09-221-017B-1017/c
; Sequence 1017, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
```

```

; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Moorov, Gladys H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEEX: 706141
; INFORMATION FOR SEQ ID NO: 1017:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1...1665
US-09-221-017B-1017

Query Match          81.0%: Score 17; DB 4; Length 1665;
Best Local Similarity 100.0%: Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTTCTTTTCTCTATTA 18
   |||||||
Db 311 TTTCTTTTCTCTATTA 295

RESULT 10
US-09-134-001C-104/c
; Sequence 104, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
```

SEO ID NO 104
LENGTH: 432
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-104

Query Match 80.0%; Score 16.8; DB 4; Length 432;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 TTTCTTTTCTCTATTAT 20
11111111111111111111
Db 188 TTCTCTTTCTCTAATAAT 169

RESULT 11

US-09-385-982-86/C
Sequence 86, Application US/09385982
Patent No. 6262334

GENERAL INFORMATION:

APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

FILE REFERENCE: CCDNA-260XX

CURRENT APPLICATION NUMBER: US/09/385,982

EARLIER FILING DATE: 1999-08-30

EARLIER APPLICATION NUMBER: 09/328,111

EARLIER FILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: 60/117,393

EARLIER FILING DATE: 1999-01-27

EARLIER APPLICATION NUMBER: 60/098,639

NUMBER OF SEQ ID NOS: 544

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 86

LENGTH: 583

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(583)

OTHER INFORMATION: n = A,T,C or G

US-09-385-982-86

Query Match 80.0%; Score 16.8; DB 4; Length 583;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 TTTCTTTTCTCTATTAT 20
11111111111111111111
Db 360 TTTTCTTTCTCTATTAT 341

RESULT 12

US-09-134-001C-760/C
Sequence 760, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

FILE REFERENCE: CTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 760

LENGTH: 696

TYPE: DNA

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-760

Query Match 80.0%; Score 16.8; DB 4; Length 696;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 TTTCTTTTCTCTATTAT 20
11111111111111111111
Db 488 TTTCTTTTCTTTATCAAT 469

RESULT 13

US-09-134-001C-993/C
Sequence 993, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

FILE REFERENCE: CTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 993

LENGTH: 1143

TYPE: DNA

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-993

Query Match 80.0%; Score 16.8; DB 4; Length 1143;
Best Local Similarity 90.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 TTTCTTTTCTCTATTAT 20
11111111111111111111
Db 533 TTTCTTTTCTTTATTAGT 514

RESULT 14

US-08-286-325A-1/C
Sequence 1, Application US/08286325A
Patent No. 5658770

GENERAL INFORMATION:

APPLICANT: PREVOT, Fabien

APPLICANT: REMY, Elisabeth

TITLE OF INVENTION: Nucleic acid sequence and plasmids

TITLE OF INVENTION: Comprising at least one phage resistance mechanism,

NUMBER OF SEQUENCES: 7 bacteria in which they are present, and their use

CORRESPONDENCE ADDRESS:

ADDRESSER: BACON & THOMAS

STREET: 625 Slaters Lane - Fourth floor

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,325A

FILING DATE: 04-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93 09 777

FILING DATE: 09-AUG-1993

```

; ATTORNEY/AGENT INFORMATION:
;   NAME: FICHTER, Richard E
;   REGISTRATION NUMBER: 26,382
;   REFERENCE/DOCKET NUMBER: REF/BDL/
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 683-0500
;   TELEFAX: (703) 683-1080
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1875 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     ORIGINAL SOURCE:
;     ORGANISM: Lactococcus lactis
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 202..1821
;       -08-286-325A-1

```

```

Query Match      80.0%; Score 16.8; DB 1; Length 1875;
Best Local Similarity 90.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 1 TTTCTTTTCTCTATTAAAT 20
    ||||| ||||| ||||| |||||
DB 988 TTTATTCTTCATTAAT 969

```

```

RESULT 15
US-09-134-001C-195/c
; Sequence 195, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucelte-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: CTC-007
; CURRENT APPLICATION NUMBER: US/09/ 4,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 195
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-195

```

```

Query Match      80.0%; Score 16.8; DB 4; Length 2667;
Best Local Similarity 90.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 1 TTTCTTTTCTCTATTAAAT 20
    ||||| ||||| ||||| |||||
DB 2603 TTTCTTTTCTCATTAAT 2584

```

```

Search completed: December 10, 2002, 22:54:23
Job time : 30.7507 secs

```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 ; Search time 27.2179 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-20

Perfect score: 21

Sequence: 1 tttctttctctattatg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NFW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	10	US-09-865-579A-10
2	21	100.0	21	10	US-09-865-579A-20
3	21	100.0	39	10	US-09-865-579A-27
4	21	100.0	2007	10	US-09-452-599-169
5	19.4	92.4	699	10	US-09-815-242-4505
6	19.4	92.4	699	10	US-09-815-242-8471
7	18.4	87.6	2000	9	US-09-938-842A-4244
8	17.8	84.8	395	10	US-09-777-564-68
9	17.8	84.8	548	10	US-09-813-358-124
10	17.8	84.8	670	10	US-09-777-564-360
11	17.8	84.8	2000	9	US-09-938-842A-4081
12	17.8	84.8	2000	9	US-09-938-842A-4149
13	17.4	82.9	21990	9	US-09-942-429A-9
14	17.4	82.9	1503841	9	US-09-946-807-1
15	17.4	82.9	1503841	10	US-09-795-668-1
16	17.4	82.9	1503841	10	US-09-795-668-1
17	17.4	82.9	1503841	10	US-09-974-300-2891
18	17	81.0	1431	10	US-09-974-300-2891
19	17	81.0	5840	10	US-09-070-927A-31

C	20	16.8	80.0	286	10	US-09-880-107-2012	Sequence 2012, Ap
C	21	16.8	80.0	380	9	US-09-933-797-438	Sequence 438, Ap
C	22	16.8	80.0	393	10	US-09-878-574-1244	Sequence 1244, Ap
C	23	16.8	80.0	453	10	US-09-880-107-2589	Sequence 2589, Ap
C	24	16.8	80.0	483	10	US-09-783-590-12266	Sequence 12266, A
C	25	16.8	80.0	496	9	US-09-954-531-1115	Sequence 1115, Ap
C	26	16.8	80.0	496	10	US-09-964-824A-149	Sequence 149, Ap
C	27	16.8	80.0	1097	10	US-09-974-300-2653	Sequence 2653, Ap
C	28	16.8	80.0	1516	10	US-09-925-302-291	Sequence 291, Ap
C	29	16.8	80.0	1571	9	US-09-981-353-86	Sequence 86, Ap
C	30	16.8	80.0	2000	9	US-09-938-842A-4131	Sequence 4131, Ap
C	31	16.8	80.0	21761	10	US-09-764-847-1680	Sequence 1680, Ap
C	32	16.8	80.0	180216	10	US-09-835-232-6	Sequence 6, Ap
C	33	16.8	80.0	326014	10	US-09-731-231A-3	Sequence 3, Ap
C	34	16.8	80.0	465237	10	US-09-933-267A-1	Sequence 1, Ap
C	35	16.8	78.1	245	10	US-09-728-445-790	Sequence 790, Ap
C	36	16.4	78.1	516	10	US-09-815-242-4261	Sequence 4261, Ap
C	37	16.4	78.1	522	10	US-09-864-761-12370	Sequence 12370, A
C	38	16.4	78.1	690	10	US-09-815-242-8293	Sequence 8293, Ap
C	39	16.4	78.1	862	9	US-09-938-842A-3058	Sequence 3058, Ap
C	40	16.4	78.1	1175	10	US-09-070-927A-660	Sequence 660, Ap
C	41	16.4	78.1	2000	9	US-09-938-842A-3106	Sequence 3106, Ap
C	42	16.4	78.1	2508	10	US-09-070-927A-623	Sequence 623, Ap
C	43	16.4	78.1	2770	10	US-09-977-269-5	Sequence 5, Ap
C	44	16.4	78.1	2863	10	US-09-954-456-1631	Sequence 1631, Ap
C	45	16.4	78.1	4187	10	US-09-764-855-252	Sequence 252, Ap

ALIGNMENTS

RESULT 1
US-09-865-579A-10
Sequence 10, Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
APPLICANT: Saito, Juichi
TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865, 579A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide capable of binding specifically to meca gene
US-09-865-579A-10

Query Match 100.0%; Score 21; DB 10; Length 21;
Best local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Caps 0;

DB 1 TTTTCTTTCTCTATTATG 21
US-09-865-579A-20
Sequence 20, Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:

```

; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
;
US-09-865-579A-20
```

```
Query Match          100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTTCTTTTCTCTATTATG 21
    |||||
DB 1 TTTCTTTTCTCTATTATG 21
```

```

RESULT 3
US-09-865-579A-27
; Sequence 27, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
;
US-09-865-579A-27
```

```
Query Match          100.0%; Score 21; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTTCTTTTCTCTATTATG 21
    |||||
DB 1 TTTCTTTTCTCTATTATG 21
```

```

RESULT 4
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
```

```

; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287-31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
;
US-09-452-599-169
```

```
Query Match          100.0%; Score 21; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTTCTTTTCTCTATTATG 21
    |||||
DB 955 TTTCTTTTCTCTATTATG 935
```

```

RESULT 5
US-09-815-242-4505/c
; Sequence 4505, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA-011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4505
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
;
US-09-815-242-4505
```

```
Query Match          92.4%; Score 19.4; DB 10; Length 699;
Best Local Similarity 95.2%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

OY 1 TTTCTTTTCTCTATTATG 21
 |||||
 DB 491 TTTCTTTTCTCTATCATG 471

RESULT 6

US-09-815-242-8471/c
 ; Sequence 8471, Application US/09815242
 ; Patent No. US2002061569A1
 ; GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlson, Karl L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
 TITLE OF INVENTION: prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8471

LENGTH: 699

TYPE: DNA

ORGANISM: Staphylococcus aureus

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(699)

US-09-815-242-8471

Query Match 92.4%; Score 19.4; DB 10; Length 699;
 Best Local Similarity 95.2%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTATG 21
 |||||
 DB 491 TTTCTTTTCTCTATCATG 471

RESULT 7

US-09-938-842A-4244
 ; Sequence 4244, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:

APPLICANT: Harper, Jeff
 APPLICANT: Kreps, Joel
 APPLICANT: Wang, Xun
 APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SRIPI300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 4244
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana

US-09-938-842A-4244

Query Match 87.6%; Score 18.4; DB 9; Length 2000;
 Best Local Similarity 95.0%; Pred. No. 2.4e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTAT 20
 |||||
 DB 536 TTTCTTTTCTCTATTAT 555

RESULT 8

US-09-777-564-68/c

Sequence 68, Application US/09777564

Patent No. US2002022591A1

GENERAL INFORMATION:

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.493

CURRENT APPLICATION NUMBER: US/09/777,564

CURRENT FILING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 1730

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 68

LENGTH: 395

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)...(395)

OTHER INFORMATION: n = A,T,C or G

US-09-777-564-68

Query Match 84.8%; Score 17.8; DB 10; Length 395;
 Best Local Similarity 90.5%; Pred. No. 3.5e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTATG 21
 |||||
 DB 177 TTTCTTTTCTCTAAGATG 157

RESULT 9

US-09-813-358-124
 ; Sequence 124, Application US/09813358
 ; Patent No. US20020048759A1
 ; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 APPLICANT: Pyle, Ruth
 APPLICANT: Stolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER

FILE REFERENCE: 210121.501

CURRENT APPLICATION NUMBER: US/09/813,358

CURRENT FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 222

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 124

LENGTH: 548

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(548)
OTHER INFORMATION: n = A,T,C or G
US-09-813-358-124

Query Match Best Local Similarity 84.8%; Score 17.8; DB 10; Length 548;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 1 TTTTCTTTTCTCTATTATG 21
|||||
Db 8 TTTTCTTTTCTCTAGTAATG 28

RESULT 10
US-09-777-564-360/C
Sequence 360, Application US/09777564
Patent No. US20020022591A1
GENERAL INFORMATION:
APPLICANT: Mannion, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.493
CURRENT APPLICATION NUMBER: US/09/777,564
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: FastSeq for Window Version 4.0
SEQ ID NO 360
LENGTH: 670
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(670)
OTHER INFORMATION: n = A,T,C or G
US-09-777-564-360

Query Match Best Local Similarity 84.8%; Score 17.8; DB 10; Length 670;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 1 TTTTCTTTTCTCTATTATG 21
|||||
Db 177 TTTTCTTTTCTCTAACAATG 157

RESULT 11
US-09-938-842A-4081
Sequence 4081, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SRRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4081
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana

US-09-938-842A-4081

Query Match Best Local Similarity 84.8%; Score 17.8; DB 9; Length 2000;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 1 TTTTCTTTTCTCTATTATG 21
|||||
Db 728 TTTTCTTTTCTCTAGTAATG 748

RESULT 12
US-09-938-842A-4149/C
Sequence 4149, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SRRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4149
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-4149

Query Match Best Local Similarity 84.8%; Score 17.8; DB 9; Length 2000;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 1 TTTTCTTTTCTCTATTATG 21
|||||
Db 1890 TTTTCTTTTCTCAATTAAG 1870

RESULT 13
US-09-867-701-2314/C
Sequence 2314, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Agiate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2314
LENGTH: 403
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(403)
OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2314

Query Match Best Local Similarity 82.9%; Score 17.4; DB 10; Length 403;

Best Local Similarity 94.7%; Pred. No. 4,8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTCTTTTCTCTATTAA 19
||| ||||| ||||| |||||
Db 210 TTTCTTTTCTCTATTAA 192

RESULT 14

US-09-942-429A-9
; Sequence 9, Application US/09942429A
; Patent No. US20020165208A1
; GENERAL INFORMATION:
; APPLICANT: JORGE H. CAPEVILLA, MICHAEL WATERMAN, AND VIJAKUMAR HOLLA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO
; FILE REFERENCE: 22000.011002
; CURRENT APPLICATION NUMBER: US/09/942,429A
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/228,947
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 21990
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NO. US20020165208A1e -
; NAME/KEY: misc_feature
; LOCATION: (1)...(21990)
; OTHER INFORMATION: n = 9, a, c or t(u)
US-09-942-429A-9

Query Match 82.9%; Score 17.4; DB 9; Length 21990;
Best Local Similarity 94.7%; Pred. No. 6e+02; 1; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTCTTTTCTCTATTAA 19
||| ||||| ||||| |||||
Db 6217 TTTCTTTTCTCTATTAA 6235

RESULT 15

US-09-946-807-1/c
; Sequence 1, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345,2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r-g or a
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)

OTHER INFORMATION: y-t/u or c

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m-a or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k-g or t/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: s-g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: w-a or t/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b-g or c or t/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d-a or g or t/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h-a or c or t/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v-a or g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: n=a or g or c or t/u
US-09-946-807-1

Query Match 82.9%; Score 17.4; DB 9; Length 1503841;
Best Local Similarity 94.7%; Pred. No. 2,5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTCTTTTCTCTATTAA 20
||| ||||| ||||| |||||
Db 1457430 TTTCTTTTCTCTATTAA 1457412

Search completed: December 11, 2002, 06:07:18
Job time : 277.218 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 ; Search time 25.9218 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-24

Perfect score: 20

Sequence: 1 tcattgctgtaattttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/ECTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	10	US-09-865-579A-14
2	20	100.0	20	10	US-09-865-579A-24
3	20	100.0	20	10	US-09-452-599-169
4	18.4	92.0	648	12	US-10-001-843-114
5	18.4	92.0	928	12	US-10-001-843-115
6	16.8	84.0	32191	10	US-09-764-864-1678
7	16.8	84.0	640681	10	US-09-790-988-1
8	16	80.0	963	10	US-09-815-242-4716
9	16	80.0	966	10	US-09-815-242-8596
10	16	80.0	966	10	US-09-815-242-8623
11	16	80.0	640681	10	US-09-790-988-1
12	15.8	79.0	124	10	US-09-783-590-6025
13	15.8	79.0	187	10	US-09-983-965-4889
14	15.8	79.0	191	10	US-09-783-590-5750
15	15.8	79.0	345	10	US-09-983-965-4863
16	15.8	79.0	364	10	US-09-764-869-2135
17	15.8	79.0	366	10	US-09-969-373-801
18	15.8	79.0	677	10	US-09-828-644-24
19	15.8	79.0	754	10	US-09-815-242-3149

20	15.8	79.0	810	10	US-09-974-300-5530	Sequence 5530, Ap
21	15.8	79.0	1981	9	US-09-258-0318-57	Sequence 57, Appl
22	15.8	79.0	2009	10	US-09-764-869-2134	Sequence 2134, Ap
23	15.8	79.0	2009	10	US-09-764-869-2139	Sequence 2139, Ap
24	15.8	79.0	2378	10	US-09-815-242-4669	Sequence 4669, Ap
25	15.8	79.0	2595	10	US-09-954-456-211	Sequence 211, App
26	15.8	79.0	2595	10	US-09-954-456-503	Sequence 503, App
27	15.8	79.0	5950	10	US-09-880-107-3346	Sequence 3346, App
28	15.8	79.0	17993	10	US-09-768-781-5	Sequence 5, Appli
29	15.8	79.0	49136	10	US-09-768-877-1	Sequence 1, Appli
30	15.8	79.0	56516	9	US-09-853-526-1	Sequence 1, Appli
31	15.8	79.0	56516	10	US-09-901-484A-1	Sequence 1, Appli
32	15.8	79.0	56520	9	US-09-853-526-179	Sequence 179, App
33	15.8	79.0	56520	10	US-09-901-484A-179	Sequence 179, App
34	15.4	77.0	162	10	US-09-783-590-5917	Sequence 5917, Ap
35	15.4	77.0	267	10	US-09-878-574-9170	Sequence 9170, Ap
36	15.4	77.0	267	10	US-09-878-574-12010	Sequence 12010, A
37	15.4	77.0	268	10	US-09-878-574-11017	Sequence 11017, A
38	15.4	77.0	280	10	US-09-878-574-11701	Sequence 11701, A
39	15.4	77.0	346	9	US-09-954-531-103	Sequence 103, App
40	15.4	77.0	392	10	US-09-867-701-6405	Sequence 6405, Ap
41	15.4	77.0	416	10	US-09-880-107-3588	Sequence 3588, Ap
42	15.4	77.0	444	10	US-09-826-312-3	Sequence 3, Appli
43	15.4	77.0	447	9	US-09-938-842A-493	Sequence 493, App
44	15.4	77.0	636	10	US-09-770-149-641	Sequence 641, App
45	15.4	77.0	761	10	US-09-833-381-894	Sequence 894, App

ALIGNMENTS

RESULT 1
US-09-865-579A-14
Sequence 14, Application US/09865579A
Patient No. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Yoshiaki
APPLICANT: Ishiguro, Takahiko
TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865,579A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-14
Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6,5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 TCATTGCTGTTAATATTTT 20
|||||
1 TCATTGCTGTTAATATTTT 20
RESULT 2
US-09-865-579A-24
Sequence 24 Application US/09865579A
Patient No. US20020098492A1
GENERAL INFORMATION:

APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865,579A
CURRENT FILING DATE: 2001-05-28
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-09-865-579A-24

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
Db 1 TCATTGCTGTTAATATTTT 20

RESULT 3
US-09-452-599-169/c
Sequence 169, Application US/09452599
Patent No. US20020055101A1
GENERAL INFORMATION:
APPLICANT: Bergeron, Michel G.
APPLICANT: Ouellette, Marc
TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
FILE REFERENCE: 12287.31
CURRENT APPLICATION NUMBER: US/09/452,599
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR FILING DATE: 1995-09-11
PRIOR APPLICATION NUMBER: 08/304,732
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 169
LENGTH: 2007
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match 100.0%; Score 20; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
Db 1234 TCATTGCTGTTAATATTTT 1215

RESULT 4
US-10-001-843-114
Sequence 114, Application US/10001843
Patent No. US20020132255A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana

APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes an
FILE REFERENCE: DEX-0267
CURRENT APPLICATION NUMBER: US/10/001,843
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,992
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 218
SOFTWARE: PatentIn version 3.1
SEQ ID NO 114
LENGTH: 648
TYPE: DNA
ORGANISM: Homo sapien
US-10-001-843-114

Query Match 92.0%; Score 18.4; DB 12; Length 648;
Best Local Similarity 95.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
Db 61 TAATTGCTGTTAATATTTT 80

RESULT 5
US-10-001-843-115
Sequence 115, Application US/10001843
Patent No. US20020132255A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes an
FILE REFERENCE: DEX-0267
CURRENT APPLICATION NUMBER: US/10/001,843
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,992
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 218
SOFTWARE: PatentIn version 3.1
SEQ ID NO 115
LENGTH: 928
TYPE: DNA
ORGANISM: Homo sapien
US-10-001-843-115

Query Match 92.0%; Score 18.4; DB 12; Length 928;
Best Local Similarity 95.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
Db 341 TAATTGCTGTTAATATTTT 360

RESULT 6
US-09-764-864-1678
Sequence 1678, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,864

```
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1678
; LENGTH: 32191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1678
```

```
Query Match      84.0%; Score 16.8; DB 10; Length 32191;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 TCATTGCTTAATATTTT 20
    ||||| ||||| ||||| |||||
Db 8813 TAATTGTTGTTAATATTTT 8832
```

```
ESUT 7
S-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: KATANABE, HIDEMI
; APPLICANT: MATSUKI, MASAHIRA
; APPLICANT: SAKAKI, YOSHITSUKI
; TITLE OF INVENTION: GENE/DNA OF BACTERIAL SYMPTOM OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
```

```
Query Match      84.0%; Score 16.8; DB 10; Length 640681;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 TCATTGCTTAATATTTT 20
    ||||| ||||| ||||| |||||
Db 517674 TCATTGATTAATATTTT 517655
```

```
RESULT 8
US-09-815-242-4716/c
; Sequence 4716, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
```

```
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4,716
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4716
```

```
Query Match      80.0%; Score 16; DB 10; Length 963;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 TTGCTGTTAATATTTT 19
    ||||| ||||| ||||| |||||
Db 64 TTGCTGTTAATATTTT 49
```

```
RESULT 9
US-09-815-242-8596/c
; Sequence 8596, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8596
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(966)
US-09-815-242-8596
```

```
Query Match      80.0%; Score 16; DB 10; Length 966;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 4 TTGCTGTAATATTTT 19
|||||
Db 64 TTGCTGTAATATTTT 49

RESULT 10

US-09-815-242-8623/C
; Sequence 8623, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8623
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(966)
US-09-815-242-8623

Query Match

Best Local Similarity 80.0%; Score 16; DB 10; Length 966;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TTGCTGTAATATTTT 19
|||||
Db 64 TTGCTGTAATATTTT 49

RESULT 11

US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:

; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match

Best Local Similarity 80.0%; Score 16; DB 10; Length 640681;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTAATAT 16
|||||
Db 306205 TCATTGCTGTAATAT 306220

RESULT 12

US-09-783-590-6025/C
; Sequence 6025, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:

; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6025
; LENGTH: 124
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (33)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (106)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (123)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-6025

Query Match

Best Local Similarity 79.0%; Score 15.8; DB 10; Length 124;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TCATTGCTGTAATATTTT 20
|||||
Db 38 TCATTGCTGTAATATTTT 19

RESULT 13

US-09-983-965-4889

```
; Sequence 4889, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 4889
; LENGTH: 187
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (114)
; OTHER INFORMATION:
; OTHER INFORMATION: Clone ID: 23-LIB34-073-Q1-E1-F3
US-09-983-965-4889

Query Match          79.0%; Score 15.8; DB 10; Length 187;
Best Local Similarity 89.5%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 19
        ||||| ||||| ||||| |||||
DB      72 TCATAGCTGTTAATATTTT 90

RESULT 14
US-09-783-590-5750/c
; Sequence 5750, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5750
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (77)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (121)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (185)
```

```
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (189)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-5750

Query Match          79.0%; Score 15.8; DB 10; Length 191;
Best Local Similarity 89.5%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 19
        ||||| ||||| ||||| |||||
DB      39 TCATTAGCTGTTAATATTTT 21

RESULT 15
US-09-983-965-4863
; Sequence 4863, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 4863
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 22-LIB34-075-Q1-E1-F5
US-09-983-965-4863

Query Match          79.0%; Score 15.8; DB 10; Length 345;
Best Local Similarity 89.5%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 19
        ||||| ||||| ||||| |||||
DB      227 TCATTGAGTTAATATTTT 245

Search completed: December 11, 2002, 06:14:01
Job time : 259.922 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 : Search time 27.2626 Seconds
(without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579a-24

Perfect score: 20

Sequence: 1 tcatgtcgttaataatttt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	2007	2	US-08-743-637B-169
C 2	20	100.0	2007	3	US-08-526-840B-169
C 3	20	100.0	2028	4	US-09-134-001C-1710
4	13	90.0	27	2	US-08-743-637B-262
5	17	85.0	330	2	US-08-437-013-4
6	17	85.0	641	2	US-08-437-013-1
7	17	85.0	641	2	US-08-437-013-28
8	17	85.0	709	2	US-08-437-013-26
9	16.8	84.0	805	1	US-08-118-469A-6
10	16.8	84.0	2119	4	US-09-509-119-6
11	16.8	84.0	11613	4	US-09-240-639-7
12	16.4	82.0	4326	4	US-09-453-702B-42
13	16	80.0	13674	2	US-08-852-807-12
14	16	80.0	13674	2	US-08-852-807-1
15	15.8	79.0	34	3	US-09-071-606-11
16	15.8	79.0	136	1	US-08-334-254-21
17	15.8	79.0	136	1	US-08-334-254-28
18	15.8	79.0	136	2	US-08-848-131-21
19	15.8	79.0	136	2	US-08-848-131-28
20	15.8	79.0	136	5	PCT-US95-14792-21
21	15.8	79.0	136	5	PCT-US95-14792-28
22	15.8	79.0	831	4	US-09-134-001C-2270
23	15.8	79.0	1607	4	US-09-853-768-13
24	15.8	79.0	1827	4	US-09-134-001C-1914
25	15.8	79.0	1929	2	US-08-892-770-2
26	15.8	79.0	1971	2	US-08-892-770-4
27	15.8	79.0	1981	4	US-09-647-590-17

28	15.8	79.0	4129	2	US-08-370-319C-12	Sequence 12, Appl
29	15.8	79.0	4129	4	US-09-224-834-12	Sequence 12, Appl
30	15.8	79.0	6506	4	US-09-453-702B-1	Sequence 1, Appl
C 31	15.8	79.0	9064	4	US-08-961-527-17	Sequence 1, Appl
C 32	15.8	79.0	10207	1	US-08-920-812-2	Sequence 2, Appl
C 33	15.8	79.0	10207	1	US-08-920-827-2	Sequence 2, Appl
C 34	15.8	79.0	10207	1	US-08-921-177-2	Sequence 2, Appl
C 35	15.8	79.0	10207	1	US-08-362-577C-2	Sequence 2, Appl
C 36	15.8	79.0	10207	2	US-08-930-828-2	Sequence 2, Appl
37	15.8	79.0	49136	4	US-09-422-869-1	Sequence 1, Appl
38	15.8	79.0	56516	2	US-08-996-306-1	Sequence 1, Appl
39	15.8	79.0	56516	4	US-09-338-907-1	Sequence 1, Appl
40	15.8	79.0	56516	4	US-09-218-207-1	Sequence 1, Appl
41	15.8	79.0	56520	4	US-09-338-907-179	Sequence 179, App
42	15.8	79.0	56520	4	US-09-218-207-179	Sequence 179, App
43	15.8	79.0	162450	4	US-09-345-882-1	Sequence 1, Appl
C 44	15.4	77.0	78	1	US-08-351-748-19	Sequence 19, Appl
C 45	15.4	77.0	78	1	US-08-430-536A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-743-637B-169/C
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
NUMBER OF INVENTIONS: 273
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: O'ARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586, 90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5591
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match 100.0%; Score 20; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
DB 1234 TCATTGCTGTTAATATTTT 1215

RESULT 2

US-08-526-840B-169/C
Sequence 169, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: APPLICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: OUELLETTE & BRADY
STREET: 411 East Wisconsin Avenue
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
DB 1234 TCATTGCTGTTAATATTTT 1215

RESULT 3

US-09-134-001C-1710/C
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 20; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
DB 1255 TCATTGCTGTTAATATTTT 1236

RESULT 4

US-08-743-637B-262
Sequence 262, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND APPLICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: OUELLETTE & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 262:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-743-637B-262

Query Match
Best Local Similarity 100.0%; Score 18; DB 2; Length 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ATTGCTGTTAATATTTT 20
DB 1 ATTGCTGTTAATATTTT 18

RESULT 5
US-08-437-013-4
Sequence 4; Application US/08437013
Patent No. 5932220
GENERAL INFORMATION:
APPLICANT: Barbours, Alan G.
TITLE OF INVENTION: Diagnostic Tests for a New Spriochrome, Borrellia
TITLE OF INVENTION: Lonestari sp. nov.
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,013
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSK:276/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-300
TELEFAX: 512/747-7577
TELEX: NA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"

US-08-437-013-4

Query Match
Best Local Similarity 100.0%; Score 17; DB 2; Length 330;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ATTGCTGTTAATATTTT 19
DB 116 ATTGCTGTTAATATTTT 132

RESULT 6
US-08-437-013-1
Sequence 1; Application US/08437013
Patent No. 5932220
GENERAL INFORMATION:
APPLICANT: Barbours, Alan G.
TITLE OF INVENTION: Diagnostic Tests for a New Spriochrome, Borrellia

TITLE OF INVENTION: Lonestari sp. nov.
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,013
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSK:276/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-300
TELEFAX: 512/747-7577
TELEX: NA
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"

US-08-437-013-1

Query Match
Best Local Similarity 100.0%; Score 17; DB 2; Length 641;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ATTGCTGTTAATATTTT 19
DB 253 ATTGCTGTTAATATTTT 269

RESULT 7
US-08-437-013-28
Sequence 28; Application US/08437013
Patent No. 5932220
GENERAL INFORMATION:
APPLICANT: Barbours, Alan G.
TITLE OF INVENTION: Diagnostic Tests for a New Spriochrome, Borrellia
TITLE OF INVENTION: Lonestari sp. nov.
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,013
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.

REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSK:276/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-300
TELEFAX: 512/747-7577
TELEX: NA
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-437-013-28

Query Match 85.0%; Score 17; DB 2; Length 641;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATTGCTGTTAATATTTT 19
|||||
Jb 253 ATTGCTGTTAATATTTT 269

RESULT 8
US-08-437-013-26
Sequence 26, /pplication US/08437013
Patent No. 5932220
GENERAL INFORMATION:
APPLICANT: Barbour, Alan G.
TITLE OF INVENTION: Diagnostic Tests for a New Spricohete, Borrelia
TITLE OF INVENTION: Ionstari sp. nov.
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,013
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSK:276/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-300
TELEFAX: 512/747-7577
TELEX: NA
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-437-013-26

Query Match 85.0%; Score 17; DB 2; Length 709;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATTGCTGTTAATATTTT 19
|||||
Db 292 ATTGCTGTTAATATTTT 308

RESULT 9
US-08-118-469A-6
Sequence 6, Application US/08118469A
Patent No. 5656451
GENERAL INFORMATION:
APPLICANT: Flavell, Richard A.
APPLICANT: Fikrig, Erol
APPLICANT: Lam, Tuan T.
APPLICANT: Kantor, Fred S.
APPLICANT: Barthold, Stephen W.
TITLE OF INVENTION: NOVEL B. BURGDORFERI POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,469A
FILING DATE: 08-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,757
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: YU-102C1P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 130..711
US-08-118-469A-6

Query Match 84.0%; Score 16.8; DB 1; Length 805;
Best Local Similarity 90.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCATGCTGTTAATATTTT 20
|||||
Db 163 TCATGCTGTTAATATTTT 182

RESULT 10
US-08-909-119-6
Sequence 6, Application US/08909119
Patent No. 5807685
GENERAL INFORMATION:
APPLICANT: Flavell, Richard A.
APPLICANT: Fikrig, Erol

```

: APPLICANT: Lam, Tuan T.
: APPLICANT: Kantor, Fred S.
: APPLICANT: Hartbold, Stephen W.
: TITLE OF INVENTION: NOVEL B. BUKGONFERE POLYPEPTIDES
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: c/o FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10022
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/909,119
: FILING DATE: 11-AUG-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/118,469
: FILING DATE: 08-SEP-1993
: APPLICATION NUMBER: US 08/099,757
: FILING DATE: 30-JUL-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Haley Jr., James F.
: REGISTRATION NUMBER: 27,794
: REFERENCE/DOCKET NUMBER: YU-102CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 805 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 130..711
: US-08-909-119-6

Query Match      84.0%; Score 16.8; DB 1; Length 805;
Best Local Similarity 90.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTCCTGTTAATATTTT 20
    |||||  |||||  |||||
Db 163 TCATTCCTGTTAATATTTT 182

RESULT 11
US-09-240-639-7
: Sequence 7, Application US/09240639
: Patent No. 6350447
: GENERAL INFORMATION:
: APPLICANT: Chadwick, Brian Paul
: APPLICANT: Frischaut, Anna-Maria
: TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
: TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
: FILE REFERENCE: 9598-066
: CURRENT APPLICATION NUMBER: US/09/240,639
: CURRENT FILING DATE: 1998-01-29
: NUMBER OF SEQ ID NOS: 29
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 7
: LENGTH: 2119
: TYPE: DNA
```

```

: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (205)..(1599)
: US-09-240-639-7

Query Match      84.0%; Score 16.8; DB 4; Length 2119;
Best Local Similarity 90.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTCCTGTTAATATTTT 20
    |||||  |||||  |||||
Db 1933 TCATTCCTGTTAATATTTT 1952

RESULT 12
US-09-453-702B-42/C
: Sequence 42, Application US/09453702B
: Patent No. 6365723
: GENERAL INFORMATION:
: APPLICANT: Blatner, Frederick R.
: Burland, Valerie
: Perna, Nicole T.
: Plunkett, Guy
: Welch, Rod
: TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Quarles & Brady
: STREET: 1 South Plinckney Street
: CITY: Madison
: STATE: WI
: COUNTRY: US
: ZIP: 53701-2113
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Word Perfect 8.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/453,702B
: FILING DATE: 03-Dec-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/110,955
: FILING DATE: 04-Dec-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Seay, Nicholas J.
: REGISTRATION NUMBER: 27386
: REFERENCE/DOCKET NUMBER: 960296,95017
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (608) 251-5000
: TELEFAX: (608) 251-9166
: INFORMATION FOR SEQ ID NO: 42:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11613
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 42:
: US-09-453-702B-42

Query Match      82.0%; Score 16.4; DB 4; Length 11613;
Best Local Similarity 94.4%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATTCGTGTTAATATTTT 19
    |||||  |||||  |||||
Db 247 CATTCGTGTTAATATTTT 230

RESULT 13
```

```

US-08-852-807-12
; Sequence 12: Application US/08852807
; Patent No. 5861298
; GENERAL INFORMATION:
; APPLICANT: Debouck, Christine
; APPLICANT: Drake, Fred
; APPLICANT: Gowen, Maxine
; APPLICANT: Rood, Julie
; APPLICANT: Hastings, Gregg
; APPLICANT: Adams, Mark
; APPLICANT: Fraser, Claire
; APPLICANT: Lee, No. 5861298man
; APPLICANT: Kirkness, Ewen
; APPLICANT: Blake, Judith
; APPLICANT: Filzgerald, Lisa
; TITLE OF INVENTION: CATHEPSIN K GENE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,807
; FILING DATE: 07-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,942
; FILING DATE: 14-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/020,273
; FILING DATE: 17-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026,273
; FILING DATE: 26-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50006-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4326 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-852-807-12

```

```

Query Match      80.0%; Score 16; DB 2; Length 4326;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 ATTGCTGTATATT 18
    |||
Db 3174 ATTGCTGTATATT 3189

```

RESULT 14

```

US-08-852-807-1
; Sequence 1: Application US/08852807
; Patent No. 5861298
; GENERAL INFORMATION:
; APPLICANT: Debouck, Christine
; APPLICANT: Drake, Fred
; APPLICANT: Gowen, Maxine
; APPLICANT: Rood, Julie
; APPLICANT: Hastings, Gregg
; APPLICANT: Adams, Mark
; APPLICANT: Fraser, Claire
; APPLICANT: Lee, No. 5861298man
; APPLICANT: Kirkness, Ewen
; APPLICANT: Blake, Judith
; APPLICANT: Filzgerald, Lisa
; TITLE OF INVENTION: CATHEPSIN K GENE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,807
; FILING DATE: 07-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,942
; FILING DATE: 14-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/020,273
; FILING DATE: 17-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026,273
; FILING DATE: 26-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50006-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-852-807-1

```

```

Query Match      80.0%; Score 16; DB 2; Length 13674;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 ATTGCTGTATATT 18
    |||
Db 8556 ATTGCTGTATATT 8571

```

RESULT 15

```

US-09-071-606-11
; Sequence 11, Application US/09071606
; Patent No. 6136365
; GENERAL INFORMATION:
; APPLICANT: Wertz et al.
; TITLE OF INVENTION: Attenuation of Negative Stranded
; TITLE OF INVENTION: RNA Viruses By Rearrangement of Their Genes and Uses Thereof
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,606
; FILING DATE: May 1, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5936
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: 777-6908
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 basepairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHEICAL: no
; ANTI-SENSE: no
; US-09-071-606-11

```

```

Query Match          79.0%; Score 15.8; DB 3; Length 34;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CATGCTGTTAATATTTT 20
        |||||
Db      15 CATGCTGTTAGTTTTT 33

```

Search completed: December 10, 2002, 22:54:47
 Job time : 32.3876 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 433.631 Seconds

(without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-24

Perfect score: 20
Sequence: 1 tcatgtcgttaataatttt 20Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Genbankl :*

1: gb_da:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_da:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_of:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	6	AX306855	AX306855 Sequence
2	20	100.0	20	6	AX306865	AX306865 Sequence
3	20	100.0	467	6	A44526	A44526 Sequence 2
4	20	100.0	1789	6	E09772	E09772 The base se
5	20	100.0	2007	6	AR089410	AR089410 Sequence
6	20	100.0	2007	6	AR093610	AR093610 Sequence
7	20	100.0	2322	1	SABBP	SABBP
8	20	100.0	2322	6	E03736	E03736
9	20	100.0	2454	1	SEMECAPB	SEMECAPB
10	20	100.0	2455	6	E09771	E09771 The base se
11	20	100.0	2456	1	SAMECAPB	SAMECAPB
12	20	100.0	2456	6	AX110445	AX110445 Sequence
13	20	100.0	5596	1	SSK8MECA	SSK8MECA
14	20	100.0	6368	1	SSK3MECA2	SSK3MECA2
15	20	100.0	9047	1	SAMECAR11	SAMECAR11
16	20	100.0	21777	1	AB063173	AB063173 Staphyloc
17	20	100.0	26090	1	AB063172	AB063172 Staphyloc
18	20	100.0	39332	1	AB033763	AB033763 Staphyloc
19	20	100.0	58237	1	D86934	D86934 Staphylococ
20	20	100.0	68256	1	AB037671	AB037671 Staphyloc
21	20	100.0	290250	1	AP004822	AP004822 Staphyloc
22	20	100.0	298050	1	AP003129	AP003129 Staphyloc
23	20	100.0	349999	1	AP003358	AP003358 Staphyloc
24	19	95.0	150964	9	AC092374	AC092374 Homo sapi
25	19	95.0	201382	9	AC092721	AC092721 Homo sapi
26	18.4	92.0	159	11	G15937	G15937 human STS C
27	18.4	92.0	3720	9	S57132	S57132 COL16A1-tyr
28	18.4	92.0	5068	1	SSK1MECA	SSK1MECA
29	18.4	92.0	5387	9	HUMCOL16A	HUMCOL16A
30	18.4	92.0	5387	11	G28574	G28574 human STS S
31	18.4	92.0	6684	1	SSK1MECA	SSK1MECA
32	18.4	92.0	10520	1	AE013857	AE013857 Yersinia
33	18.4	92.0	68398	2	AC131045	AC131045 Homo sapi
34	18.4	92.0	73141	2	AC025123	AC025123 Homo sapi
35	18.4	92.0	97194	2	AC127723	AC127723 Rattus no
36	18.4	92.0	97786	2	AC111926	AC111926 Rattus no
37	18.4	92.0	97968	9	AF003530	AF003530 Homo sapi
38	18.4	92.0	111290	2	AC115462	AC115462 Rattus no
39	18.4	92.0	115184	2	AC127170	AC127170 Medicago
40	18.4	92.0	129677	2	AC127035	AC127035 Homo sapi
41	18.4	92.0	135631	9	AL512649	AL512649 Human DNA
42	18.4	92.0	141386	2	AC119454	AC119454 Rattus no
43	18.4	92.0	143813	9	AC002994	AC002994 Homo sapi
44	18.4	92.0	143909	9	AC104454	AC104454 Homo sapi
45	18.4	92.0	148661	2	AC126738	AC126738 Rattus no

ALIGNMENTS

RESULT 1
AX306855
LOCUS AX306855
DEFINITION Sequence 14 from Patent EP1160333.
ACCESSION AX306855
VERSION AX306855.1 GI:17894677
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.

REFERENCE
1 Taya, T., Ishiguro, T. and Saito, J.
Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
Patent: EP 1160333-A 14 05-DEC-2001;
JOURNAL

FEATURES Tosoh Corporation (JP)
Location/Qualifiers
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide capable of binding specifically to
mecca gene or RNA derived from said gene"

BASE COUNT 4 a 2 c 2 g 12 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTTAATATTTT 20
|||||
1 TCATTGCTGTTAATATTTT 20

DB 1 TCATTGCTGTTAATATTTT 20

RESULT 2
X306865 AX306865 20 bp DNA linear PAT 14-DEC-2001
ACCESSION Sequence 24 from Patent EP1160333.
VERSION AX306865.1 GI:17894687
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.

REFERENCE 1
AUTHORS Taya,T., Ishiguro,T. and Saito,J.
TITLE Oligonucleotides and method for detection of mecca gene of
methicillin-resistant Staphylococcus aureus
JOURNAL Patent: EP 1160333-A 24 05-DEC-2001;
Tosoh Corporation (JP)
Location/Qualifiers
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 4 a 2 c 2 g 12 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTTAATATTTT 20
|||||
1 TCATTGCTGTTAATATTTT 20

RESULT 3
A44526 A44526 467 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 2 from Patent WO9513395.
ACCESSION A44526
VERSION A44526.1 GI:2299344
KEYWORDS
SOURCE
ORGANISM
Staphylococcus aureus.
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1 (bases 1 to 467)
AUTHORS Springer,W. and Endermann,R.
TITLE SPECIFIC GENE PROBES AND METHODS FOR QUANTITATIVE DETECTION OF
METHICILLIN-RESISTANT STAPHYLOCOCCI
JOURNAL Patent: WO 9513395-A 2 18-MAR-1995;
BAYER AG (DE)
Other publication DE 4338119 950511.
Location/Qualifiers
1..467
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

FEATURES
source

BASE COUNT 187 a 73 c 85 g 122 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTTAATATTTT 20
|||||
210 TCATTGCTGTTAATATTTT 191

DB 210 TCATTGCTGTTAATATTTT 191

RESULT 4
E09772 E09772 1789 bp RNA linear PAT 29-SEP-1997
LOCUS The base sequence of modified mecca DNA.
DEFINITION E09772
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS
SOURCE
ORGANISM
Staphylococcus aureus.
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1 (bases 1 to 1789)
AUTHORS Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
TITLE NOVEL MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 2 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC
C12R1:19)
CC (C12P21/02,C12R1:19);
CC Strandedness: Double;
CC Topology: Linear;
FH Key
FH source
FT 1..1789 /organism="Staphylococcus aureus" FT CNS
FT 1..1608 /product="Modified mecca".
FT Location/Qualifiers
1..1789
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

BASE COUNT 735 a 263 c 302 g 489 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1789;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTTAATATTTT 20
|||||
835 TCATTGCTGTTAATATTTT 816

DB 835 TCATTGCTGTTAATATTTT 816

RESULT 5
AR089410 AR089410 2007 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 169 from patent US 5994066.
DEFINITION AR089410
ACCESSION AR089410
VERSION AR089410.1 GI:10016167
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2007)

AUTHORS Bergeron, M.G., Picard, F.J., Ouellette, M., and Roy, P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
FEATURES location/Qualifiers
SOURCE 1. 2007
BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
DB 1234 TCATTGCTGTTAATATTTT 1215

RESULT 6
LOCUS AR093610/c AR093610 2007 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 169 from patent US 6001564.
ACCESSION AR093610
VERSION AR093610.1 GI:10020359
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron, M.G., Ouellette, M., and Roy, P.H.
TITLE Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
FEATURES location/Qualifiers
SOURCE 1. 2007
BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TCATTGCTGTTAATATTTT 20
DB 1234 TCATTGCTGTTAATATTTT 1215

RESULT 7
LOCUS SARPBP 2322 bp DNA linear RCT 12-SEP-1993
DEFINITION Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
ACCESSION Y00688.1 GI:46628
VERSION Y00688.1
KEYWORDS penicillin-binding protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
REFERENCE 1 (bases 1 to 2322)
AUTHORS Song, M.D., Machi, M., Doi, M., Ishino, F., and Matsubashi, M.
TITLE Evolution of an inducible penicillin-target protein in methicillin-resistant Staphylococcus aureus by gene fusion
JOURNAL FEBS Lett. 221 (1), 167-171 (1987)
MEDLINE 87304805
PUBMED 3305073
REFERENCE 2 (bases 1 to 2322)
AUTHORS Kyte, J.C., Tesch, W., Birch-Machin, I., Reynolds, P.E.,

TITLE Barberis-Maino, L., Kayser, F.H., and Berger-Bachi, B.
JOURNAL Sequence comparison of mecA genes isolated from epidermidis
MEDLINE 91033056
PUBMED 2227446
COMMENT Data kindly reviewed (13.1.88) by Matsubashi.
FEATURES location/Qualifiers
SOURCE 1. 2322
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"
1. 2013
/note="penicillin-binding protein (AA 1-670)"
/codon_start=1
/transl_table=11
/protein_id="CA68684.1"
/db_xref="GI:46629"
/db_xref="SWISS-PROT:P07944"
/translation="MKKIKIPLILIVVVGFCIYVASKDK:INNTIDAIEDKFKQ
VYKDSYISKSDNGEVEETPERIKIYNSIGVGIQIDRKIKKSKKRVDAQKIK
TNGNIDIRNVGFNFVEDGMKRLMDHSVILPGMKDSIHIEELKSEBKKIDRNV
ELANTGTHMRIGIYPRNVSKKDYKAIKELISIEDYINNKIKIGIKMISFHKTYK
KMDRTLSDPAKRFHITNETSRNPPIGKATSHLGVGPINSEFIKOEKKGKIDA
VIGKGLLEKLYDKLQHDGCVKPIVAVDQSNITAHLLIEKKKIDKDIQITIDAKV
OKSIYNNKKNIDYGSCTAHPQICELALVSPSYDVYFPMQSNIEYNNKLTEDKEP
LANKFOITTSPTGOKILTAMIGLNKTLDDKTSYKIDGKMGOKSMGCVNTRYEV
VNGNIDIKOATIESDNIFFARVALLEGSKREKMKLGVEDIPSYPYNAQISNK
MLDNEIILADSGVGGELLINPVQILISYSLAENGNINAPHILIKDKNNVYMKNIIS
KENINLNDGQGVNKTTHKEDTIRSYANLIGKSGTALMKKOCETROQIGPISYK
DNPMMATINVDVODKGMASYNKISCKYVDELYENCKRYDIDE"

BASE COUNT 940 a 324 c 389 g 669 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 2322;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
DB 1240 TCATTGCTGTTAATATTTT 1221

RESULT 8
LOCUS E03736/c E03736 2322 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence of PBP2' gene for determination of methicillin resistance.
ACCESSION E03736
VERSION E03736.1 GI:2171951
KEYWORDS JP 1992169200-A/9.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2322)
AUTHORS Watanabe, Y., Nakamura, E., Teraoka, H., Wada, K., Minamide, W., and Murakami, K.
TITLE DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
JOURNAL Patent: JP 1992169200-A 9 17-JUN-1992;
COMMENT SHIONOGI & CO LTD
OS (methicillin resistant)staphylococcus aureus
PN JP 1992169200-A/9
PD 17-JUN-1992
PF 31-OCT-1990 JP 199026708
PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI, MINAMIDE WAKIO, MURAKAMI KAZUHISA
PC C12Q1/68.C12N15/11;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FH key location/Qualifiers


```

FT      misc_feature      1..2322
FT      FT                /note='PBP2' gene for determination of FT
FT      FT                methicillin
FT      FT                resistance'
FEATURES
  source      1..2322
               /organism="unidentified"
               /db_xref="taxon:32644"
BASE COUNT   939 a 324 c 390 g 669 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 2322;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 20
        |||||||
Db      1240 TCATTGCTGTTAATATTTT 1221

RESULT 9
LOCUS      SMCAPB      2454 bp      DNA      linear      BCF 12-SEP-1993
DEFINITION S.epidermidis meca gene for PBP2' (penicillin binding protein 2').
ACCESSION  X52592.1
VERSION     X52592.1 GI:46993
KEYWORDS    meca gene; methicillin resistance; penicillin-binding protein;
             penicillin-binding protein 2'.
SOURCE      Staphylococcus epidermidis
ORGANISM    Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1 (bases 1 to 2448)
            Ryfel,C.
            Direct Submission
            Submitted (05-APR-1990) Ryfel C., University of Zuerich, Inst of
            Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE   2 (bases 1 to 2454)
            Ryfel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
            Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
            Sequence comparison of meca genes from methicillin-resistant
            Staphylococcus aureus and Staphylococcus epidermidis
            Gene (1990) In press
            3 (bases 1 to 2454)
            Ryfel,C.
            Direct Submission
            Submitted (23-JUL-1990) Ryfel C., University of Zuerich, Inst of
            Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE   4 (bases 1 to 2454)
            Ryfel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
            Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
            Sequence comparison of meca genes isolated from
            methicillin-resistant Staphylococcus aureus and Staphylococcus
            epidermidis
            Gene 94 (1), 137-138 (1990)
JOURNAL     MEDLINE      9103056
            PUBMED      2227446
COMMENT     See also <X52593-4> and <Y00688>.
            Data kindly reviewed (23-JUL-1990) by C. Ryfel.
FEATURES
  source      1..2454
               /organism="Staphylococcus epidermidis"
               /strain="WT55"
               /db_xref="taxon:1282"
               /clone="MT80/MT79"
               80..85
               /note="35 region"
               101..105
               /note="10 region"
               130..134
               /note="ribosome binding site"
               141..2159
               /note="primary transcript"
               141..2147
CDS

```

```

/note="PBP2' (AA 1 - 668)"
/codon_start=1
/transl_table=11
/protein_id="CAA36828.1"
/db_xref="GI:46994"
/db_xref="SPTREMBL:054113"
/translation="MKRIKIVPLIVVVGFIYFVASKDEINNTIDAIEDKNEKQ
YKDSYISKSDGVEEMTERPIKIYNSGVKDINODRKIKVSKNRKVDVQYKIK
TNYGNDIRNVQFNVKEDGMKMDMDSYIIPGMKDOSIHIENIKSHCKIIDDYK
ELANTGTAEVIGIVPKRVSKKDYKAIKALKLSISHDYTKQMOMNVQDPTVPLKTVK
KMDYISDFAKRHILTNTEFESRNPUGKATSHIIGYGPINSEIKQEVKGYDDA
VIGKRGLEKLYDKLQHDGYRYTVIVDQSNNTIAHTLEKKRKDEKDIQLTIDAAYQK
SIYNNMKNDYSGSTAIHPQTGELLAVSPSYDVPFMYGMSNEEYKLTEDKKEPL
NKFQITSPSGSTOKILITAMIGLNKTLDDTKSYKIDGKMGKSMGKYNTRYEVYN
GNIDLKQALSSDNIPFARVALEIGSKREKMGKRIQGEIDIPSDYPIYNAOISKNV
DNEILLADSGGCGELLINPVQILSTYSALENNCGINAPHLIKDKKVMYKKNISKE
NINLLTDGMQVYVKNKTHKEDIYRSYANLIGKSGTALAKKQGTQRQIGWISYQKDN
PNMKMAINVKDVQDKGMASYNMKISGYVDLEYENGNKRYDIDE"
441..448
/note="altaaac was ac in [1]"
/citation=11
641..643
/note="agc was ac in [1]"
/citation=11
652..653
/note="ta was tta in [1]"
/citation=11
731..733
/note="caa was ca in [1]"
/citation=11
780..781
/note="ct was ctt in [1]"
/citation=11
old_sequence
old_sequence
old_sequence
old_sequence

BASE COUNT   997 a 345 c 714 t
ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 2454;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 20
        |||||||
Db      1374 TCATTGCTGTTAATATTTT 1355

RESULT 10
LOCUS      E09771/C      2455 bp      RNA      linear      PAT 29-SEP-1997
DEFINITION The base sequence of meca DNA.
ACCESSION  E09771
VERSION     E09771.1 GI:22026400
KEYWORDS    JP 1995209294-A/1.
SOURCE      Staphylococcus aureus.
ORGANISM    Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1 (bases 1 to 2455)
            Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
            NOVEL 'MECA PROTEIN' CODING DNA THEREFOR, AND DETECTION METHOD FOR
            METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
            Patent: JP 1995209294-A 1 11-AUG-1995;
            KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
            OS Staphylococcus aureus
            PN JP 1995209294-A/1
            PD 11-AUG-1995
            PF 10-JAN-1994 JP 1994012226
            PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
            MASAHISA,
            PI SUGURO KAZUYA
            PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,(C12N1/21, PC
            C12R1:19),
            PC (C12P21/02,C12R1:19);
            CC strandedness: Double;
            CC topology: Linear;

```

```

FH      Key      Location/Qualifiers
FH      source      1. 2455
FH      FT          /organism='Staphylococcus aureus' FT      CDS
FH      FT          134. 2146 /product='meca protein'.
FEATURES
source      1. 2455
            /organism='Staphylococcus aureus'
            /db_xref='taxon:1280'
BASE COUNT      997 a      344 c      401 g      713 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 2456;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 TCATTGCTGTTAATATTTT 20
        11111111111111111111
        1373 TCATTGCTGTTAATATTTT 1354

```

```

RESULT 11
LOCUS      SAMCABP      2456 bp      DNA      linear      BCT 12-SEP-1993
DEFINITION      S. aureus meca gene for PBP2' (penicillin binding protein 2').
ACCESSION      X52593
VERSION      X52593.1 GI:46610
KEYWORDS      meca gene; methicillin resistance; penicillin-binding protein;
              penicillin-binding protein 2.
SOURCE      Staphylococcus aureus.
ORGANISM      Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE      1 (bases 1 to 2456)
AUTHORS      Ryffel, C.
TITLE      Direct Submission
JOURNAL      Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
              Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE      2 (bases 1 to 2456)
AUTHORS      Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P.E.,
              Barberis-Maino, L., Kayser, F.H. and Berger-Bachli, B.
TITLE      Sequence comparison of meca genes isolated from
              methicillin-resistant Staphylococcus aureus and Staphylococcus
              epidermidis
JOURNAL      Gene 94 (1), 137-138 (1990)
MEDLINE      91033056
PUBMED      2227446
COMMENT      See also <X52592>, <X52594> and <Y00688>.
              Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source      1. 2456
            /organism='Staphylococcus aureus'
            /strain='NCTC8325, Isolate-BB270'
            /db_xref='taxon:1280'
            /clone_lib='EMBL-3'
            80. 85
            /note='--35 region'
            101. 105
            /note='--10 region'
            130. 134
            /note='--10 region'
            141. 2153
            /note='ribosome binding site'
            141. 2147
            /note='primary transcript'
            141. 2147
            /note='PBP2' (AA 1-668)'
            /codon_start=1
            /transl_table=11
            /protein_id='CAA36829.1'
            /db_xref='GI:46611'
            /db_xref='SPTREMBL:053707'
            /translation='MKKIKIVPLILIVVVGSGIYFASKKEINNTIDAIEDKNEKO
              VTKSSYISKNGEYTERPIKITYNSIGVADINIDRKIKVSKNKKRVIAOTKIK
              TNYGNIDRNVPFVKEDGMKLDWDHSVITPGMKDSDIHENLSEKSKTLDRNVP

```

```

ELANTGTHMRILGIVPKNVSKKDYAKIAKEISISEDY INNKMIKIGYKMI1P5THPKTVK
KMEDEYLSDFAKKPHLTTESETSRNRYPLEKATSHLIGYGVGINSELEKOEKYGKDYK
VICKKGEKLYDKRQKHEDGYRRTIYDONSRTIARLEKKKCKXDLTLTDKAYOK
SYNNMKNDYSGSRIHPOTGELLALVSTPSYDIPREYIGNSNEKYLTEDEKKEPL
NKFOITTSPTGTOKILTAMIGLNNNTLDDKTSYKIDGKWKDCKSMGYNVTRIEVN
CENIDLOAIESSDNIFFARVALELOSKKPEKGMKICGEDI1PSIYPPYNAOI1SKNI
DNEILLADSGYGGCEILLINPYOJIS1SYALENNNGMINAPHILKIPYKNVYKNI1SKK
NINILLNDGMOOVNKTKEED1YRSYANLIGKSGTAEIKMKOCFSGROI1SYDKDN
PMMMAIVKRVOKMGASYNKISGYKYEDELKNGKKNKYDIDE'
BASE COUNT      1001 a      344 c      396 g      715 t
ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 2456;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 TCATTGCTGTTAATATTTT 20
        11111111111111111111
        1374 TCATTGCTGTTAATATTTT 1355

```

```

RESULT 12
LOCUS      AX110445/c      2456 bp      DNA      linear      PAT 30-APR-2001
DEFINITION      Sequence 1178 from Patent WO0123604.
ACCESSION      AX110445
VERSION      AX110445.1 GI:13926737
KEYWORDS
SOURCE      Staphylococcus aureus subsp. aureus NCTC 8325.
              Staphylococcus aureus subsp. aureus NCTC 8325.
              Bacteria; Firmicutes; Bacilli res; Staphylococcus.
              1 (bases 1 to 2456)
              Bergeron, M.G., Boissinot, M., Huelsky, A., m Nard, C., Ouellette, M.,
              Picard, F.J. and Roy, P.H.
              Highly conserved genes and their use to generate probes and primers
              for detection of microorganisms
              Patent: WO 0123604-A 1178 05-APR-2001;
              Infectio Diagnostic (I.D.I.) INC. (CA)
              Location/Qualifiers
              1. 2456
              /organism='Staphylococcus aureus subsp. aureus NCTC 8325'
              /db_xref='taxon:93061'
BASE COUNT      1001 a      344 c      396 g      715 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 2456;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 TCATTGCTGTTAATATTTT 20
        11111111111111111111
        1374 TCATTGCTGTTAATATTTT 1355

```

```

RESULT 13
LOCUS      SSR8MECA/c      5596 bp      DNA      linear      BCT 16-JAN-1998
DEFINITION      S.sciuri meca gene, strain K8 (ATCC700063).
ACCESSION      Y13096
VERSION      Y13096.1 GI:2791919
KEYWORDS      meca gene; mecI gene; NFOR101; NFOR78; ORF142.
SOURCE      Staphylococcus sciuri.
ORGANISM      Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE      1 (bases 1 to 5596)
AUTHORS      Wu, S., de Lencastre, H. and Tomasz, A.
              Genetic organization of the meca region in methicillin-susceptible
              and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL      J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE      98101461
PUBMED      9440511
REFERENCE      2 (bases 1 to 5596)
AUTHORS      Wu, S.

```

TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences X53818, X54660, L14020, X52593, Y09223.
FEATURES
source
1..5596
/organism="Staphylococcus sciuri"
/strain="K8 (ATCC700063)"
/sub_species="rodentius"
/db_xref="taxon:1296"
1..236
/gene="NTORF78"
/gene="NTORF78"
/codon_start=3
/transl_table=11
/protein_id="CAA73540.1"
/db_xref="GI:2791920"
/db_xref="SPTREMBL:054284"
/translation="AFKLRPDCSTSYLNLLIEDHRIHKVTKRQSYNTAKNTLK
GICITAYLKKNRSLQITGFSPCHEISIMLAS"
complement(485..856)
/gene="mecI"
/gene="mecI"
complement(485..856)
/gene="mecI"
/codon_start=1
/transl_table=11
/product="MecI protein"
/protein_id="CAA73545.1"
/db_xref="GI:2791921"
/db_xref="SPTREMBL:054285"
/translation="MDNKTYEISSAEWEVNNI..MKRYASANYIEETIOMOKDSPKT
IRTLIRLYKGFIDRDKNKIKQYSLVESDQIKYTSKNFINKVYKGGNSLVNLF
VERKDIODEIEIRNLNKK"
complement(join(856..2613,2620..2626,2638..2643))
gene
/gene="mecR1"
complement(856..2613)
/gene="mecR1"
/codon_start=1
/transl_table=1
/product="MecR1 protein"
/protein_id="CAA73546.1"
/db_xref="GI:2791922"
/translation="MLSSFMLSLIISLLTICVILVRLMYIKYTONIMSHKWLVL
VSTLIPILIPYKISNTPFSKDMNRNVDSTSSVSHMLDGOSSVTDLAINVQFET
SNITVYMLLIMVFGSLCLPYMIKAPQIDVIRKSSLESSYLNERLKYCOSKQFYK
HITISYSSINDPNVFGLVKSOIVLPVVEVTMDKELEYLILHELSHVKSQDLIFNO
LYVFERKIFPNPALYISKTMDCCEKQCDRNLKILNREHTRVGSSTIKGLS
QHINNAQYILGFSNINIKERKITALYDSKPRNRKRIVATVCSISLILQPLLS
AHVQODKYEETNASTKRLNQLAPYKFGDSVFLNEREQATSYNEPESKQRYSPNT
YKJYLALMAPDQNLISLNTHQOMDKHQYPRKENVQDQNISSMKYSVNMYPLNHL
LRQDEKSYIDLIFYGNELISGNENYNESLSLKISALIDQVNI..KNMKQNMHFPNKA
IKVENSMTLKQDHYKYVGKTCGICIVNHKANGWFGVYVETKQNTYVFATHLKCEDNA
NGERAOOISERILKEMELI"
complement(865..869)
gene
/gene="mecI"
complement(865..869)
RBS
/gene="mecI"
complement(2620..2626)
/gene="mecR1"
complement(2638..2643)
-10_signal
/gene="mecR1"
2652..2657
/gene="mecA"
2652..2657
-35_signal
/gene="mecA"
complement(2663..2668)
/gene="mecR1"
complement(2663..2668)
/gene="mecR1"
2676..4719
/gene="mecA"
2676..2681
-10_signal

RBS
/gene="mecA"
2702..2707
/gene="mecA"
2713..4719
/gene="mecA"
/codon_start=1
/transl_table=11
/product="MecI protein"
/protein_id="CAA73547.1"
/db_xref="GI:2791923"
/db_xref="SPTREMBL:054286"
/translation="MKKIKVPLILIVVVGFIYFASKKEINNTIDAIEDKFNKO
VYKSSYSIKSDNGEVEMERPIKIVYSLVGVQDNIODRKIKVSKKKRVADQYKIK
TNYGINDIRNVQFNPKEDGMMKLDMDISVYIPGQKQSHIENLSEKGIIDRNV
ELANTGAYEIGVIPKRVSKDKAIKELISIDYIKQMDQNVQDDTPVPLKTYK
KMDYELSDFAKKFPLTNTNESRNPLEKATSHLGVGPINSBELKQYKQKIDA
VIGKGLLEKLYDKKLOHEIDYRVYIVDONSNTLAHTLIEKKKDKGNDIQLTIDAKVOK
SIYNNMKNDGSGTAIHPOTGELLATVSTPSDYVPYPMYQMSNEEYKLTEDKKEPLL
NKQIITTSPSGSTOKILFAMIGLNKKTLDKTSYKIDGKQKDSMGVQVTVREYVN
GNIDLKQATSSSDNIFPRAVALDELGSKKFKKMKKILGVGDIPSDYFPYVAOISNNKL
DNEILADSCGQCEILINPYQLISYSALENNGNINAPHLKQTKKKVYKKNIIKRE
NINILTDGMOQVNVKTKHEDIYRSYAWLICKSGTAEILMKQCEGTGQIGFISTDKDN
PNMMAINVDVODKMAVNAKISGVYDELVENCKKYYDIE"
complement(4765..5266)
/gene="ORF142"
complement(4765..5193)
/gene="ORF142"
/codon_start=1
/transl_table=11
/protein_id="CAA73548.1"
/db_xref="GI:2791924"
/db_xref="SPTREMBL:054520"
/translation="MKYDDPIVCEPFTKSLIHITFEELIQTATTPDQYMHIDKEKAE
OSRKGIIASGMHTLSISPKLWPEKGEYVAGTQMNWVKIKIPVYPCNTLTVIAE
ITNKSITKKEGLVTSISTYNEENELVFRGEVYALINNS"
complement(5200..5205)
/gene="ORF142"
complement(5238..5243)
/gene="ORF142"
complement(5261..5266)
/gene="ORF142"
complement(5290..5596)
/gene="NTORF101"
complement(5290..5596)
/gene="NTORF101"
/codon_start=2
/transl_table=1
/protein_id="CAA73549.1"
/db_xref="GI:2791925"
/db_xref="SPTREMBL:054616"
/translation="SPNVVIVKLAIEIMPQYNRAVIFHTTSPFEDMKRTLLDYCNKIV
NTEDAKLTAKKVKVWKGAGYELNWTGVNKKPARANQLANMCVDCIFFDNADKMYHLSSO"
BASE COUNT 1991 a 856 c 821 g 1928 t
ORIGIN
Query Match 100.0% Score 20; DB 1; Length 5596;
Best local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCATGCTGTTAATATTTT 20
DB 3946 TCATTGCTGTATATTTT 3927
RESULT 14
SSK3MECA2/c SSK3MECA2 6368 bp DNA linear BCT 16-JAN-1998
LOCUS S_sciuri_mecA2 gene, strain K3 (MM2).
DEFINITION Y13095
ACCESSION Y13095.1 GI:2791912
VERSION Y13095.1
KEYWORDS CTORF261 gene; mecA2 gene; mecI gene; NTORF101; ORF142.
SOURCE Staphylococcus sciuri.
ORGANISM Staphylococcus sciuri

REFERENCE 1 Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic Organization of the mecA region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 96101461
PUBMED 9440511
REFERENCE 2 (bases 1 to 6368)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences U14020, X52593, Y09223.
FEATURES
source Location/Organism
1. .6368
/organism="Staphylococcus sciuri"
/strain="K3 (M2)"
/sub_species="rodentilis"
/db_xref="taxon:1296"
gene complement(1. .883)
/gene="CtorF261"
complement(<1. .784)
/gene="CtorF261"
/codon_start=1
/transl_table=11
/protein_id="CAA73539.1"
/db_xref="GI:2791913"
-35_signal /db_xref="SPTREMBL:O54280"
gene /translation="MENILNINDNEKRVLRREIYNHHNISRTOISKNEINKATISSIL
NKLKYSLVNEVGEGDSTSGGRKPIILKNVHLGYFSLDLYTSVEVMYNDGY
IKHESYLDPEKVSSTISITIKHTIDIOEKIDTNGILGYSIHGYVDNEHYTLPE
HETEGISIAKKIKETITVPVVEFANLSALYERFNHNSLYNMLALSTHKGIGAGL
IINQOLRGANGEGEIGKTLVSKVSONVEIFKIEDIFSOEA"
RBS complement(791. .797)
/gene="CtorF261"
complement(855. .860)
/gene="CtorF261"
complement(878. .883)
gene /gene="CtorF261"
complement(1257. .1628)
/gene="mecI"
complement(1257. .1628)
CDS /gene="mecI"
/codon_start=1
/transl_table=11
/product="MecI protein"
/protein_id="CAA73540.1"
/db_xref="GI:2791914"
-35_signal /db_xref="SPTREMBL:O54281"
gene /translation="MDNKTYEISAEWEVNNIIMKKYASANNIIEEIQMRDHPKT
IKRLIRLYKKCFIDRKKDKKIPQYISLVEESDIKKTYSKFIKKYKGGFNSLVLP
VEKEDLSQDEIEELRNILNKK"
RBS complement({join(1628. .3385,3392. .3398,3410. .3415)})
/gene="mecR1"
complement(1628. .3385)
/gene="mecR1"
/codon_start=1
/transl_table=11
/product="MecR1 protein"
/protein_id="CAA73541.1"
/db_xref="GI:2791915"
-35_signal /db_xref="SPTREMBL:O54282"
gene /translation="MLSSFLMICLISLLTTCVFLVRLMLYIKYTQIMSHKIMLVI
VSTLPIIPYKISNFTFSKDMNRNVSDDTTSVSHMLDGOSSVTDLAINVQFET
SNITMILLIWFGLCLFLYKIKAFQIDIVIKSSLESSLYNERLKVCOCKQFYFK
HRTISYSSNIDNPMVEGLVRSQIVLPVVVEITMDKEIEYIILHELSHVSHDIFNQ
LYVFKMIEFNPALYISKTMNDCEKVCDDRYLKLINRHEIRYGESTIKGSIIS
OHINVAAGYLGFNSNIKEKRVYIALYDMPKPNRKRIVAYIVCSISILGIPILS
AHVOODKYEFTNVSKYKLNOLAPYFKGDSFVLVNEEQAYSTNPEPSQORSPNS
KYTIALMAFDONLISNHTEOODKHQYFPKENDQNLNNSKKYSNNYTENLNKH
LRDEVKSTIDLIEIGNEEISGNENTWESSLKISALEOVNLLKDMQOHNNHFONKAI
EKVNSMTLKQKDTYKVGKTGTGIVNHRKANGFVGIVETKDMTYFATHLKGEDNA

gene NGEKAOISERLKEMLI"
complement(1636. .1640)
/gene="mecI"
complement(1636. .1640)
RBS /gene="mecI"
complement(3392. .3398)
RBS /gene="mecR1"
complement(3410. .3415)
-10_signal /gene="mecR1"
complement(3429. .3429)
gene /gene="mecR1"
complement(3429. .3429)
-35_signal /gene="mecA2"
complement(3433. .3438)
/gene="mecR1"
complement(3433. .3438)
gene /gene="mecR1"
complement(3448. .5491)
3448. .5491
/gene="mecA2"
3448. .3453
/gene="mecA2"
3474. .3479
RBS /gene="mecA2"
3485. .5491
CDS /gene="mecA2"
/codon_start=1
/transl_table=11
/product="MecA2 protein"
/protein_id="CAA73542.1"
/db_xref="GI:2791916"
-35_signal /db_xref="SPTREMBL:O54283"
gene /translation="MKTKIYPLIIVVVGFGIYFVSKKEENNTIDAIGKNFKQ
VYKDSYISKSDNCEVENTERP IRYNSLGVKDINIDOK I KYSKNKKRDAQYK I K
TYNGNIDRNVQFNVEYEDGMKLPMDHSVILIPGQKQSIHIFNLKSRGKILIRNNV
ELANTGTAYEIGIYVAPKNYSKKDYKALAKELISEDY IKQKDDMMVODDTPVLYKTV
KMEYLSDFKAPHLTNETESRNPLEKATSHLGYGPIINSEILOKEKVGKDYK
VIGKKGLEKLYDKKLOHEDGYRVTIVDNSNTIATLIEKKRKGKIDQZLIDAKYOK
SIYNMKMDGSGGTAIHPOTELALVSTPSYDYPTMTGSKSNEEYNKLTIDKKEPL
NKFOITTSYPSGTOKILYAMIGLNKTYLDDKTSYKIDGGMQDSMGQVNTREYVN
DNILDKOATIESSDNIFFARVALIELGSKKFEKGMKLAGHDJPSIDYFYNQOISKNL
DNELLADSGYGOCEIILINPOILSYSALENNGNINAPHLIKDTKNVKKNNIISKE
NINLTDGMOOVNKTREKEDIYRSYANLIGSGTAELKMKOGEGRIQWGISYDKDN
PHLMALINVKDVPKGMASNAKISGKYIDELYENKKNKYIDE"
complement(5537. .6038)
/gene="ORF142"
complement(5537. .5965)
CDS /gene="ORF142"
/codon_start=1
/transl_table=11
/protein_id="CAA73543.1"
/db_xref="GI:2791917"
-35_signal /db_xref="SPTREMBL:O54520"
gene /translation="MKYDDEYVGEYFPTKSLHITTEEIIOFATTFDPQYMHILKEKAE
OSRFGIASGMHTLSISTEKLAVEEGGEEVAVGTOMNNYKFIKPYPGNTLVIAE
ITNKKSIKKENGLTVSLSTNENDEIYKGEVALLINNS"
RBS complement(5972. .5977)
/gene="ORF142"
complement(6010. .6015)
-10_signal /gene="ORF142"
complement(6033. .6038)
-35_signal /gene="ORF142"
complement(6062. .6368)
gene /gene="NTORF101"
complement(6062. .6368)
CDS /gene="NTORF101"
/codon_start=2
/transl_table=11
/protein_id="CAA73544.1"
/db_xref="GI:2791918"
-35_signal /db_xref="SPTREMBL:O54616"
gene /translation="SPNVVLAKLAEEIIMPQYNAVIFHTTSFREDMPTLLDYCNAKIV
NTEPAKTLKAIVKAVKAGYELANVTYVTKPARANQLANMGVDGIFTDNADKMHVLSQ"

BASE COUNT 2230 a 998 c 884 g 2256 t

/translation-"MNYFRYKQFNKDVITVAVGYLYLRYTLSTYRDISSEILBERGVNVHH
STVYRWQCEYAPILYOIMKKKKKAYKKRIDETVYIKIKGKWSYLYRAIDAEGHTLDI
WLRKORDNHSATAFIKRLIKQKPKOKVITTDAPSTKVMAMKVIKAFKLPDCHCTSK
YJNNLIEQDHRHIKVKRTYOSINTAKNTLKGIECIYALYKKNRSLQIYG+SPCHEI
SIMLAS"

BASE COUNT 3099 a 1469 c 1257 g 3222 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; length 9047;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
Db 4705 TCATTGCTGTTAATATTTT 4686

Search completed: December 10, 2002, 20:17:07
Job time : 437.756 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 ; Search time 1025.47 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-24

Perfect score: 20

Sequence: 1 tcaatgctgtaataatttc 20

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthu:*
3: em_estin:*
4: em_estlu:*
5: em_estlo:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vtl:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	95.0	436	17	A0063885 HS_2186_B
2	18.4	92.0	205	14	BM874740 1a607h11
3	18.4	92.0	274	9	AA770215 ab72h12.s
4	18.4	92.0	283	9	AA821323 v867d07.r
5	18.4	92.0	289	12	BF223892 7q36a07.x
6	18.4	92.0	298	9	A1656575 tt51h06.x

C	7	18.4	92.0	332	9	A1565925	tr94h12.x
C	8	18.4	92.0	336	9	AA682251	ab52d11.s
C	9	18.4	92.0	337	10	AW192414	X183c10.x
C	10	18.4	92.0	339	9	AA620929	a196d02.s
C	11	18.4	92.0	345	9	A1644998	v867d07.y
C	12	18.4	92.0	352	10	AW594048	h944d02.x
C	13	18.4	92.0	356	9	AA678445	ah01c08.s
C	14	18.4	92.0	382	9	A1679677	tue5c09.x
C	15	18.4	92.0	383	14	T29062	EST67294.hu
C	16	18.4	92.0	390	9	A15926275	vs67d07.x
C	17	18.4	92.0	390	9	A1582517	w043q08.x
C	18	18.4	92.0	395	9	AU088039	ts01h09.x
C	19	18.4	92.0	395	9	AA791476	vs66f07.r
C	20	18.4	92.0	402	9	A169276	wp81g01.x
C	21	18.4	92.0	405	9	AA330228	EST33974
C	22	18.4	92.0	411	9	A1686616	LX08h12.x
C	23	18.4	92.0	437	9	A1783833	tu79f01.x
C	24	18.4	92.0	456	14	W95831	zc09c10.r1
C	25	18.4	92.0	456	14	W96115	zc09c10.s1
C	26	18.4	92.0	463	12	BF058423	7K30f11.x
C	27	18.4	92.0	479	9	AA682133	OL48C02.s
C	28	18.4	92.0	485	9	A1589349	lr61c11.x
C	29	18.4	92.0	486	9	A1206895	qr35a11.x
C	30	18.4	92.0	488	9	AA088202	zk71c02.s
C	31	18.4	92.0	488	9	AA088202	zk71c02.s
C	32	18.4	92.0	489	9	A1089082	ou86h10.s
C	33	18.4	92.0	494	9	A1624537	ts30a08.x
C	34	18.4	92.0	494	10	AW950459	EST362529
C	35	18.4	92.0	502	10	A1131021	qb82c12.x
C	36	18.4	92.0	502	10	BE645315	7e60c05.x
C	37	18.4	92.0	518	12	BF063391	7h89c02.x
C	38	18.4	92.0	521	17	BH185493	027.L-23-
C	39	18.4	92.0	521	17	CNS0706W	TL622442.T3
C	40	18.4	92.0	531	10	BE049264	xw98g05.x
C	41	18.4	92.0	549	14	BM672887	UI-R-C00-
C	42	18.4	92.0	558	9	A1801156	co85h11.x
C	43	18.4	92.0	558	12	Hf434543	7o78b04.x
C	44	18.4	92.0	569	13	BM314325	1953a12.x
C	45	18.4	92.0				

ALIGNMENTS

RESULT 1
A0063885/c
LOCUS
DEFINITION
HS_2186_H1.C01_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2186 Col=1 Row=N, DNA sequence.

ACCESSION
A0063885
VERSION
A0063885.1 GI:3379783
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Hood, L., Kulkarny, S., Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 436)
Mahairas, G.G., Wallace, J.C., Smith, R., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and

TITLE
JOURNAL
MEDLINE
COMMENT
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2186 row: N column: 1

Class: BAC ends
High quality sequence stop: 436.

FEATURES
Source
Location/Qualifiers
1. 436
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT
147 a 87 c 62 g 133 t 7 others

ORIGIN
Query Match 95.0%; Score 19; DB 17; Length 436;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 19
|||||
198 TCATTGCTGTTAATATTTT 180

RESULT 2
BM874740 205 bp mRNA linear EST 07-MAR-2002
LOCUS la07h11.y1 8 5 week embryo anterior tongue 8 5 EAT Homo sapiens
DEFINITION cDNA 5' mRNA sequence.
ACCESSION BM874740
VERSION BM874740.1 GI:19242406
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 205)
Tidwell,R., Clifton,S., Marra,M., Hillier,L., Page,D., Martin,J.,
Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Rilter,E., Bennet,J.,
Ronko,I., Tsagarisshvili,R., Belaygorod,L., Grow,A., Maguire,L.,
Waterston,R. and Wilson,R.
Washu Stem cell EST Project
Unpublished (2002)
TITLE JOURNAL
COMMENT Contact: Rose Tidwell
Washu Stem cell EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Tissue provided by Rose Tidwell Library was constructed by Yulia
and Rose Tidwell Library re-arrayed by Rose Tidwell DNA sequencing
by: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell
(rtidwell@genetics.wustl.edu)
putative full length read
vector to vector length is 206
Seq primer: -40RP from Gldco.
Location/Qualifiers
1. 205
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="8 5 week embryo anterior tongue 8 5 EAT"
/dev_stage="8.5 week embryo"
/lab_host="DH10B"
/note="Vector: PAMPI; Site: 1: no restr sites used in
cloning; Site 2: no restr sites used in cloning; UDG
cloning; oligo dt primed 1st strand cDNA library"

BASE COUNT
82 a 23 c 37 g 62 t 1 others

ORIGIN
Query Match 92.0%; Score 18.4; DB 14; Length 205;
Best Local Similarity 95.0%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
Db 129 TAATTGCTGTTAATATTTT 148

RESULT 3
AA770215/c 274 bp mRNA linear EST 29-DEC-1998
LOCUS ah72h12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321223 3'
DEFINITION similar to SW:CAIF_HUMAN 007092 COLLAGEN ALPHA 1(XVI) CHAIN
PRECURSOR.; mRNA sequence.
ACCESSION AA770215
VERSION AA770215.1 GI:2821453
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 274)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
cDNA Library Preparation: M. Hento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCG; clone distribution information can be
found through the I.M.A.G.E. consortium/LLNL at:
www.bio.llnl.gov/btrp/image/image.html
Insert Length: 418 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
1. 274
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="1321223"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCCGCAATTTTATTTT 3'].
(Pharmacia), digested with Not I and Eco RI adaptors
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
80 a 65 c 57 g 72 t

ORIGIN
Query Match 92.0%; Score 18.4; DB 9; Length 274;
Best Local Similarity 95.0%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
Db 46 TAATTGCTGTTAATATTTT 27

RESULT 4
AA821323 283 bp mRNA linear EST 17-FEB-1998
LOCUS vs67d07.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION IMAGE:1151341 5', mRNA sequence.
ACCESSION AA821323
VERSION AA821323.1 GI:2891191
KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 283)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, N., Dietrich, N., Dubuque, T., Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and Waterston, R.
TITLE The Mashu-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
Mashu-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:624549
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 248.
Location/Qualifiers
1..283
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1151341"
/clone_1lb="Stralagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mce. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACACAG 3' -3' adaptor sequence: 5' CTCGACGTTTTTTTTTTTTTTTTTTT 3' "

BASE COUNT 87 a 49 c 53 g 94 t
ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 283;
Best Local Similarity 95.0%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 TCATTGCTGTATATTTT 20
Db 165 TTATTGCTGTATATTTT 184

RESULT 5
LOCUS BF223892 289 bp mRNA linear EST 30-MAR-2001
DEFINITION B936a07.x1 NCI CGAP GC6 Homo sapiens CDNA clone IMAGE:3700141 3'
Similar to SW:CAIF_HUMAN Q07092 COLLAGEN ALPHA 1(XVI) CHAIN
PRECUSOR. : mRNA sequence.
ACCESSION BF223892
VERSION BF223892.1 GI:11131079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 289)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov.
Location/Qualifiers
1..289
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3700141"
/clone_1lb="NCI CGAP GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pTRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 83 a 70 c 67 g 69 t
ORIGIN

Query Match 92.0%; Score 18.4; DB 12; Length 289;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCATTGCTGTATATTTT 20
Db 42 TATTGCTGTATATTTT 23

RESULT 6
LOCUS A1656575 298 bp mRNA linear EST 04-MAY-1999
DEFINITION tt51h06.x1 NCI CGAP GC6 Homo sapiens CDNA clone IMAGE:2244347 3'
Similar to SW:CAIF_HUMAN Q07092 COLLAGEN ALPHA 1(XVI) CHAIN
PRECUSOR. : mRNA sequence.
ACCESSION A1656575
VERSION A1656575.1 GI:4740554
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 298)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbfp/image/image.html
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..298
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2244347"

/clone_1lb-"NCI.CGAP.GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
 from the normalized library NCI.CGAP.GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (cloneds
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Felina Bonaldo."

Query Match	92.0%	Score 18.4	DB 9	length 298
Best Local Similarity	95.0%	Pred. No. 1.6e+03		
Matches 19; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1 TCATGCTGCTAATATTTT	20		
	1			
	51 TTAATGCTGCTAATATTTT	32		

RESULT	7
A165925/c	
LOCUS	332 bp mRNA linear EST 14-MAY-1999
DEFINITION	t14ah12.x1 NC1_CCAP_Pan1 Homo sapiens cDNA clone IMAGE:222679 3'
similar to	SW:CAIF_HUMAN O07092 COLLAGEN ALPHA 1(XVI) CHAIN
PRECUSOR	; mRNA sequence.
A165925	
ACCESSION	A165925

ACCESSION	AF665925	GI:4524377
VERSION	AF665925.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 332)	
AUTHORS	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .	
URL		

JOURNAL COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bnbp/image/image.html

Insert Length: 2303 Std Error: 0.00

Seq Primer: -40UP from Gldco

High quality sequence stop: 225

POLYA=NO.

FEATURES	SOURCE	Location/Qualifiers
		1..332
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone IMAGE:2226791"
		/clone_id="NCI_CGAP_Pan1"
		/tissue_type="adenocarcinoma"
		/lab_host="DH10B"
		/note="Organ: pancreas; Vector: pCMV-Sport6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.72 kb. Life Technologies catalog #:
		11548-013"
BASE COUNT		90 a 82 c 72 g 86 t 2 others
ORIGIN		

Query Match	92.0%	Score 18.4	DB 9	Length 332
Best Local Similarity	95.0%	Pred. No. 1.6e+03		
Matches 19; Conservative	0	Mismatches 1	Indels 0	Gaps 0
0Y	1	TCATTCGTGTTAATATTTT	20	

```

DB              47  TAAATGCTGTTAATATTTT  28
1  |||||||||||||||||||
RESULT 8
LOCUS          AA682251/c
DEFINITION    ah52d11.s1 Soares_testis_MHT Homo sapiens cDNA clone 1293141 3'
               similar to SW:CA1F_HUMAN 007092 COLLAGEN ALPHA 1(XVI) CHAIN
               PRECURSOR.; mRNA sequence.
ACCESSION     AA682251
VERSION       AA682251.1  GI:2669383
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 336)
               MCI-CGAP http://www.ncbi.nlm.nih.gov/mcicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
JOURNAL       Contact: Robert Strausberg, Ph.D.
COMMENT       Email: rstra@nci.nih.gov

```

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fátima Bonaldo
Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/HLNLT at:
www.bio.linn.gov/bdbp/image/image.html
Insert Length: 265 Std Error: 0.00
Seq primer: -40ml3 fwd: ET from Amersham.

FEATURES

Source

Location/Qualifiers

1..336

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="1293141"

/clone.lib="Soares_testis_NHT"

/sex="male"

/lab_host="DH10B"

/note="Vector: pPT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dt) primer [5', TGTTACCAATCTGACATGCGAGCGCCGCCATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pPT73 vector. Library was through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonafido."

88 a 84 c 76 g 87 t 1 others

BASE COUNT

ORIGIN

Query Match	92.0%;	Score 18.4;	DB 9;	Length 336;
Best Local Similarity	95.0%;	Pred. No. 1.6e+03;		
Matches 19;	Conservative	0;	Mismatches 1;	Indels 0;
				Caps 0;
OY	1	TCATTGCGCTAATATTTTT	20	
Db	46	TAATTGCGTTAATATTTTT	27	
RESULT 9				
LOCUS	AM192414/c			
DEFINITION	AM192414	337 bp	MRNA	linear
	x183c10.x1	NCI-CGAP-Panl Homo sapiens cDNA clone IMAGE:2681298 3'		
		similar to contains PTR5.t3 PTR5 repetitive element ;		MRNA
ACCESSION	AM192414			
VERSION	AM192414.1	GI:6471038		
KEYWORDS	EST.			
SOURCE	human.			

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 337)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, ph.D.
 Email: cgaps-femail.nih.gov
 Life Technologies catalog #: 11548-013
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrr/image/image.html
 Possible reversed clone: polyT not found
 Seq primer: -400P from Gibco
 High quality sequence stop: 335.
 Location/Qualifiers
 1..337
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2681298"
 /clone_1lb="NCI-CGAP_Pan1"
 /issue_type="adenocarcinoma"
 /lab_host="DH10B"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1; Salt:
 Site_2: Not; Cloned unidirectionally. Primer: Oligo df.
 Average insert size 1.72 kb. Life Technologies catalog #:
 11548-013"

BASE COUNT 89 a 84 c 75 g 88 t 1 others
 ORIGIN
 Query Match 92.0%; Score 18.4; DB 10; Length 337;
 Best Local Similarity 95.0%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
 1 |||||
 Db 48 TAAATCGCTTAATATTTT 29

RESULT 10 339 bp mRNA linear EST 02-MAR-1998
 AA620929
 LOCUS at96402.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1055619
 DEFINITION 3' similar to SW:CAIF.HUMAN Q07092 COLLAGEN ALPHA 1(XVI) CHAIN
 PRECURSOR. ; mRNA sequence.
 AA620929
 ACCESSION AA620929.1 GI:2524868
 VERSION
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 339)
 AUTHORS Hillier, D., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
 J., Moore, B., Scheinberg, K., Steptoe, M., Tan, F., Theising, B.,
 White, Y., Wylie, T., Waterson, R. and Wilson, R.
 White, Y., Wylie, T., Waterson, R. and Wilson, R.
 TITLE WashU-NCI human EST Project
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.
 Insert Length: 297 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amersham.

FEATURES
 source Location/Qualifiers
 1..339
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1055619"
 /clone_1lb="Soares_testis_NHT"
 /sex="male"
 /lab_host="DH10B"
 /note="Vector: pT73D-pac (pharmacia) with a modified
 polylinker; Site_1: Not; Site_2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech laboratories
 , Inc., and primed with a Not I - Oligo(dT) primer [5'.
 TGTACCAATCTGACGAGCGGCGCCCATATTTTTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors
 (pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Benito Soares and M. Fatima Bonaldo."

BASE COUNT 93 a 84 c 76 g 86 t
 ORIGIN
 Query Match 92.0%; Score 18.4; DB 9; Length 339;
 Best Local Similarity 95.0%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
 1 |||||
 Db 48 TAAATCGCTTAATATTTT 29

RESULT 11 345 bp mRNA linear EST 29-APR-1999
 A1644998
 LOCUS vs67607.y1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 DEFINITION IMAGE:1151341 5', mRNA sequence.
 A1644998
 ACCESSION A1644998.1 GI:4723473
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 345)
 AUTHORS Marra, M., Hillier, D., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterson, R. and Wilson, R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.
 This read is a RESSEQUENCE of a previously sequenced mouse clone
 correct orientation)
 Seg primer: -40RP from Gibco
 High quality sequence stop: 333.
 Location/Qualifiers
 1..345
 /organism="Mus musculus"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:1151341"
 /clone_1lb="Stratagene mouse skin (#937313)"
 /sex="females"
 /tissue_type="whole skin"

```

/dev-stage-"11 weeks old"
/lab host="SOLR (kanamycin resistant)"
/notes="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-TAG XR Vector: ~5'
Adaptor sequence: 5' GAATTCGCGACGAP 3' adaptor
sequence: 5' CTCGACGTTTTTTTTTTTTTTT 3'"
BASE COUNT      120 a      54 c      68 g      103 t
ORIGIN

```

Query Match	92.0%	Score 18.4	DB 9	length 345
Best Local Similarity	95.0%	Pred. No. 1.6e+03		
Matches 19	Conservative	0	Mismatches 1	Indels 0
				Gaps 0
QY	1	TCATGCGCTGAATATTTT	20	
Db	166	TTATTCGCTGTAATATTTT	185	

RESULT 12	352 bp	mRNA	linear	EST 22-MAR-2000
LOCUS	1594048/c			
DEFINITION	h444b02.x1	NCI CGAP GC6 Homo sapiens CDNA clone IMAGE:2948427 3		
	similar to	SM:CALF_HUMAN 007092 COLLAGEN ALPHA 1(XVI) CHAIN		
	PRECUSOR	'' mRNA sequence.		
ACCESSION	AM594048			
VERSION	AM594048.1	GI:7281306		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 352)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CCAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg Ph.D.

JOURNAL COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Pimmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI, at: image.llnl.gov/image/html/irsources.shtml
Seq primer: -400p from Glco.

ATURES
 SOURCE
 Location/Qualifiers
 1.352
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:2948427"
 /clone_lib="NCI_CGAP-C6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP-C64 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonetrads 1287096-128631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT
 92 a 88 c 81 g 91 t

Query Match	92.0%	Score 18.4	DB 10	Length 352
Best Local Similarity	95.0%	Pred. No. 1.6e+03		
Matches 19: Conservative	0	Mismatches 1	Indels 0	Gaps 0

OY	1	TCATTGCTGTTAATATTTT	20
Db	49	TAATTGCTGTTAATATTTT	30

RESULT 13	AA678445/c	LOCUS	AA678445	356 bp	mRNA	linear	EST 02-DEC-1997
DEFINITION	IMAGE:1153398 3' similar to SM-CALF HUMAN Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR. ;, mRNA sequence.	AA678445	356 bp	mRNA	linear	EST 02-DEC-1997	
ACCESSION	AA678445						

VERSION	AA678445.1	GI:2658967
KEYWORDS	EST.	
SOURCE	human.	

REFERENCE
Euharipota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 356)
AUTHORS
Hallier, D., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S., Kitzman, L., Kucuba, T., Lacy, M., Le, N., Lennon, G., Marfa, M., Mart, J., Moore, B., Schellenberg, K., Sleptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE
JOURNAL
Mashu-NCI human EST Project
COMMENT
Unpublished (1997)
Contact: Wilson RK

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.linnl.gov) for further information.
Seq primer: -40m3 fwd. Et from Amersham.
Location/Qualifiers
1. .356

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1155398"
/clone_1lb="Gessler Wilms tumor"
/sex="Pooled (6)"
/lab_host="DH108"
/note="Vector: pSPOR1; Site_1: SalI; Site_2: NotI; RNA
was prepared from a pool of 6 anonymous Wilms' tumor RNAs
oligo dT selection. cDNA library preparation was with
the BRL/Life Tech. Superscript plasmid system. An
oligo-dT NotI primer for first strand synthesis generated
ggcgccggcc(t)n at the 3' end of the clones. A 5' SalI
adapter was used with sequence 5'-gtcagaccacggcg-3'.
Resulting cDNAs were size selected (average size 2 kb),
NotI digested, and ligated into NotI/SalI-cut pSPOR1.
Library was constructed by Dr. Manfred Gessler."

```

```

Query Match      92.0%:  Score 18.4:  DB 9:      Length 356;
Best Local Similarity 95.0%:  Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCATTTGCTGTTAATATTTTT 20
          | | | | | | | | | | | | | |
Db       43 TAAATGCTGTTAATATTTTT 24

```

RESULT 14	LOCUS	DEFINITION	ACCESSTION
A1679677/c	382 bp	linear	EST 26-MAY-1999
A1679677	NCI-CGAP_Gas4	mouse sapiens cDNA	IMAGE:2255920 3'
tug6509.x1	similar to	SM:CA1F_HUMAN Q07092	COLLAGEN ALPHA 1(XVI) CHAIN
precursor.	;', mRNA sequence.		
A1679677			

```

VERSION      A1679677.1  GI:4889859
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE        1 (bases 1 to 382)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT      Tumor Gene Index
              Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabs-remail.nih.gov
              Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
              Emmert-Buck, M.D., Ph.D.
              CDNA library preparation: Life Technologies, Inc.
              CDNA library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LINL at:
              www.bio.liml.gov/bdrip/image/image.html
              Seq primer: -40UP from Gibco
              High quality sequence stop: 274.
FEATURES
  source
    1..382
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:2255920"
    /clone_1b="NCI-CGAP_Gas4"
    /lissue_type="poorly differentiated adenocarcinoma with
    signed ring cell features"
    /lab_host="DH10B"
    /note="Organ: stomach; Vector: PCMV-SPORT6; Site:1: Sal1;
    Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
    Average insert size 1.69 kb. Life Technologies catalog #:
    11549-011"
BASE COUNT   96 a 98 c 94 g 92 t 2 others
ORIGIN
Query Match      92.0%; Score 18.4; DB 9; Length 382;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCATTGCTGTTAATATTTT 20
1 ||||||||||||||||
Db 44 TAAATGCTGTTAATATTTT 25

ESTUT 15
-29062/c
LOCUS        T29062      383 bp      mRNA      linear      EST 06-SEP-1995
DEFINITION   EST; J294 Human lung Homo sapiens cDNA 3' end similar to collagen,
              TYP: XVI, alpha 1 (Ht:293), mRNA sequence.
ACCESSION    T29062
VERSION      T29062.1  GI:611160
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 383)
              Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
              ,C.J., Lee,N., Kitzness,E.F., Weissman,K.G., Gockayne,J.D., White
              ,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A.,
              Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
              ,J.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S.M., Glodex,A.,
              Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkleir,P.S., Kelley,J.M.,
              Klimke,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
              Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M.,
              Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
              Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
              Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J.,
              Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W.,

```

```

TITLE
JOURNAL      Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L.,
MEDLINE      Kunsch,C., Ji,H., Li,H., Melsner,P.S., Olsen,H., Raymond,L., Wei
              ,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Pannon
              ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
              Venter,J.C.
              Initial Assessment of Human Gene Diversity and Expression Patterns
              Based Upon 83 Million Basepairs of cDNA Sequence
              Nature 377, 3-174 (1995)
              96026280
COMMENT      Other ESTs: EST67295 THC23485
              Contact: Venter, JC
              The Institute for Genomic Research
              932 Clopper Rd, Gaithersburg, MD 20878
              Tel: 3018699056
              Fax: 3018699423
              Email: tdbinfo@tdb.tigr.org
              For clone availability, additional sequence and expression
              information related to this EST, please contact the TIGR Database
              (tdbinfo@tdb.tigr.org)
              Seq primer: M13-21.
FEATURES
  source
    1..383
    /organism="Homo sapiens"
    /db_xref="ATCC (lnhost):105192"
    /db_xref="taxon:9606"
    /clone_1b="Human Lung"
    /note="Organ: lung"
BASE COUNT   105 a 86 c 74 g 116 t 2 others
ORIGIN
Query Match      92.0%; Score 18.4; DB 14; Length 383;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCATTGCTGTTAATATTTT 20
1 ||||||||||||||||
Db 42 TAAATGCTGTTAATATTTT 23

```

Search completed: December 10, 2002, 22:50:14
 Job time : 1029.47 secs


```

PT mRNA -
XX
XX Claim 1; Page 17; 28pp; English.
PS
XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in
CC Staphylococcus aureus) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the mecA gene as template. Also disclosed is a detection
CC method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant S. aureus in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the mecA gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 2 C; 2 G; 12 T; 0 other:
XX
Query Match 100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCATTGCTGTTAATATTTT 20
    |||||||
DB 1 TCATTGCTGTTAATATTTT 20

RESULT 2
ABK85924
ID ABK85924 standard; DNA; 20 BP.
XX
XX ABK85924;
AC
XX
XX 16-AUG-2002 (first entry)
DT
XX
XX Methicillin resistant Staphylococcus aureus detection primer #24.
DE
XX
XX Methicillin resistant Staphylococcus aureus; MRSA; primer; ss;
KW
XX
XX mecA; probe.
XX
XX Staphylococcus aureus.
XX
XX
XX EPI160333-A2.
PD
XX
XX 05-DEC-2001.
PD
XX
XX 29-MAY-2001; 2001EP-0112100.
PF
XX
XX 29-MAY-2000; 2000JP-0163149.
PR
XX
XX 09-JUN-2000; 2000JP-0179394.
PR
XX
XX (TOYO ) TOSOH CORP.
PA
XX
XX Taya T, Ishiguro T, Saito J;
PI
XX
XX WPI; 2002-395832/43.
DR
XX
XX
XX New oligonucleotide specific for the mecA methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related
PT mRNA -
XX
XX Claim 5; Page 20; 28pp; English.
PS
XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in

```

```

CC Staphylococcus aureus) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the mecA gene as template. Also disclosed is a detection
CC method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant S. aureus in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the mecA gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 2 C; 2 G; 12 T; 0 other:
XX
Query Match 100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCATTGCTGTTAATATTTT 20
    |||||||
DB 1 TCATTGCTGTTAATATTTT 20

RESULT 3
AAQ86977/c
ID AAQ86977 standard; DNA; 467 BP.
XX
XX AAQ86977;
AC
XX
XX 16-JAN-1996 (first entry)
DT
XX
XX Polynucleotide probe for methicillin resistant Staphylococcus aureus.
DE
XX
XX MRSA; methicillin resistant Staphylococcus aureus; probe;
KW
XX
XX hybridisation; mecA; MRSE; Staphylococcus epidermis; ss.
XX
XX
XX Staphylococcus aureus.
OS
XX
XX
XX DE4338119-A1.
PN
XX
XX 11-MAY-1995.
PD
XX
XX 08-NOV-1993; 93DE-4338119.
PF
XX
XX 08-NOV-1993; 93DE-4338119.
PR
XX
XX 08-NOV-1993; 93DE-4338119.
PR
XX
XX (FARB ) BAYER AG.
PA
XX
XX Endermann R, Springer W;
PI
XX
XX WPI; 1995-180108/24.
DR
XX
XX
XX Detection of methicillin resistant Staphylococcus - using an
PT oligo:nucleotide derived from the mecA gene
PT
XX
XX Claim 2; Page 11; 14pp; German.
PS
XX
XX An oligonucleotide probe having the 467 nucleotide sequence shown
CC isolated from S. aureus, is capable of hybridising with the DNA or
CC RNA of methicillin resistant S. aureus (MRSA). The probe is
CC specifically derived from the mecA gene of S. aureus and S. epidermidis.
CC The mecA gene product has no homology with known PBPs
CC (penicillin-binding proteins). The new probes allow for the rapid
CC identification of all MRSA, eradicated need for labour intensive in
CC vitro cultivation and physiological assays.
XX
XX Sequence 467 BP; 187 A; 73 C; 85 G; 122 T; 0 other:
SQ

```


KM Haemophilus influenzae; Moraxella catarrhalis; septicæmia; meningitis;
 KM infection: intra-abdominal infection; skin infection;
 KM bacterial resistance; beta-lactam antibiotic; ds.
 XX
 OS Synthetic.
 XX
 PN MO9608582-A2.
 XX
 PD 21-MAR-1996.
 XX
 PF 12-SEP-1995; 95MO-CA00528.
 XX
 PR 12-SEP-1994; 94US-0304732.
 XX
 PA (BERG/) BERGERON M G.
 PA (OUEL/) OUELLETTE M.
 PA (ROYP/) ROY P H.
 XX
 PI Bergeron MG, Ouellette M, Roy PH;
 XX
 R WPI: 1996-179953/18.
 T Method for the detection of bacterial species using probes and
 PT primers - allows detection and quantification of antibiotic
 PT resistant bacteria in patients, the environment and food
 XX
 PS Claim 91: Page 144-145; 216pp; English.
 XX
 CC The sequences given in AAT28560-76 represent fragments derived from
 CC bacterial antibiotic resistance genes which were used as probes in the
 CC method of the invention for the detection of bacterial species in a
 CC sample. The method of the invention comprises using probes and/or
 CC amplification primers which are specific, ubiquitous and sensitive for
 CC determining the presence and/or amount of nucleic acids from selected
 CC bacterial species in any sample, where the bacterial nucleic acid
 CC comprises a selected target region hybridisable with the probes or
 CC primers. The method comprises contacting the sample with the probes
 CC or primers and detecting the presence and/or amount of hybridised
 CC primers or amplification products as and indication of the presence
 CC and/or amount of the bacterial species. This method may be used to
 CC detect commonly encountered bacterial pathogens, e.g. Escherichia coli,
 CC Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis,
 CC Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus
 CC epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus,
 CC Streptococcus pyogenes, Haemophilus influenzae and Moraxella
 CC catarrhalis. These bacterial species are associated with approx. 90% of
 CC urinary tract infections and with a high percentage of other severe
 CC infections including septicæmia, meningitis, pneumonia, intra-abdominal
 CC infections, skin infections and other severe respiratory tract
 CC infections. The method may also be used to evaluate a bacterial
 CC resistance to beta-lactam antibiotics.
 XX
 SQ Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
 XX
 QY Query Match 100.0%; Score 20; DB 17; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1234 TCATTGCTGTTAATATTTT 20
 1234 TCATTGCTGTTAATATTTT 1215

RESULT 7
 ID AAV68337/C
 XX AAV68337 standard; DNA; 2007 BP.
 AC AAV68337;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Penicillin binding protein PBP2A meca-27R gene of S. aureus 27R.
 XX

KM Penicillin binding protein; PBP2A-27A; meca-27R gene;
 KM methicillin resistance; antibiotic; assay; purification; ss.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP875578-A2.
 XX
 PD 04-NOV-1998.
 XX
 PF 18-MAR-1992; 92EP-0302298.
 XX
 PR 19-MAR-1991; 91US-0672704.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Blaszcak LC, Skatrud PL, Smith MC, Wu CE;
 XX
 DR WPI: 1998-559443/48.
 DR P-PSDB; AAW81149.
 XX
 PT New Staphylococcus aureus soluble penicillin-binding proteins and
 PT their derivatives - useful for screening for compounds effective
 PT against methicillin resistant organisms
 XX
 PS Disclosure; Page 14-16; 97pp; English.
 XX
 CC This meca-27R gene encodes penicillin binding protein 2A (PBP2A-27R)
 CC responsible for the methicillin resistance of Staphylococcus aureus
 CC strain 27R. The invention provides new PBPs of formula SP-L-PBP2As,
 CC where: SP is 0 or a signal peptide (preferably from the ampC, ompA or
 CC beta-lactamase gene product); L is Met-Val or a compound of formula
 CC Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see
 CC AAW81151-58) of formula (His)x-(A)y-(His)z and A=an amino acid,
 CC x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above
 CC polypeptide where each monomer unit is the same or different; Pro
 CC is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see
 CC AAW81159-62). Also claimed are polynucleotides encoding specific
 CC soluble PBP2A compounds. The new PBP2A-27R proteins are useful for
 CC assaying for agents useful as antibiotics against methicillin
 CC resistant Staphylococcus strains by creating a kinetically inert
 CC complex between a support-immobilised transition ion and a modified
 CC soluble PBP2A protein comprising a chelating agent, which screens
 CC for agents which bind to PBP2A proteins (disclosed). Soluble forms
 CC of PBP2A-27R protein facilitate crystallisation as they lack their
 CC transmembrane association region, and so are useful for x-ray
 CC crystallography studies of the protein, assisting in the design of
 CC antibiotic compounds against methicillin resistant Staphylococcus
 CC strains (disclosed). The chelating peptide operably linked to the
 CC PBP2A-27R proteins is useful for purifying PBPs.
 XX
 SQ Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
 XX
 QY Query Match 100.0%; Score 20; DB 19; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1234 TCATTGCTGTTAATATTTT 20
 1234 TCATTGCTGTTAATATTTT 1215

RESULT 8
 ID ABA76993/C
 XX ABA76993 standard; DNA; 2007 BP.
 AC ABA76993;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Antibiotic resistance detection polynucleotide SEQ ID NO 169.
 XX
 DE Detection; bacterial species; animal; food; environment;
 KM antibiotic resistance; ds.

```

XX OS Unidentified.
XX PN NZ501596-A.
XX PD 29-JUN-2001.
XX PF 12-SEP-1995: 95NZ-0501596.
XX PR 12-SEP-1995: 95NZ-0501596.
XX PA (ID11-) IDI INPECTIO DIAGNOSTIC INC.
XX PI Bergeron MG, Ouellette M, Roy PH;
XX DR MPI: 2001-615034/71.
XX PT Method for detecting target bacterial species in a sample, comprises
XX PR detecting the presence or amount of bacterial nucleic acid amplified by
XX T a primer derived from bacterial DNA, specific for the target bacterial
XX f species.
XX PS Claim 16: Page 159-160; 168pp; English.
XX CC The invention relates to detecting target bacterial species suspected to
XX CC be present in a sample, comprising contacting nucleic acids of target
XX CC bacterial species with an amplification primer pair derived from a
XX CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target
XX CC bacterial species but ubiquitous for different strains, amplifying the
XX CC nucleic acid and detecting the presence or amount of an amplified
XX CC sequence as an indication of the presence or amount of the target
XX CC bacterial species. The invention includes primers and probes
XX CC (ABA76862-ABA76984) against the target bacterial species, especially
XX CC E.coli, K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae,
XX CC S.aureus, S.epidermidis, E.faecalis, S.saprophyticus, S.progenes,
XX CC H.influenzae, M.cattarrhalis and/or group A Streptococci producing
XX CC exotoxin A gene spe A, suspected to be present in a sample which is
XX CC obtained from human patients, animals, environment or food, and which
XX CC consists of one or more bacterial colonies. Oligonucleotide
XX CC probes and primers complementary to the bacterial genes encoding
XX CC resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadB,
XX CC aac(1), aac(2), aac(3), aac(4), mecA, vanA, vanH, vanX, aacA-aphD, vat,
XX CC vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify
XX CC commonly encountered and clinically important resistance genes. The
XX CC invention provides a rapid method of bacterial identification that can be
XX CC achieved, which reduces the time currently required for the
XX CC identification of pathogens in the clinical laboratory.
XX YX
Q Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
Query Match 100.0%; Score 20; DB 22; Length 2007;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATTGCTGTTAATATTTT 20
Db 1234 TCATTGCTGTTAATATTTT 1215
RESULT 9
ABN92247/c
ID ABN92247 standard; DNA; 2028 BP.
XX AC
XX AC ABN92247;
XX XX
XX DT 24-JUL-2002 (first entry)
XX XX
XX DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.
XX XX
XX KM Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX KM antibacterial; gene therapy; gene; ds.
XX XX
XX OS Staphylococcus epidermidis.

```

```

XX XX US6380370-B1.
XX PN
XX PD 30-APR-2002.
XX PF
XX PF 13-AUG-1998; 98US-0134001.
XX PR 14-AUG-1997: 97US-055779P.
XX PR 08-NOV-1997: 97US-064964P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Doucette-Stamm LA, Bush D;
XX PT
XX DR MPI: 2002-381255/41.
XX DR P-PSDB; ABP39702.
XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
XX PR polypeptide, useful for diagnosing and treating bacterial infections -
XX PS Disclosure; SEQ ID 1710; 267pp; English.
XX CC AN90538 to ABN93374 represent Staphylococcus epidermidis open reading
XX CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
XX CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
XX CC antibacterial activity and can be used in gene therapy. The sequences
XX CC can also be used in the diagnosis and treatment of bacterial infections,
XX CC particularly S. epidermidis infections. The sequences can be used to
XX CC screen for compounds able to interfere with the S. epidermidis life
XX CC cycle or inhibit S. epidermidis infection.
XX CC N.B. The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from the
XX CC USPTO web site.
XX SO Sequence 2028 BP; 861 A; 273 C; 346 G; 547 T; 1 other;
Query Match 100.0%; Score 20; DB 24; Length 2028;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATTGCTGTTAATATTTT 20
Db 1255 TCATTGCTGTTAATATTTT 1236
RESULT 10
AAQ35213/c
ID AAQ35213 standard; DNA; 2110 BP.
XX AC
XX AC AAQ35213;
XX XX
XX DT 06-JUN-1993 (first entry)
XX XX
XX DE Sequence of the mec A gene.
XX XX
XX KM Methicillin-resistant staphylococci; detection; primer; PCR; ss.
XX OS Staphylococcus aureus.
XX XX
XX XX Key location/Qualifiers
XX FT 105..2110
XX FT CDS /*tag= a
XX PN EP527628-A.
XX XX
XX PD 17-FEB-1993.
XX PF
XX PF 10-AUG-1992; 92EP-0307307.
XX PR
XX PR 13-AUG-1991: 91US-0744770.
XX XX
XX PA (ELIL ) LILLY & CO ELI.
XX XX

```

```

P1 Skatrud PL, Unal S;
XX
DR WPI: 1993-054352/07.
DR P-PSDB: AAR30845.
XX
PT Detection of methicillin-resistant staphylococci - using
PT polymerase chain reaction method, and DNA primers, for rapid,
PT sensitive and accurate detection
XX
PS Disclosure: Pages 7-10; 16pp; English.
XX
CC The inventors claim a method for detecting methicillin-resistant
CC staphylococcal infections which involves the use of the PCR primed
CC by fragments of the Staphylococcus meca gene. More specifically, the
CC initial primers used are nucleotides 141-160 and the inverse
CC complement of nucleotides 1929-1952 of the S. aureus meca gene. The
CC interior primers are nucleotides 568-593 and the inverse complement
CC of 1647-1670 of the S. aureus meca gene.
XX
SQ Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;
Query Match 100.0%; Score 20; DB 14; Length 2110;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCATTGCTGTTAATATTTT 20
DB 1338 TCATTGCTGTTAATATTTT 1319

RESULT 11
AAQ25905/C
ID AAQ25905 standard; DNA; 2322 BP.
XX
AC AAQ25905;
XX
DT 18-JAN-1993 (first entry)
XX
DE PBP2'.
XX
KW Polymerase chain reaction; PCR; amplification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1581..1598
FT /tag= a
FT /label= Probe_binding_site
XX
JP04169200-A.
XX
17-JUN-1992.
XX
PF 31-OCT-1990; 90JP-0296708.
XX
PR 31-OCT-1990; 90JP-0296708.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
DR WPI: 1992-253403/31.
XX
PT Detection of PBP2' gene for determ. of methicillin-resistance -
PT useful esp. for detection of methicillin-resistance
PT Staphylococcus aureus
XX
PS Disclosure: Fig 1; 9pp; Japanese.
XX
CC The sequence given is the PBP2' gene. This gene could be detected
CC by the primer sequences given in AAQ25897-904. Due to the results of
CC this amplification reaction resistance to methicillin in Staphylococcus
CC aureus could be determined.
XX
SQ Sequence 2322 BP; 940 A; 324 C; 389 G; 669 T; 0 other;

```

```

Query Match 100.0%; Score 20; DB 13; Length 2322;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCATTGCTGTTAATATTTT 20
DB 1240 TCATTGCTGTTAATATTTT 1221

RESULT 12
AAT04538/C
ID AAT04538 standard; CDNA to mRNA; 2455 BP.
XX
AC AAT04538;
XX
DT 11-APR-1996 (first entry)
XX
DE Staphylococcus aureus meca protein coding sequence.
XX
KW methicillin-resistant Staphylococcus aureus; MRSA; 'meca protein;
KW antibiotic resistance; ds.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT CDS 134..2146
FT /tag= a
FT /product= mec_A protein
XX
JP07209294-A.
XX
PD 11-AUG-1995.
XX
PF 10-JAN-1994; 94JP-0012226.
XX
PR 10-JAN-1994; 94JP-0012226.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KAWA/) KAWANO M.
PA (MITU ) MITSUBISHI CHEM CORP.
XX
DR WPI: 1995-313917/41.
DR P-PSDB: AAR80036.
XX
PT New 'mec A protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
XX
PS Example 2; Page 8-10; 15pp; Japanese.
XX
CC The present sequence codes for the mec A protein. DNA coding for
CC the 'mec A protein, which controls methicillin resistance in
CC methicillin-resistant Staph. aureus (MRSA), was obtained by PCR
CC amplification of the mec A sequence using primers AAT04537 and
CC AAT04539. The 'mec A protein (mol. wt. 40000) is useful for
CC preparation of antiserum specific for MRSA, thereby allowing
CC methicillin-resistant and methicillin-sensitive strains to be
CC distinguished.
XX
SQ Sequence 2455 BP; 997 A; 344 C; 401 G; 713 T; 0 other;
Query Match 100.0%; Score 20; DB 16; Length 2455;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCATTGCTGTTAATATTTT 20
DB 1373 TCATTGCTGTTAATATTTT 1354

RESULT 13
AAH01187/C
ID AAH01187 standard; DNA; 2456 BP.

```

```

XX AC AAH01187;
XX DT 24-JUL-2001 (first entry)
XX DE Staphylococcus aureus nucleotide sequence SEQ ID NO:1178.
XX
XX Species specific; genus specific; family specific; probe; detection;
XX Identification; algal; archaeal; bacterial; fungal; parasitical;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial;
XX vaccine; primer; ds.
XX
XX Staphylococcus aureus.
XX
XX WO200123604-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000MO-CA01150.
XX
XX 28-SEP-1999; 99CA-2283458.
XX
XX 19-MAY-2000; 2000CA-2307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (ID1) INC.
XX
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
XX Picard FJ, Roy PH;
XX
XX WP1; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and
XX primers which can be used to identify and detect the presence of algal,
XX archaeal, bacterial, fungal and parasitcal species in a test sample -
XX
XX Disclosure: Page 1048-1049; 1580pp; English.
XX
XX The present invention describes a method for generating a repertory of
XX nucleic acids of tuf, fts, atpD and/or recA genes from which probes
XX and/or primers are derived. The method comprises amplifying the nucleic
XX acids of determined algal, archaeal, bacterial, fungal and parasitcal
XX species with a combination of defined primer pairs. The method can be
XX used for producing probes and/or primers for detecting one or more
XX related microorganisms e.g. algae, archaea, bacteria, fungi and
XX parasites, for universal detection and for specific and ubiquitous
XX detection and identification of an algal, archaeal, bacterial, fungal
XX and parasitcal species, genus, family and group. A nucleic acid (I)
XX obtained using the method of the invention can be used for the universal
XX detection of any bacterium, fungus or parasite in a sample and for the
XX detection of at least one antimicrobial agent resistance gene or at
XX least one toxin gene. hea nucleic acids are used for the specific and
XX ubiquitous detection and for identification of Streptococcus pneumoniae.
XX (I) can be used to design a therapeutic agent which is effective against
XX microorganisms. Microbial species or genus or family or phylum or group
XX which can be detected include Abiotrophia adhaerens, Bordetella sp.,
XX Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
XX Mycobacteriaceae family, Pseudomonas group, Streptococcus sp.,
XX Neisseria gonorrhoeae and Staphylococcus sp.. using DNA based tests
XX provides faster results than substrate specificity tests as results can
XX be determined in an hour and improved accuracy is also achieved.
XX AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
XX which are given in the exemplification of the present invention.
XX
XX Sequence 2456 BP; 1001 A; 344 C; 396 G; 715 T; 0 other.
XX
XX Query Match 100.0%; Score 20; DB 22; Length 2456;
XX Best Local Similarity 100.0%; Pred. No. 27;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TCATGCTGTTAATATTTT 20
XX |||||||||||||||||||
XX DB 1374 TCATGCTGTTAATATTTT 1355

```

```

XX RESULT 14
XX AAV37097
XX ID AAV37097 standard; DNA; 27 BP.
XX
XX AC AAV37097;
XX
XX DT 04-SEP-1998 (first entry)
XX DE PCR primer for antibiotic resistance gene meca.
XX
XX PCR primer for antibiotic resistance gene; bacteria;
XX fungal species; identification; PCR primer; ss.
XX
XX Synthetic.
XX
XX OS
XX
XX PN WO9820157-A2.
XX
XX PD 14-MAY-1998.
XX
XX XX 04-NOV-1997; 97WO-CA00829.
XX
XX PR 04-NOV-1996; 96US-0743637.
XX
XX (ID11-) ID1 INFECTIO DIAGNOSTIC INC.
XX
XX Bergeron MG, Ouellette M, Picard FJ, Roy PH;
XX
XX WP1; 1998-286967/25.
XX
XX Use of oligo:nucleotide primers and probes - for detection,
XX identification and quantification of bacteria, fungi and bacterial
XX antibiotic resistance gene(s)
XX
XX Claim 21; Page 103; 167pp; English.
XX
XX PCR primers AAV37096-97 are used to amplify antibiotic resistance gene
XX meca. They are used in the course of the invention. The specification
XX describes the use of probes and/or amplification primers which are
XX specific, ubiquitous and sensitive for determining the presence and
XX amount of nucleic acids from a bacterial antibiotic resistance gene
XX and specific bacterial and fungal species in any sample suspected of
XX containing the bacterial or fungal nucleic acids, where each of the
XX nucleic acid or variant or part comprises a selected target region
XX hybridisable with the probes or primers. The method of use comprises
XX contacting the sample with the probes or primers and detecting the
XX presence of hybridised probes or amplified products as an indication
XX of the presence of the specific bacterial or fungal species and
XX bacterial antibiotic resistance genes. The methods and products can
XX be used to detect and identify the bacterial and fungal species and
XX genera and determine the bacterial resistance to antibiotics.
XX
XX Sequence 27 BP; 7 A; 1 C; 5 G; 14 T; 0 other.
XX
XX Query Match 90.0%; Score 18; DB 19; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 ATTGCTGTTAATATTTT 20
XX |||||||||||||||||||
XX DB 1 ATTGCTGTTAATATTTT 18
XX
XX RESULT 15
XX AAL05956/C
XX ID AAL05956 standard; DNA; 6987 BP.
XX
XX AC AAL05956;
XX
XX DT 21-NOV-2001 (first entry)
XX DE Human reproductive system related antigen DNA SEQ ID NO: 8644.

```

XX Human: reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX Homo sapiens.
OS WO200155320-A2.
XX 02-AUG-2001.
PD 17-JAN-2001; 2001WO-US01339.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 05-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251990.

PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI: 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
PT is used in preventing, treating or ameliorating a medical condition -
XX
XX Disclousure; SEQ ID NO 8644; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.
Y
Y Sequence 6987 BP; 1740 A; 1642 C; 1626 G; 1979 T; 0 other:
Query Match 87.0%; Score 17.4; DB 22; Length 6987;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TCATTGCTGTATAATTT 19
|||||
DB 197 TCATTGCTGTATAATTT 179

Search completed: December 10, 2002, 17:32:40
Job time : 132.391 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 : Search time 27.2626 Seconds

(without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579A-23

Perfect score: 1 tctcttttctcgttla 20

Sequence: 1 tctcttttctcgttla 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

al number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_MA:*
2: /cgn2_6/plodata/1/ina/5A.COMB.seq:*
3: /cgn2_6/plodata/1/ina/5B.COMB.seq:*
4: /cgn2_6/plodata/1/ina/6A.COMB.seq:*
5: /cgn2_6/plodata/1/ina/6B.COMB.seq:*
6: /cgn2_6/plodata/1/ina/PCTUS.COMB.seq:*
7: /cgn2_6/plodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	2007	2	US-08-743-637B-169
2	20	100.0	2007	3	US-08-526-840B-169
3	20	100.0	2028	4	US-09-134-001C-1710
4	16.8	84.0	30549	4	US-09-134-001C-322
5	16.4	82.0	267	4	US-09-134-001C-1218
6	15.8	79.0	1820	2	US-08-757-046A-4
7	15.8	79.0	1820	3	US-09-447-208-4
8	15.8	79.0	1820	3	US-09-135-988-4
9	15.8	79.0	1820	3	US-09-277-716-4
10	15.8	79.0	1820	4	US-08-597-274A-4
11	15.8	79.0	1820	4	US-08-908-909-4
12	15.8	79.0	1820	4	US-09-609-161B-4
13	15.8	79.0	1820	4	US-08-990-103-4
14	15.8	79.0	3033	1	US-08-003-311B-1
15	15.8	79.0	3033	1	US-08-261-432-1
16	15.8	79.0	3145	4	US-09-221-017B-855
17	15.8	79.0	4692	4	US-08-961-527-220
18	15.8	79.0	5630	2	US-08-937-931-1
19	15.8	79.0	5630	4	US-09-285-502-1
20	15.8	79.0	5630	4	US-09-709-126-1
21	15.8	79.0	5630	4	US-09-871-385A-1
22	15.8	79.0	5873	1	US-07-928-464-4
23	15.8	79.0	5873	5	PCT-US93-07347-4
24	15.8	79.0	5890	1	US-07-928-464-3
25	15.8	79.0	5890	1	US-07-928-464-5
26	15.8	79.0	5890	1	US-07-928-464-6
27	15.8	79.0	5890	5	PCT-US93-07347-3

28	15.8	79.0	5890	5	PCT-US93-07347-5	Sequence 5, Appli
29	15.8	79.0	5890	5	PCT-US93-07347-6	Sequence 6, Appli
30	15.8	79.0	6295	1	US-08-003-311B-4	Sequence 4, Appli
31	15.8	79.0	6295	1	US-08-261-432-4	Sequence 4, Appli
32	15.8	79.0	6312	1	US-08-003-311B-3	Sequence 3, Appli
33	15.8	79.0	6312	1	US-08-003-311B-5	Sequence 5, Appli
34	15.8	79.0	6312	1	US-08-003-311B-6	Sequence 6, Appli
35	15.8	79.0	6312	1	US-08-003-311B-7	Sequence 7, Appli
36	15.8	79.0	6312	1	US-08-261-432-3	Sequence 3, Appli
37	15.8	79.0	6312	1	US-08-261-432-5	Sequence 5, Appli
38	15.8	79.0	6312	1	US-08-261-432-6	Sequence 6, Appli
39	15.8	79.0	6312	1	US-08-261-432-7	Sequence 7, Appli
40	15.8	79.0	169998	4	US-09-676-610B-24	Sequence 24, Appli
41	15.4	77.0	834	4	US-09-134-001C-2775	Sequence 2775, Ap
42	15.4	77.0	9919	3	US-08-880-179-1	Sequence 1, Appli
43	15.4	77.0	19250	4	US-08-961-527-35	Sequence 35, Appli
44	15.4	77.0	43676	3	US-09-356-952-12	Sequence 12, Appli
45	15.2	76.0	562	3	US-09-038-909-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-743-637B-169/C
Sequence 169 Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: COULETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSER: QUARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/743,637B
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0%; Score 20; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTATCTCGGTTA 20
Db 1167 TTTCTTTTATCTCGGTTA 1148

RESULT 2

US-08-526-840B-169/c
Sequence 169, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:

APPLICANT: BERGERON, Michel G.
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: APPLICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESSES:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
08-526-840B-169

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 2007;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTATCTCGGTTA 20
Db 1167 TTTCTTTTATCTCGGTTA 1148

RESULT 3

US-09-134-001C-1710/c
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelle-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 2028;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTATCTCGGTTA 20
Db 1188 TTTCTTTTATCTCGGTTA 1169

RESULT 4

US-09-134-001C-322/c
Sequence 322, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelle-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 322
LENGTH: 30549
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-322

Query Match
Best Local Similarity 84.0%; Score 16.8; DB 4; Length 30549;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCTTTTATCTCGGTTA 20
Db 22626 TTTCTTTTATCTCGGTTA 22607

RESULT 5

US-09-134-001C-1218/c
Sequence 1218, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelle-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
SEQ ID NO: 1218
LENGTH: 267
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1218

Query Match 82.0%; Score 16.4; DB 4; Length 267;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CTTTTFATCTCGCTTA 20
|||||
Db 49 CTTTTFATCTACGCTTA 32

RESULT 6
US-08-757-046A-4/C
Sequence 4, Application US/08757046A
Patent No. 5876995

GENERAL INFORMATION:

APPLICANT: Bryan, Bruce
TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,046A
FILING DATE: 11-25-96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,274
FILING DATE: 02-06-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE//DOCKET NUMBER: 6680-105B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062

TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1664
OTHER INFORMATION: Vargula (cypridina) luciferase
PUBLICATION INFORMATION:
AUTHORS: Thompson et al.
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 86
PAGES: 1326-1332
DATE: (1989)
DOCUMENT NUMBER: JP 3-30678 Osaka (Tsuji)

Query Match 79.0%; Score 15.8; DB 2; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTTFATCTCGCTT 19
|||||
Db 1719 TTTTTFATCTCGCTT 1701

RESULT 7
US-09-447-208-4/C
Sequence 4, Application US/09447208
Patent No. 6113886

GENERAL INFORMATION:

APPLICANT: Bryan, Bruce
TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Erman White & McAlliff
STREET: 4250 Executive Square, 7th floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/447,208
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0909/135,988
FILING DATE: 08-17-98
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/757,046
FILING DATE: 11-25-96
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,274
FILING DATE: 02-06-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE//DOCKET NUMBER: 24727-105C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-450-8499

TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1664
OTHER INFORMATION: Vargula (cypridina) luciferase
PUBLICATION INFORMATION:
AUTHORS: Thompson et al.
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 86
PAGES: 1326-1332
DATE: (1989)
US-09-447-208-4

Query Match 79.0%; Score 15.8; DB 3; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGCTT 19
|||||
Db 1719 TTCTTTTATCTTCGCT 1701

RESULT 8
US-09-135-988-4/c

Sequence 4, Application US/09135988

Patent No. 6152358

GENERAL INFORMATION:

APPLICANT: Bryan, Bruce

TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Heller Ehrman White & McCauliffe

STREET: 4250 Executive Square, 7th Floor

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/135,988

FILING DATE:

CLASSIFICATION:

PRIORITY INFORMATION:

PRIORITY NUMBER: 08/597,274

FILING DATE: 02-06-96

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 24727-105C

TELEPHONE: 619-450-8400

TELEFAX: 619-450-8499

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1820 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1..1664

OTHER INFORMATION: Vargula (cypridina) Luciferase

PUBLICATION INFORMATION: JP 3-30678 Osaka (Tsuji)

AUTHORS: Thompson et al.

JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

VOLUME: 86

PAGES: 1326-1332

DATE: (1989)

US-09-135-988-4

Query Match 79.0%; Score 15.8; DB 3; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGCTT 19
|||||
Db 1719 TTCTTTTATCTTCGCT 1701

RESULT 9
US-09-277-716-4/c

Sequence 4, Application US/09277716A

Patent No. 6232107

GENERAL INFORMATION:

APPLICANT: Bryan, Bruce

APPLICANT: Szent-Gyorgyi, Christopher

APPLICANT: PROLOME, LTD.

TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THI

CURRENT APPLICATION NUMBER: US/09/277,716A

EARLIER FILING DATE: 1999-03-26

EARLIER FILING DATE: 1998-10-01

EARLIER FILING DATE: 1998-06-15

EARLIER FILING DATE: 1998-03-27

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 1820

TYPE: DNA

ORGANISM: Vargula cypridina

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1664)

FEATURE:

OTHER INFORMATION: Vargula (cypridina) Luciferase

PUBLICATION INFORMATION:

PATENT DOCUMENT NUMBER: JP 3-30678

PATENT FILING DATE: 1989-06-29

PUBLICATION DATE: 1991-02-08

AUTHORS: Thompson, E.M.

TITLE: Cloning and expression of cDNA for the luciferase from the marine ostracod

JOURNAL: Proc. Natl. Acad. Sci. USA

VOLUME: 86(17)

PAGES: 1326-1332

DATE: 1989-09

US-09-277-716-4

Query Match 79.0%; Score 15.8; DB 4; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGCTT 19
|||||
Db 1719 TTCTTTTATCTTCGCT 1701

RESULT 10
US-08-597-274A-4/c

Sequence 4, Application US/08597274A

Patent No. 6247995

GENERAL INFORMATION:

APPLICANT: Bryan, Bruce

TITLE OF INVENTION: BIOLUMINESCENT NOVELTY ITEMS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/597,274A

1
FILING DATE: 02/06/96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L,
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6680-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1664
OTHER INFORMATION: Vargula (cypridina) luciferase
PUBLICATION INFORMATION:
AUTHORS: Thompson et al.
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 86
PAGES: 6567-6571
DATE: (1989)
US-08-597-274A-4
Query Match 79.0%; Score 15.8; DB 4; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 TTCTTTTATCTTCGTT 19
|||||
Db 1719 TTCTTTTATCTTCGTT 1701
RESULT 11
US-08-908-909-4/c
Sequence 4, Application US/08908909
Patent No. 6416960
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
TITLE OF INVENTION: DETECTION AND VISUALIZATION OF
TITLE OF INVENTION: NEOPLASTIC TISSUES AND OTHER TISSUES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,909
FILING DATE: 08-Aug-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,374
FILING DATE: 08-Aug-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L,
REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6680-108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1664
OTHER INFORMATION: Vargula (cypridina) luciferase
PUBLICATION INFORMATION:
AUTHORS: Thompson et al.
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 86
PAGES: 1326-1332
DATE: (1989)
US-08-908-909-4
DOCUMENT NUMBER: JP 3-30678 Osaka (Tsuji)
Query Match 79.0%; Score 15.8; DB 4; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 TTCTTTTATCTTCGTT 19
|||||
Db 1719 TTCTTTTATCTTCGTT 1701
RESULT 12
US-09-609-161B-4/c
Sequence 4, Application US/09609161B
Patent No. 6436682
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS,
FILE REFERENCE: 24729-121B
CURRENT APPLICATION NUMBER: US/09/609,161B
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/277,716
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/102,939
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR FILING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: 60/079,624
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentia Ver. 2.0
SEQ ID NO 4
LENGTH: 1820
TYPE: DNA
ORGANISM: Vargula cypridina
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1664)
OTHER INFORMATION: Vargula (cypridina) luciferase
PUBLICATION INFORMATION:
PATENT DOCUMENT NUMBER: JP 89167689
PATENT FILING DATE: 1989-02-29
PUBLICATION DATE: 1991-02-08
PUBLICATION INFORMATION:
AUTHORS: Thompson, E.M.
AUTHORS: Nagata, S.

1 ; AUTHORS: Tsuji, F.I.
2 ; TITLE: Cloning and expression of cDNA for the luciferase from the marine
3 ; TITLE: ostracod Vargula hilgendorfii
4 ; JOURNAL: Proc. Natl. Acad. Sci. USA
5 ; VOLUME: 86(17)
6 ; PAGES: 1326-1332
7 ; DATE: 1989-09
8 ; US-09-609-161B-4

Query Match 79.0%; Score 15.8; DB 4; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTTTTATCTTCGCT 19
1719 TCTTTTATCTTCGCT 1701

RESULT 13
US-08-990-103-4/c

Sequence 4, Application US/08990103
Patent No. 6458547

GENERAL INFORMATION:

APPLICANT: Bruce J. Bryan

APPLICANT: Stephen Gaalema

APPLICANT: Randall B. Murphy

TITLE OF INVENTION: APPARATUS AND METHOD FOR DETECTING AND

TITLE OF INVENTION: IDENTIFYING INFECTIOUS AGENTS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Brown, Martin, Haller & McClain

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE:

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/990,103

FILING DATE: 12-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,675,

FILING DATE: 02-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/033,745

FILING DATE: 12-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6680-112

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1820 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1...1664

OTHER INFORMATION: Vargula (Cypridina) luciferase

PUBLICATION INFORMATION:

AUTHORS: Thompson et al.

JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

1 ; VOLUME: 86
2 ; PAGES: 1326-1332
3 ; DATE: (1989)
4 ; DOCUMENT NUMBER: JP 3-30678 Osaka (Tsuji)
5 ; US-08-990-103-4

Query Match 79.0%; Score 15.8; DB 4; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTTTTATCTTCGCT 19
1719 TCTTTTATCTTCGCT 1701

RESULT 14

US-08-003-311B-1/c

Sequence 1, Application US/0800311B

Patent No. 544166

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.

APPLICANT: Kiebert, Joseph J.

TITLE OF INVENTION: Constitutive Triple Response Gene

TITLE OF INVENTION: and Mutations

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESS: Woodcock Washburn Kurtz Mackiewicz and

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/003,311B

FILING DATE: January 12, 1993

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/928,464

FILING DATE: August 10, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Lori Y. Beardsell

REGISTRATION NUMBER: 34,293

REFERENCE/DOCKET NUMBER: UPN-1108

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3033 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 118..2583

US-08-003-311B-1

Query Match 79.0%; Score 15.8; DB 1; Length 3033;

Best Local Similarity 89.5%; Pred. No. 2.7e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCTTTTATCTTCGCTA 20

1719 TCTTTTATCTTCGCTA 2993

RESULT 15
US-08-261-432-1/C
Sequence 1, Application US/08261432
Patent No. 5602322
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5602322ris
STREET: One Liberty Place - 46th Floor
City: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE//DOCKET NUMBER: UPN-1864
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 118..2583
US-08-261-432-1

Query Match 79.0%; Score 15.8; DB 1; Length 3033;
Best Local Similarity 89.5%; Pred. No 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 2 TCTTTTATCTCGGTTA 20
||||||| ||||| ||
Db 3011 TCTTTTACCTCGCTTA 2993

Search completed: December 10, 2002, 22:54:42
Job time : 34.3876 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 : Search time 25.9218 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-23
Perfect score: 20
Sequence: 1 tttcttttatcttcggtta 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PC1_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PC1US_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	US-09-865-579A-13	Sequence 13, Appl
2	20	100.0	20	US-09-865-579A-23	Sequence 23, Appl
3	20	100.0	2007	US-09-452-599-169	Sequence 169, App
4	17.4	87.0	910	US-09-974-300-1089	Sequence 1089, Ap
5	17.4	87.0	1911	US-09-938-842A-3533	Sequence 3533, Ap
6	16.8	84.0	1641	US-09-070-927A-582	Sequence 582, App
7	16.8	84.0	173808	US-10-003-806-10	Sequence 10, Appl
8	16.4	82.0	2000	US-09-938-842A-4201	Sequence 4201, Appl
9	16.4	82.0	147309	US-09-742-312-3	Sequence 3, Appl
10	15.8	79.0	140	US-09-910-430-21	Sequence 21, Appl
11	15.8	79.0	323	US-09-878-574-4955	Sequence 4955, Ap
12	15.8	79.0	516	US-09-728-444-1101	Sequence 1101, Ap
13	15.8	79.0	1119	US-09-815-242-7059	Sequence 7059, Ap
14	15.8	79.0	1820	US-09-803-211-4	Sequence 4, Appl
15	15.8	79.0	1820	US-09-746-485A-4	Sequence 4, Appl
16	15.8	79.0	2468	US-09-925-301-293	Sequence 293, App
17	15.8	79.0	5630	US-09-871-388-1	Sequence 1, Appl
18	15.8	79.0	6560	US-09-808-602-76	Sequence 76, Appl
19	15.8	79.0	9729	US-09-808-602-12	Sequence 12, Appl

C 20	15.8	79.0	9826	9	US-09-808-602-7
C 21	15.8	79.0	12566	10	US-09-764-869-2035
C 22	15.4	77.0	1099	10	US-09-925-300-736
C 23	15.4	77.0	1626	10	US-09-119-855-6
C 24	15.4	77.0	2000	10	US-09-887-576-128
C 25	15.4	77.0	2694	10	US-09-119-855-4
C 26	15.4	77.0	3977	10	US-09-801-574-33
C 27	15.4	77.0	9919	12	US-10-079-035-1
C 28	15.2	76.0	116	10	US-09-815-242-723
C 29	15.2	76.0	129	10	US-09-815-242-408
C 30	15.2	76.0	216	10	US-09-983-965-2187
C 31	15.2	76.0	239	10	US-09-983-965-4010
C 32	15.2	76.0	267	10	US-09-815-242-3863
C 33	15.2	76.0	284	10	US-09-815-242-275
C 34	15.2	76.0	289	10	US-09-815-242-156
C 35	15.2	76.0	291	10	US-09-815-242-6454
C 36	15.2	76.0	309	10	US-09-815-242-265
C 37	15.2	76.0	382	10	US-09-864-761-206
C 38	15.2	76.0	385	10	US-09-960-352-8405
C 39	15.2	76.0	411	10	US-09-964-824A-205
C 40	15.2	76.0	418	10	US-09-960-352-4845
C 41	15.2	76.0	529	10	US-09-983-965-2109
C 42	15.2	76.0	585	10	US-09-864-761-15399
C 43	15.2	76.0	670	10	US-09-867-550-903
C 44	15.2	76.0	774	9	US-09-870-759-15
C 45	15.2	76.0	867	10	US-09-974-300-6287

ALIGNMENTS

Sequence 7, Appl
Sequence 2035, Ap
Sequence 736, App
Sequence 6, Appl
Sequence 128, App
Sequence 4, Appl
Sequence 33, Appl
Sequence 1, Appl
Sequence 723, App
Sequence 408, App
Sequence 2187, Ap
Sequence 4010, Ap
Sequence 3863, Ap
Sequence 275, App
Sequence 156, App
Sequence 654, Ap
Sequence 265, App
Sequence 206, App
Sequence 8405, App
Sequence 205, App
Sequence 4845, Ap
Sequence 2109, Ap
Sequence 15399, A
Sequence 903, App
Sequence 15, Appl
Sequence 6287, Ap

RESULT 1
US-09-865-579A-13
; Sequence 13, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865, 579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to meca gene
; OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-13
Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCTTTATCTTCGCTTA 20
DB 1 TTTCTTTATCTTCGCTTA 20
RESULT 2
US-09-865-579A-23
; Sequence 23, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:

```
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-23
```

```
Query Match          100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTCTTTTATCTTCGGTTA 20
    |||
Db 1 TTCTTTTATCTTCGGTTA 20
```

```
RESULT 3
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169
```

```
Query Match          100.0%; Score 20; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTCTTTTATCTTCGGTTA 20
    |||
Db 1167 TTCTTTTATCTTCGGTTA 1148
```

```
RESULT 4
US-09-974-300-1089/c
; Sequence 1089, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Betka, Randy M.
```

```
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: Expression
; FILE REFERENCE: 10085,500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1089
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-1089
```

```
Query Match          87.0%; Score 17.4; DB 10; Length 910;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 TTCTTTTATCTTCGGTT 19
    |||
Db 552 TCCTTTTATCTTCGGTT 534
```

```
RESULT 5
US-09-938-842A-3533/c
; Sequence 3533, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMB: : US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3533
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3533
```

```
Query Match          87.0%; Score 17.4; DB 9; Length 1911;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 TTCTTTTATCTTCGGTT 19
    |||
Db 219 TTCATTTTATCTTCGGTT 201
```

```
RESULT 6
US-09-070-927A-582/c
; Sequence 582, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; APPLICANT: Patrick J. Dillon
; APPLICANT: Steven Barash
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
```

```

CORRESPONDENCE ADDRESS:
ADDRESSSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: P8369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 582:
SEQUENCE CHARACTERISTICS:
LENGTH: 1641 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 582:
US-09-070-927A-582

Query Match
Best Local Similarity 84.0%; Score 16.8; DB 10; Length 1641;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 1581 TTCTTTTATCTTCGGTTA 1562

RESULT 7
US-10-003-806-10/C
Sequence 10, Application US/10003806
Patent No. US2002011929A1
GENERAL INFORMATION:
APPLICANT: Bishop, Colin E.
APPLICANT: Agoulalik, Alexander I.
APPLICANT: Zhu, Qichao
TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
FILE REFERENCE: P020606US/10024824
CURRENT APPLICATION NUMBER: US/10/003,806
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/245,872
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 10
LENGTH: 173808
TYPE: DNA
ORGANISM: Mouse
US-10-003-806-10

Query Match
Best Local Similarity 84.0%; Score 16.8; DB 12; Length 173808;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 TTCTTTTATCTTCGGTTA 20
Db 140864 TTCTTTTATCTTCGGTTA 140845

RESULT 8
US-09-938-842A-4201
Sequence 4201, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Mang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: S001300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO: 4201
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-4201

Query Match
Best Local Similarity 82.0%; Score 16.4; DB 9; Length 2000;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGT 18
Db 1919 TTCTTTTATCTTCGGT 1936

RESULT 9
US-09-742-312-3/C
Sequence 3, Application US/09742312
Patent No. US20020045166A1
GENERAL INFORMATION:
APPLICANT: CHANDRAMOULISARAN, Ishwar et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: C0000838
CURRENT APPLICATION NUMBER: US/09/742,312
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 3
LENGTH: 147309
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1) --(147309)
OTHER INFORMATION: n = A,T,C or G
US-09-742-312-3

Query Match
Best Local Similarity 82.0%; Score 16.4; DB 10; Length 147309;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCTTTTATCTTCGGTT 19
Db 93310 TCTTTTATCTTCGGTT 93293
```



```
RESULT 10
US-09-910-430-21
; Sequence 21, Application US/09910430
; Patent No. US2002012735A1
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Boulle, Alex
; APPLICANT: Lebouille, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CPI
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 140
; TYPE: DNA
; ORGANISM: Ixodes ricinus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3)
; OTHER INFORMATION: A,C,T or G
; NAME/KEY: unsure
; LOCATION: (10)
; OTHER INFORMATION: A,C,T or G
; NAME/KEY: unsure
; LOCATION: (30)
; OTHER INFORMATION: A,C,T or G
US-09-910-430-21

Query Match          79.0%; Score 15.8; DB 10; Length 140;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTT 19
    |||||  |||||
Db 54 TTCTTTTATCTTCGGTT 72

RESULT 11
US-09-878-574-4955
; Sequence 4955, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 4955
; LENGTH: 323
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: L1B3028-005-Q1-B1-B4
US-09-878-574-4955

Query Match          79.0%; Score 15.8; DB 10; Length 323;
Best Local Similarity 89.5%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 TTCTTTTATCTTCGGTTA 20
    |||||  |||||
Db 170 TTCTTTTATCTTCGGTTA 188

RESULT 12
US-09-728-444-1101/C
; Sequence 1101, Application US/09728444
; Patent No. US20020161207A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020161207A1 Murine Polynucleotide Sequences
; TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
; FILE REFERENCE: LEX-0100-USA
; CURRENT APPLICATION NUMBER: US/09/728,444
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,360
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 1206
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1101
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(516)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-444-1101

Query Match          79.0%; Score 15.8; DB 9; Length 516;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTT 19
    |||||  |||||
Db 299 TTCTTTTATCTTCGATT 281

RESULT 13
US-09-815-242-7059/C
; Sequence 7059, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA-011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
```


DOCUMENT NUMBER: JP 3-30678 Osaka (Tsu)1)
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-746-485A-4

Query Match 79.0%; Score 15.8; DB 10; Length 1820;
Best Local Similarity 89.5%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTT 19
|||||
Db 1719 TTCTTTTATCTTCGCT 1701

Search completed: December 11, 2002, 06:10:07
Job time : 75.9218 secs

Email: acameron@caltech.edu
Plate: 73 row: G column: 7

Seq primer: 17
Class: BAC ends

High quality sequence stop: 534.

Location/Qualifiers

1. 534

/organism="Strongylocentrotus purpuratus"

/db_xref="taxon:7668"

/clone="Plate-73 Col-7 Row-G"

/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"

/note="Organ: sperm; Vector: BAC63.6; BAC Clones in E-Coli DH10B"

BASE COUNT 162 a 108 c 76 g 177 t 11 others

ORIGIN

Query Match 92.0%; Score 18.4; DB 17; Length 534;

Best Local Similarity 95.0%; Pred. No. 9.5e+03;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 TTCTTTTATCTTCGCTTA 20

||||||| |||||||||

Db 443 TTCTTTTATCTTCGCTTA 462

RESULT 2
BI180052/c 676 bp mRNA linear EST 09-JUL-2001

LOCUS EST520997 cSTE Solanum tuberosum cDNA clone cSTE21B11 5' sequence.

DEFINITION mRNA sequence.

BI180052

BI180052.1 GI:14645863

KEYWORDS EST.

SOURCE potato.

ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 676)

van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Cho, J.,

Chieningo, A., Bougril, O., Buell, C.R., Konning, C., Tanksley, S. and

Baker, B.

Generation of ESTs from in vitro grown microtubers

Contact: Cathy Romning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries

Division tel 1-800-711-6195, email cdna@resgen.com

Seq primer: MJ3F-R.

FEATURES

source

Location/Qualifiers

1. 676

/organism="Solanum tuberosum"

/cultivar="Bintje"

/db_xref="taxon:4113"

/clone="cSTE21B11"

/clone_lib="cSTE"

/tissue_type="axillary buds of stem explants; growing sink-tubers"

/dev_stage="7, 8 and 10 days"

/lab_host="SOLR"

/note="Vector: Bluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Tissue supplied by Christian Bachem and Richard Visser (Department of Plant Breeding, Wageningen University, The Netherlands). The cSTA libraries will attempt to capture the induction and initiation/initial growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal, 1996). Small microtubers developed from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets

those genes involved in induction of the microtubers. The following libraries, cSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as p3 in Tanksley lab notebooks."

BASE COUNT 245 a 123 c 111 g 197 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 13; Length 676;

Best Local Similarity 95.0%; Pred. No. 8.7e+03;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 TTCTTTTATCTTCGCTTA 20

||||||| |||||||||

Db 82 TTCTTTTATCTTCGCTTA 63

RESULT 3
BI179988/c 725 bp mRNA linear EST 09-JUL-2001

LOCUS EST520933 cSTE Solanum tuberosum cDNA clone cSTE21A12 5' sequence.

DEFINITION mRNA sequence.

BI179988

BI179988.1 GI:14645799

KEYWORDS EST.

SOURCE potato.

ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 725)

van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Cho, J.,

Chieningo, A., Bougril, O., Buell, C.R., Konning, C., Tanksley, S. and

Baker, B.

Generation of ESTs from in vitro grown microtubers

Contact: Cathy Romning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries

Division tel 1-800-711-6195, email cdna@resgen.com

Seq primer: MJ3F-R.

FEATURES

source

Location/Qualifiers

1. 725

/organism="Solanum tuberosum"

/cultivar="Bintje"

/db_xref="taxon:4113"

/clone="cSTE21A12"

/clone_lib="cSTE"

/tissue_type="axillary buds of stem explants; growing sink-tubers"

/dev_stage="7, 8 and 10 days"

/lab_host="SOLR"

/note="Vector: Bluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Tissue supplied by Christian Bachem and Richard Visser (Department of Plant Breeding, Wageningen University, The Netherlands). The cSTA libraries will attempt to capture the induction and initiation/initial growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal, 1996). Small microtubers developed from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, cSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as p3 in Tanksley lab notebooks."

BASE COUNT 257 a 137 c 120 g 211 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 13; Length 725;

Best Local Similarity 95.0%; Pred. No. 8.4e+03;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY	1	TTCCTTTTATCCTTGCTTA	20
Db	82	TTCCTTTTATCCTTGCTTA	63
RESULT 4			
H1436018/c	B1436018	822 bp	mRNA
LOCUS	EST53679 cstd	Solanum tuberosum	cDNA clone cSTD21A12 5' sequence,
DEFINITION	mRNA sequence.		
ACCESSION	B1436018		
VERSION	B1436018.1	GI:15260708	
KEYWORDS	EST.		
SOURCE	Potato.		
ORGANISM	Solanum tuberosum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophytas; Magnoliophyta; eudicotyledons; core eudicots;		
	Asteridae; euasteroids I; Solanales; Solanaceae; Solanum.		
	(bases 1 to 822)		
REFERENCE	van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemlingo,A.,		
AUTHORS	Bongri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.		
TITLE	Generations of ESTs from dormant potato tubers		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Cathy Ronning The Institute for Genomic Research For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdnaresgen.com Seq primer: M13F-R.		
FEATURES			
source	Location/Qualifiers		
	1..822		
	/organism="Solanum tuberosum"		
	/cultivar="Kennebec"		
	/db_xref="taxon:4113"		
	/clone="cSTD21A12"		
	/clone_1fb="cSTD"		
	/tissue_type="dormant tuber"		
	/dev_stage="one month post-harvest"		
	/lab_host="SOLR"		
	/note="Vector: pBluescript SK(-); Site1: EcoRI; Site2:		
	XhoI; This library targets genes expressed in dormant		
	tubers. This library was made from sections of dormant		
	tuber, avoiding the buds and epidermis. Tubers were stored		
	for one month post-harvest at 40C. The tuber was peeled,		
	well away from the surface. Then it was chopped into 1-2		
	mm cubes and immediately frozen in liquid nitrogen. This		
	library is noted as P4 in Tankeley lab notebooks."		
BASE COUNT	280 a	151 c	150 g
ORIGIN		241 t	
Query Match	92.0%, Score 18.4; DB 13; Length 822;		
Best Local Similarity	95.0%; Pred. NO. 8e+03;		
Matches	19; Conservative	0; Mismatches	1; Indels
	0; Gaps	0;	
Oy	1	TTCCTTTTATCCTTGCTTA	20
Db	82	TTCCTTTTATCCTTGCTTA	63
RESULT 5			
H8301848	B8301848	294 bp	mRNA
LOCUS	B8301848 RIKEN full-length enriched, adult male corpora		
DEFINITION	quadrigenitina Mus musculus cDNA clone B23003M19 3', mRNA sequence.		
ACCESSION	B8301848		
VERSION	B8301848.1	GI:9002553	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	(bases 1 to 294)		
REFERENCE	Komno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci		
AUTHORS			

TITLE
JOURNAL
COMMENT

Riken Mouse ESTs (Konno H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho,
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasakawa,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermoadaptation and thermoregulation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Katsunari,T., Akiyama,J., Shibata,K., Iwama,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

Location/Qualifiers

1. 294
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="B23003M19"
/clone_lib="RIKEN full-length enriched, adult male corpora quadrigenima"
/sex="male"
/tissue_type="corpora quadrigenima"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site.1: SalI; Site.2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was pplied with a primer [5', GAGGACAGAGAAGATCCACGGCTTTTGTTCCTTTTAA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGACAGATTCGAGATTAAATTAATTCACCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PLC I.

BASE COUNT 65 a 62 c 57 g 110 t
ORIGIN

Query Match 87.0% Score 17.4; DB 10; Length 294;
Best Local Similarity 94.7%; Pred. No. 2.5e+04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TTTCTTTTATCTCGGTT 19

```

|||||
Db      192 TTCTTTTCTTCGCTT 210

RESULT 6
BH385341
LOCUS
DEFINITION BH385341 RIKEN full-length enriched, 0 day neonate cerebellum mus
ACCESION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

1 (bases 1 to 303)
Kono,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadoh,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
Y., Shigemoto,Y., Shinagawa,A., Shitaki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya
T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamataka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Kono,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resesc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermostactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (22), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.

FEATURES
source
1..303
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="C23003BL24"
/clone_lib="RIKEN full-length enriched, 0 day neonate
cerebellum"
/lisse_type="cerebellum"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/Note="Site 1: Sall; Site 2: BamHI. cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAAAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was

```

```

prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 479.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GACAGAGAGATCTCGAGTTAAATTAATCCCGCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
PhC 1."

BASE COUNT      62 a      74 c      63 g      104 t
ORIGIN
Query Match      87.0%; Score 17.4; DB 10; Length 303;
Best Local Similarity 94.7%; Pred. No.2.5e+04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGCTT 19
Db      243 TTCTTTTCTTCGCTT 261

RESULT 7
BQ451096/c
LOCUS
DEFINITION BQ451096 PfESToab03903.y1 Plasmodium falci-parum 3D7 asexual cDNA Plasmodium
ACCESION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

1 (bases 1 to 419)
Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D.,
Marta,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Kono,T.,
Tsagarisvilli,K., Belaygorod,L., Franklin,C., Carr,L., Grow,A.,
Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D.,
Waterston,R., Wilson,R. and Sibley,D.
Unpublished (2001)
Contact: L. David Sibley
Washu Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: L. David Sibley
(sibley@dcrlm.wustl.edu), Washington University
Seq primer: -400P from Gibco.

FEATURES
source
1..419
/organism="Plasmodium falci-parum"
/db_xref="taxon:5833"
/clone_lib="Plasmodium falci-parum 3D7 asexual cDNA"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/Note="Vector: pBluescript SK plus; Site 1: EcoRI; Site 2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%) lysed P. falci-parum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
mRNA isolation system (Promega, WI) using streptavidin
magnosphere particles. Directional cDNA libraries were
constructed by oligo d(T) priming of poly(A)+ RNA (5mg)
into EcoRI and XhoI sites of 1 ZapII vector using the Zap
cDNA synthesis kit (Stratagene, CA) The average size of the
cDNA inserts in the library was between 1.0 and 1.5kb.
Clones were mass excised using the Exassist helper phage
(Stratagene), the phagemids were precipitated with PEG

```

8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."

BASE COUNT

167 a 39 c 44 g 169 t

ORIGIN

Query Match

87.0%: Score 17.4; DB 14; Length 419;

Best Local Similarity 94.7%: Pred. No. 2.2e+04;

Matches 18: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TCTTTTATCTTCGCTTA 20

Db 289 TCTTTTATCTTCGCTTA 271

RESULT 8

HO596612/c 428 bp mRNA linear EST 24-JUN-2002

LOCUS P1EST0ab20b10.y1 Plasmodium falciparum 3D7 asexual cDNA Plasmodium

DEFINITION falciparum cDNA 5', mRNA sequence.

CESSION HO596612.1 GI:21543338

KEYWORDS EST.

SOURCE malaria parasite P. falciparum.

ORGANISM Plasmodium falciparum

REFERENCE

1 (bases 1 to 428)

AUTHORS

Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D., Barra, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Tsagaris, V., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I., Tsagaris, V., Richey, J., Wadkins, J., Franklin, C., Carr, L., Grow, A., Maguire, L., Wilson, R., and Sibley, D.

TITLE

Washu Plasmodium EST Project

JOURNAL

Unpublished (2001)

COMMENT

Contact: L. David Sibley
Washu Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -400p from Gibco.

FEATURES

source

1..428

/organism="Plasmodium falciparum"

/db_xref="taxon:5833"

/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"

/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"

/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2: XhoI; Library was constructed by Debopam Chakrabarti.

Total RNA samples were isolated from mixed stage

saponin(0.1%) lysed P. falciparum 3D7 infected

erythrocytes by the acidic guanidium-phenol chloroform

method. The poly A+ RNA was isolated by the polyAT-triact

mRNA isolation system (Promega, WI) using streptavidin

Magnosphere particles. Directional cDNA libraries were

constructed by oligo d(T) priming of poly(A)+ RNA (5mg)

into EcoRI and XhoI sites of 1 ZapII vector using the Zap

cDNA synthesis kit (Stratagene, CA). The average size of the

cDNA inserts in the library was between 1.0 and 1.5kb.

Clones were mass excised using the Exassist helper phage

(Stratagene), the phagemids were precipitated with PEG

8000 and extracted with phenol/chloroform. Phagemid DNA

Matches 18: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TCTTTTATCTTCGCTTA 20

Db 289 TCTTTTATCTTCGCTTA 271

RESULT 9

BU031040 477 bp mRNA linear EST 23-AUG-2002

LOCUS OHJ17D20.yg.ab1 OH_EFGHJ sunflower RHA280 Helianthus annuus cDNA

DEFINITION clone OHJ17D20, mRNA sequence.

ACCESSION BU031040

VERSION BU031040.1 GI:22466560

KEYWORDS EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lal, Z., Church, S., Jackson, L., and Bradford, K.

TITLE

Letuce and Sunflower ESTs from the Compositae Genome Project

JOURNAL

Unpublished (2002)

COMMENT

Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Assumundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig OH_CA.Contig194465, see http://cgpdb.ucdavis.edu/
for details.

FEATURES

source

1..477

/organism="Helianthus annuus"

/cultivar="RHA280"

/db_xref="taxon:4232"

/clone_lib="OHJ17D20"

/lab_host="E.coli"

/note="Vector: pBRCDNA51AB: The library was constructed from 11 different sources of RNA from a single genotype.

Separate cDNAs were generated using primers that

incorporated unique 5' and 3' tags to distinguish each

source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and

transformations made with four size classes to minimize

size bias. Details of each source of RNA and library

construction can be obtained at http://cgpdb.ucdavis.edu/

TAG_LIB-OH_EFGHJ sunflower RHA280

TAG_TISSUE-flowers environmental stress

TAG_SEQ-CGATGCGC

BASE COUNT

167 a 76 c 80 g 154 t

ORIGIN

Query Match

87.0%: Score 17.4; DB 14; Length 477;

Best Local Similarity 94.7%: Pred. No. 2e+04; 1; Indels 0; Gaps 0;

Matches 18: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TCTTTTATCTTCGCTTA 20

Db 197 TCTTTTATCTTCGCTTA 215

RESULT 10

AW622642

LOCUS AM622642 543 bp mRNA linear EST 18-MAY-2001
 DEFINITION EST313442 tomato root during/after fruit set, Cornell University
 ACCESSION Lycopersicon esculentum cDNA clone CLEX15012 5', mRNA sequence.
 VERSION AM622642
 KEYWORDS EST.
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.
 REFERENCE 1 (bases 1 to 543)
 AUTHORS van der Hoeven, R.S., Garvin, D., Matern, A.L., Holt, I.E., Kochian, L.,
 Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Romling, C.M.,
 Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
 S.D.
 TITLE Generation of ESTs from tomato root, during and after fruit set
 JOURNAL Unpublished (1999)
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.
 FEATURES
 source
 Location/Qualifiers
 1..543
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="CLEX15012"
 /clone_lib="tomato root during/after fruit set, Cornell
 University"
 /issue_type="root"
 /dev_stage="plants during and after fruit-set"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin
 (USDA-ARS, Ithaca, NY 14850)."
 BASE COUNT 145 a 107 c 92 g 199 t
 ORIGIN
 Query Match 87.0%; Score 17.4; DB 10; Length 543;
 Best Local Similarity 94.7%; Pred. No. 1.9e+04;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TCTTTTATCTTCGGTTA 20
 |||||||
 Db 171 TCTTTTATCTTCGGTTA 189
 :SULT 11
 JAI95C01P 548 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone J95C01, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL477924
 VERSION AL477924.1 GI:11841736
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei.
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 REFERENCE 1 (bases 1 to 548)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
miles@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v+ i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 details of T. brucei sequencing at the Sanger Centre are available
 at <http://www.sanger.ac.uk/Projects/T-brucei/>.
 Location/Qualifiers
 1..548
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="J95C01"
 BASE COUNT 158 a 130 c 43 g 217 t
 ORIGIN
 Query Match 87.0%; Score 17.4; DB 17; Length 548;
 Best Local Similarity 94.7%; Pred. No. 1.9e+04;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCTTTTATCTTCGGTT 19
 |||||||
 Db 8 TCTTTTATCTTCGGTT 26
 RESULT 12
 LOCUS B1509735/c 552 bp mRNA linear EST 08-APR-2002
 DEFINITION BBI70019A10C12.5 Bee Brain Normalized/Subtracted Library, BBI7 Apis
 mellifera cDNA clone BBI70019A10C12 5', mRNA sequence.
 ACCESSION B1509735
 VERSION B1509735.1 GI:15360109
 KEYWORDS EST.
 SOURCE honeybee.
 ORGANISM Apis mellifera
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 Apidae; Apis.
 REFERENCE 1 (bases 1 to 552)
 AUTHORS Whitfield, C.W., Hand, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
 Pardinas, J., Robertson, H.M., Soares, R. and Robinson, G.E.
 TITLE Annotated expressed sequence tags and cDNA microarrays for studies
 JOURNAL of brain and behavior in the honey bee
 MEDLINE Genome Res. 12 (4), 555-566 (2002)
 COMMENT 21929762
 CONTACT: Gene E. Robinson
 Department of Entomology
 University of Illinois
 505 S. Goodwin Ave., Urbana, IL 61801, USA
 Tel: 217 265 0309
 Fax: 217 244 3499
 Email: gene@life.uiuc.edu
 This research was funded by the University of Illinois Critical
 Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
 Award in Functional Genomics to G.E. Robinson and an NSF
 Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
 REPEAT IN THE SEQUENCE
 Simple_repeat STRAND (+) ELEMENT (ATC)n LOCATION [39,63].
 PCR Primers
 FORWARD: TATAGCTACCTATAGG
 BACKWARD: ATTACCTACTAAG
 Plate: BBI70019A10 row: C column: 12
 Seq primer: AGCGATACCAATTGCACAGCA
 High quality sequence stop: 552.
 Location/Qualifiers
 1..552
 /organism="Apis mellifera"
 /strain="mixed strains of European bees, predominantly
 A.m. ligustica"
 /db_xref="taxon:7460"

```

/c/clone="BB170019A10C12"
/c/clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
/sex="Female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/notice="Organ: brain; Vector: pT73-Pac; Site:1; EcoRI;
Site:2; NotI; This BB17 cDNA library was generated by
subtraction of the BB16 library with 4000 previously
sequenced clones. The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups."
BASE COUNT      175 a      83 c      97 g      197 t
ORIGIN
Query Match      87.0%; Score 17.4; DB 13; Length 552;
Best Local Similarity 94.7%; Pred. No. 1.9e+04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  TTCTTTTACTTCGGCT 19
          ||||||| |||||||
Db      435  TTCTTTTCTTCGCTT 417

RESULT 13
AA579610/c      582 bp      mRNA      linear      EST_03-SEP-1997
LOCUS DEFINITION nm79b03.s1 NCI-CGAP_C09 Homo sapiens cDNA clone IMAGE:1074413.3'
similar to contains Alu repetitive element;contains element MER22
repetitive element ; , mRNA sequence.
AA579610
AA579610.1 GI:2357794
EST.
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CCAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI, at:
www-bio.lnli.gov/bdrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 475.
Location/Qualifiers
1..582
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1074413"
/clone_lib="NCI-CGAP_C09"
/tissue_type="Colon tumor RER+"
/lab_host="DH10B"
/notice="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Not I -
oligo(47) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo (Soares4

```

```

BASE COUNT      207 a      115 c      122 g      138 t
ORIGIN
Query Match      87.0%; Score 17.4; DB 9; Length 582;
Best Local Similarity 94.7%; Pred. No. 1.9e+04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  TTCTTTTACTTCGGCT 19
          ||||||| |||||||
Db      466  TTCTTTCTATTCGCTT 448

RESULT 14
AZ369836/c      582 bp      DNA      linear      GSS_02-OCT-2000
LOCUS DEFINITION 1M0120C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0120C09 R, DNA sequence.
AZ369836
AZ369836.1 GI:10483536
GSS.
house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 582)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0120 row: C column: 09
Seq primer: CACACAGCAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 582.
Location/Qualifiers
1..582
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0120C09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-."
/notice="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydridynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g114732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

```

BASE COUNT 160 a 126 c 108 g 188 t and selected for ampicillin resistance."

ORIGIN

Query Match 87.0%; Score 17.4; DB 17; Length 582;
 Best Local Similarity 94.7%; Pred. No. 1.9e+04;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 TTCTTTTATCTCGGT 19
 |||
 Db 214 TTCTTTTATCTCGGT 196

BASE COUNT 174 a 127 c 159 g 157 t and selected for ampicillin resistance."

ORIGIN

Query Match 87.0%; Score 17.4; DB 17; Length 617;
 Best Local Similarity 94.7%; Pred. No. 1.8e+04;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 TTCTTTTATCTCGGT 19
 |||
 Db 161 TTCTTTTATCTCGGT 143

Search completed: December 10, 2002, 22:50:10
 Job time : 1030.47 secs

RESULT 15
 AZ810395/c 617 bp DNA linear GSS 20-FEB-2001
 LOCUS
 DEFINITION 2M0074F22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0074F22 R, DNA sequence.
 ACCESSION AZ810395
 VERSION AZ810395.1 GI:12977613
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 617)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meen J.E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tinge,A., von Niederhausen,A.
 and Wright,D., Weiss R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 385 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0074 row: F column: 22
 Seq primer: CACACGCAACACGATGACCC
 Class: plasmid ends
 High quality sequence stop: 617.
 Location/Qualifiers
 1..617
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0074F22"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g11473211419b/AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells

FEATURES
 source

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 : Search time 91.2737 Seconds
(without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579A-19
Perfect score: 14
Sequence: 1 gaagtggtgcttac 14

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	14	24	ABK85917
2	14	100.0	14	24	ABK85919
3	14	100.0	467	16	AAQ86977
4	14	100.0	1789	16	AAAT04536
5	14	100.0	2007	13	AAQ28599
6	14	100.0	2007	17	AAAT28568
7	14	100.0	2007	19	AAV68337
8	14	100.0	2007	22	ABA76993
9	14	100.0	2028	24	ABN92247

C	10	14	100.0	2110	14	AAQ35213
C	11	14	100.0	2322	13	AAQ25905
C	12	14	100.0	2455	16	AAAT04538
C	13	14	100.0	2456	22	AAH01187
C	14	13	92.9	301	23	AAQ35747
C	15	13	92.9	422	22	AAK72181
C	16	13	92.9	422	22	AAK72185
C	17	13	92.9	441	22	AAK72186
C	18	13	92.9	804	24	ABN66368
C	19	13	92.9	1065	20	AAH82169
C	20	13	92.9	1377	22	AAQ85064
C	21	13	92.9	1758	22	AAH56344
C	22	13	92.9	1758	24	ABL92573
C	23	13	92.9	2068	17	AAAT28283
C	24	13	92.9	2826	23	AAAT7488
C	25	13	92.9	2826	23	AAAT79117
C	26	13	92.9	2827	23	AAQ69657
C	27	13	92.9	5253	24	ABL92628
C	28	13	92.9	5253	24	ABL92704
C	29	13	92.9	5265	21	AAH64756
C	30	13	92.9	5265	22	AAH56259
C	31	13	92.9	5265	24	ABL92488
C	32	13	92.9	6735	19	AAV52237
C	33	13	92.9	8766	24	ABN72581
C	34	13	92.9	11484	22	ABAT7409
C	35	13	92.9	11484	22	ABAT17410
C	36	13	92.9	11853	22	AAQ32785
C	37	13	92.9	14111	22	AAQ57100
C	38	13	92.9	14111	23	ABL10392
C	39	13	92.9	2155561	24	ABN71557
C	40	12.6	90.0	248	24	ABL93129
C	41	12.4	88.6	20	20	AAQ95153
C	42	12.4	88.6	20	20	AAQ92677
C	43	12.4	88.6	233	16	AAQ75124
C	44	12.4	88.6	233	23	ABV16438
C	45	12.4	88.6	275	23	ABV16229

ALIGNMENTS

RESULT 1
ABK85917
ID ABK85917 standard: DNA: 14 BP.
XX
AC ABK85917;
XX
16-AUG-2002 (first entry)
DT
DE Methicillin resistant Staphylococcus aureus detection primer #17.
XX
KW Methicillin resistant Staphylococcus aureus; MRSA; primer; ss;
KW meca; probe.
XX
OS Staphylococcus aureus.
XX
PN EP1160333-A2.
XX
PD 05-DEC-2001.
XX
PF 29-MAY-2001; 2001EP-0112100.
XX
PR 29-MAY-2000; 2000JP-0163149.
XX
PR 09-JUN-2000; 2000JP-0179394.
XX
PA (TORJ) TOSOH CORP.
XX
PI Taya T, Ishiguro T, Saito J;
XX
DR WPI: 2002-395832/43.
XX
PT New oligonucleotide specific for the meca methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related

Sequence of the me
pmp2'. Synthetic.
Staphylococcus aur
Staphylococcus aur
DNA encoding novel
Human immune/haema
Human immune/haema
Streptococcus poly
p. vivax Pvs28 pol
Mouse apoptosis me
DNA encoding Chlam
Chlamydia trachoma
A. niger Bo-1 geno
DNA encoding novel
DNA encoding novel
Chlamydia trachoma
Chlamydia trachoma
Chlamydia trachoma
Chlamydia DNA sequ
Streptococcus pneu
Streptococcus agal
Human nervous syst
Human genomic DNA
DNA encoding Dros
Drosophila melanog
Streptococcus poly
Ral metastatic tum
PCR primer used to
PCR primer used to
E. carotovora nucle
Human prostate exp
Human prostate exp

PT mRNA - :
XX Claim 1; Page 18; 28pp: English.
PS
CC This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the meca gene (associated with methicillin resistance in
CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the meca gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the meca gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
XX
XX Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 14; DB 24; Length 14;
Best Local Similarity 100.0%; Pred. NO. 84;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGTCGCTTAC 14
Db 1 GAAGGTGTGCTTAC 14
|||||
1 GAACGTCGCTTAC 14
RESULT 2
ABK85919
10 ABK85919 standard; DNA; 14 BP.
XX
XX ABK85919;
AC
XX 16-AUG-2002 (first entry)
DT
XX Methicillin resistant *Staphylococcus aureus* detection primer #19.
DE
XX Methicillin resistant *Staphylococcus Aureus*; MRSA; primer; ss;
KW meca; probe.
RW
XX
XX *Staphylococcus aureus*.
CS
/ EP1160333-A2.
XX
XX 05-DEC-2001.
PD
XX 29-MAY-2001; 2001EP-0112100.
PP
XX 29-MAY-2000; 2000JP-0163149.
PR 09-JUN-2000; 2000JP-0179394.
PR
XX (TOYJ) TOSOH CORP.
PA
XX
XX Taya T, Ishiguro T, Saito J;
PI
XX WPI: 2002-395832/43.
DR
XX
XX New oligonucleotide specific for the meca methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related
PT mRNA -
XX
XX Claim 5; Page 19; 28pp: English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the meca gene (associated with methicillin resistance in
CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the meca gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the meca gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
XX
XX Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 14; DB 24; Length 14;
Best Local Similarity 100.0%; Pred. NO. 84;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGTCGCTTAC 14
Db 1 GAAGGTGTGCTTAC 14
|||||
1 GAACGTCGCTTAC 14
RESULT 2
ABK85919
10 ABK85919 standard; DNA; 14 BP.
XX
XX ABK85919;
AC
XX 16-AUG-2002 (first entry)
DT
XX Methicillin resistant *Staphylococcus aureus* detection primer #19.
DE
XX Methicillin resistant *Staphylococcus Aureus*; MRSA; primer; ss;
KW meca; probe.
RW
XX
XX *Staphylococcus aureus*.
CS
/ EP1160333-A2.
XX
XX 05-DEC-2001.
PD
XX 29-MAY-2001; 2001EP-0112100.
PP
XX 29-MAY-2000; 2000JP-0163149.
PR 09-JUN-2000; 2000JP-0179394.
PR
XX (TOYJ) TOSOH CORP.
PA
XX
XX Taya T, Ishiguro T, Saito J;
PI
XX WPI: 2002-395832/43.
DR
XX
XX New oligonucleotide specific for the meca methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related
PT mRNA -
XX
XX Claim 5; Page 19; 28pp: English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the meca gene (associated with methicillin resistance in
CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the meca gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the meca gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
XX
XX Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 14; DB 24; Length 14;
Best Local Similarity 100.0%; Pred. NO. 84;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGTCGCTTAC 14
Db 1 GAAGGTGTGCTTAC 14
|||||
1 GAACGTCGCTTAC 14
RESULT 2
ABK85919
10 ABK85919 standard; DNA; 14 BP.
XX
XX ABK85919;
AC
XX 16-AUG-2002 (first entry)
DT
XX Methicillin resistant *Staphylococcus aureus* detection primer #19.
DE
XX Methicillin resistant *Staphylococcus Aureus*; MRSA; primer; ss;
KW meca; probe.
RW
XX
XX *Staphylococcus aureus*.
CS
/ EP1160333-A2.
XX
XX 05-DEC-2001.
PD
XX 29-MAY-2001; 2001EP-0112100.
PP
XX 29-MAY-2000; 2000JP-0163149.
PR 09-JUN-2000; 2000JP-0179394.
PR
XX (TOYJ) TOSOH CORP.
PA
XX
XX Taya T, Ishiguro T, Saito J;
PI
XX WPI: 2002-395832/43.
DR
XX
XX New oligonucleotide specific for the meca methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related
PT mRNA -
XX
XX Claim 5; Page 19; 28pp: English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the meca gene (associated with methicillin resistance in
CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the meca gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the meca gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
XX
XX Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 14; DB 24; Length 14;
Best Local Similarity 100.0%; Pred. NO. 84;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGTCGCTTAC 14
Db 1 GAAGGTGTGCTTAC 14
|||||
1 GAACGTCGCTTAC 14
RESULT 2
ABK85919
10 ABK85919 standard; DNA; 14 BP.
XX
XX ABK85919;
AC
XX 16-AUG-2002 (first entry)
DT
XX Methicillin resistant *Staphylococcus aureus* detection primer #19.
DE
XX Methicillin resistant *Staphylococcus Aureus*; MRSA; primer; ss;
KW meca; probe.
RW
XX
XX *Staphylococcus aureus*.
CS
/ EP1160333-A2.
XX
XX 05-DEC-2001.
PD
XX 29-MAY-2001; 2001EP-0112100.
PP
XX 29-MAY-2000; 2000JP-0163149.
PR 09-JUN-2000; 2000JP-0179394.
PR
XX (TOYJ) TOSOH CORP.
PA
XX
XX Taya T, Ishiguro T, Saito J;
PI
XX WPI: 2002-395832/43.
DR
XX
XX New oligonucleotide specific for the meca methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related
PT mRNA -
XX
XX Claim 5; Page 19; 28pp: English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the meca gene (associated with methicillin resistance in
CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
CC a

CC	Staphylococcus aureus) or its derived RNA. The invention also comprises
CC	a detection method employing an RNA amplification process, using RNA
CC	derived from the mecA gene as template. Also disclosed is a detection
CC	method for a methicillin-resistant <i>S. aureus</i> (MRSA), comprising an RNA
CC	amplification process in the presence of a complementary oligonucleotide
CC	probe labeled with an intercalated fluorescent dye, where complementary
CC	binding of the probe to the RNA transcription product results in a
CC	change in the fluorescent property relative to that of a situation where
CC	a complex formation is absent, and then measuring the fluorescence
CC	intensity of the reaction solution. The oligonucleotides may be used as
CC	primers or probes, for detecting methicillin-resistant <i>S. aureus</i> in
CC	clinical samples. They may also be used therapeutically to inhibit RNA
CC	reverse transcription or translation. These oligonucleotides permit
CC	rapid and very sensitive detection/identification of the mecA gene, at a
CC	relatively low temperature without the need for heat denaturation of
CC	target RNA. The present sequence represents a methicillin resistant
CC	<i>Staphylococcus aureus</i> (MRSA) detection oligonucleotide of the invention.
XX	
XX	Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 other:
XX	
Qy	1 GAAGCGTGCCTTAC 14
Db	1 GAAGGTGTCTTAC 14
XX	
XX	RESULT 3
XX	AA086977/C
ID	AA086977 standard; DNA; 467 BP.
XX	
AC	AA086977:
XX	
DT	16-JAN-1996 (first entry)
XX	
DE	Polynucleotide probe for methicillin resistant <i>Staphylococcus aureus</i> .
XX	
KM	MRSA: methicillin resistant <i>Staphylococcus aureus</i> ; probe:
KW	hybridisation: mecA; MRSE; <i>Staphylococcus epidermidis</i> ; ss.
XX	
OS	<i>Staphylococcus aureus</i> .
XX	
PN	DEA338119-A1.
XX	
PD	11-MAY-1995.
XX	
PF	08-NOV-1993; 93DE-4338119.
XX	
PR	08-NOV-1993; 93DE-4338119.
XX	
PA	(FARB) BAYER AG.
XX	
PI	Endermann R, Springer W;
XX	
DR	WPI; 1995-180108/24.
XX	
PT	Detection of methicillin resistant <i>Staphylococcus</i> - using an
XX	oligo:nucleotide derived from the mecA gene
XX	
PS	Claim 2; Page 11; 14pp; German.
XX	
XX	An oligonucleotide probe having the 467 nucleotide sequence shown
CC	isolated from <i>S. aureus</i> , is capable of hybridising with the DNA or
CC	RNA of methicillin resistant <i>S. aureus</i> (MRSA). The probe is
CC	specifically derived from the mecA gene of <i>S. aureus</i> and <i>S. epidermidis</i> .
CC	The mecA gene product has no homology with known PBPs
CC	(penicillin-binding proteins). The new probes allow for the rapid
CC	identification of all MRS, eradicating need for labour intensive in
CC	vitro cultivation and physiological assays.
XX	
XX	
XX	Sequence 467 BP; 187 A; 73 C; 85 G; 122 T; 0 other:

```

Query Match      100.0%; Score 14; DH 16; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GAAGCTGCTTAC 14
        |||
Db       70 GAAGCTGCTTAC 57

RESULT 4
AAT04536/c
ID      AAT04536 standard; cDNA to mRNA; 1789 BP.
XX
AC      AAT04536;
XX
DT      11-APR-1996 (first entry)
XX
DE      Staphylococcus aureus 'meca' protein coding sequence.
X
Y        methicillin-resistant Staphylococcus aureus; MRSA; 'meca' protein;
XX      antibiotic resistance; ds.
XX
OS      Staphylococcus aureus.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..1608
FT      /*tag= a
FT      /product= 'mecA' protein
XX
XX      JP07209294-A.
XX
PD      11-AUG-1995.
XX
PF      10-JAN-1994; 94JP-0012226.
XX
PR      10-JAN-1994; 94JP-0012226.
XX
PA      (DENK-) DENKA SEIKEN KK.
PA      (KAWA-) KAWANO M.
PA      (MITU) MITSUBISHI CHEM CORP.
XX
XX      WPI: 1995-31917/41.
DR      P-PSDB; AAR80035.
XX
XX      New 'mecA' protein and DNA encoding it - used for the detection of
PT      methicillin-resistant Staphylococcus aureus
XX
S        Claim 5; Page 11-13; 15pp; Japanese.
XX
CC      The present sequence codes for the 'mecA' protein which controls
CC      methicillin resistance in methicillin-resistant Staph. aureus. The
CC      'mecA' protein (mol. wt. 40000) is useful for preparation of
CC      antiserum specific for MRSA, thereby allowing methicillin-resistant
CC      and methicillin-sensitive strains to be distinguished. The coding
CC      sequence was obtained by PCR amplification of the mecA sequence
CC      (see AAT04536) using primers AAT04537 and AAT04539.
CC      N.B. in the sequence listing of the patent specification, the
CC      sequence length is stated to be 1785 bp.
XX
XX      Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;
XX
SO
Query Match      100.0%; Score 14; DH 16; Length 1789;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GAAGCTGCTTAC 14
        |||
Db       695 GAAGCTGCTTAC 682

RESULT 5
AAQ28599/c

```

```

ID      AAQ28599 standard; DNA; 2007 BP.
XX
AC      AAQ28599;
XX
DT      19-FEB-1993 (first entry)
XX
DE      Encodes penicillin binding protein PBP2A-27R.
XX
XX      Penicillin; antibiotic; bacteria; methicillin; staphylococci;
XX      soluble; chelating peptide; MRS infection; methicillin resistant;
XX      strain.
XX
XX      Staphylococcus aureus strain 27R.
XX
OS      Staphylococcus aureus strain 27R.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..2007
FT      /*tag= a
XX
XX      EP505151-A.
XX
PD      23-SEP-1992.
XX
PF      18-MAR-1992; 92EP-0302298.
XX
PR      19-MAR-1991; 91US-0672704.
XX
PA      (ELIL) LILLY & CO ELI.
XX
XX      Blaszcak LC, Skatrud PL, Smith MC, Wu CYE;
XX      WPI: 1992-318034/39.
XX
DR      Polynucleotide cpd. encoding PBP 2A-27R protein or its deriv. -
XX      contains PBP isolated from Staphylococcus aureus and is used to
XX      treat methicillin resistant staphylococci
XX
PS      Disclosure: Page 14; 101pp; English.
XX
XX      This sequence encodes a PBP2a penicillin binding protein isolated
XX      from S. aureus strain 27R. A cDNA library was constructed from
XX      S. aureus DNA in lambda phage EMBL3. Packaging extracts from this
XX      were then used to infect E. coli CJ236. Plaques were screened for the
XX      presence of the mecA-27R gene by a probe produced by PCR amplification
XX      of the mecA gene using primers 028600.1. Positive plaques were purified
XX      and digested with HindIII, and this fragment digested with XbaI and
XX      cloned into M13mp18 and M13mp19 for sequencing.
XX
XX      Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
XX
SO
Query Match      100.0%; Score 14; DH 13; Length 2007;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GAAGCTGCTTAC 14
        |||
Db       1094 GAAGCTGCTTAC 1081

RESULT 6
AAT28568/c
ID      AAT28568 standard; DNA; 2007 BP.
XX
AC      AAT28568;
XX
DT      01-APR-1997 (first entry)
XX
DE      Bacterial antibiotic resistance gene, mecA, probe.
XX
XX      Detection; probe; amplification primer; bacterial pathogen; pneumonia;
XX      Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
XX      Proteus mirabilis; Streptococcus pneumoniae; staphylococcus aureus;
XX      staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
XX      staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
XX

```

```

KW Haemophilus influenzae; Moraxella catarrhalis; septicæmia; meningitis;
KM infection; intra-abdominal infection; skin infection;
KM bacterial resistance; beta-lactam antibiotic; ds.
OS Synthetic.
XX
XX MO9608582-A2.
XX
XX 21-MAR-1996.
XX
XX 12-SEP-1995; 95WO-CA00528.
XX
XX 12-SEP-1994; 94US-0304732.
XX
XX (BERG/) BERGERON M G.
XX (OUEL/) OUELLETTE M.
XX (ROYP/) ROY P H.
XX
XX Bergeron MG, Ouellette M, Roy PH;
XX
XX WP1: 1996-179953/18.
XX
XX Method for the detection of bacterial species using probes and
XX primers - allows detection and quantification of antibiotic
XX resistant bacteria in patients, the environment and food
XX
XX Claim 91; Page 144-145; 216pp; English.
XX
XX The sequences given in AA728560-76 represent fragments derived from
XX bacterial antibiotic resistance genes which were used as probes in the
XX method of the invention for the detection of bacterial species in a
XX sample. The method of the invention comprises using probes and/or
XX amplification primers which are specific, ubiquitous and sensitive for
XX determining the presence and/or amount of nucleic acids from selected
XX bacterial species in any sample, where the bacterial nucleic acid
XX comprises a selected target region hybridisable with the probes or
XX primers. The method comprises contacting the sample with the probes
XX or primers or amplification products as and indication of the presence
XX and/or amount of the bacterial species. This method may be used to
XX detect commonly encountered bacterial pathogens, e.g. Escherichia coli,
XX Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis,
XX Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus
XX epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus,
XX Streptococcus pyogenes, Haemophilus influenzae and Moraxella
XX catarrhalis. These bacterial species are associated with approx. 90% of
XX urinary tract infections and with a high percentage of other severe
XX infections including septicaemia, meningitis, pneumonia, intra-abdominal
XX infections, skin infections and other severe respiratory tract
XX infections. The method may also be used to evaluate a bacterial
XX resistance to beta- lactam antibiotics.
XX
XX Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
XX
XX Query Match 100.0%; Score 14; DB 17; Length 2007;
XX Best Local Similarity 100.0%; Pred. NO. 1.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GAAGCGTGCCTTAC 14
DB 1094 GAAGCTGTCTTAC 1081
RESULTS
AAV68337/C
AAV68337 standard; DNA; 2007 BP.
AAV68337;
21-JUN-1999 (first entry)
Penicillin binding protein PBP2A mecA-27R gene of S. aureus 27R.

```

KW	Penicillin binding protein: PBP2A-27r: meca-27r gene:
KM	methicillin resistance: antibiotic: assay: purification: ss.
XX	
OS	Staphylococcus aureus.
XX	
PN	EP875578-A2.
PD	04-NOV-1998.
XX	
PE	18-MAR-1992; 92EP-0302298.
XX	
PR	19-MAR-1991; 91US-0672704.
XX	
PA	(ELIL) LILLY & CO ELI.
XX	
PI	Blaszczak LC, Skatrud PL, Smith MC, Wu CE;
XX	
XX	WPI: 1998-559443/48.
DR	P-PSDB; AAM81149.
XX	
XX	New Staphylococcus aureus soluble penicillin-binding proteins and
PT	their derivatives - useful for screening for compounds effective
PT	against methicillin resistant organisms
XX	
PS	Disclosure: page 14-16; 97pp; English.
XX	
XX	This meca-27r gene encodes penicillin binding protein 2A (PBP2A-27r)
CC	responsible for the methicillin resistance of Staphylococcus aureus
CC	strain 27r. The invention provides new PBPs of formula SP-L-PBP2As,
CC	where: SP is 0 or a signal peptide (preferably from the ampC, ompA or
CC	beta-lactamase gene product); L is Met-Val or a compound of formula
CC	Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see
CC	AAM81151-58) of formula (His)x-(Ala)y-(His)z and A-an amino acid,
CC	x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above
CC	polypeptide where each monomer unit is the same or different; Pro
CC	is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27r protein (see
CC	AAM81159-62). Also claimed are polynucleotides encoding specific
CC	soluble PBP2A compounds. The new PBP2A-27r proteins are useful for
CC	assaying for agents useful as antibiotics against methicillin
CC	resistant Staphylococcus strains by creating a kinetically inert
CC	complex between a support-immobilised transition ion and a modified
CC	soluble PBP2A protein comprising a chelating agent, which screens
CC	for agents which bind to PBP2A proteins (disclosed). Soluble forms
CC	of PBP2A-27r protein facilitate crystallisation as they lack their
CC	transmembrane association region, and so are useful for x-ray
CC	crystallography studies of the protein, assisting in the design of
CC	antibiotic compounds against methicillin resistant Staphylococcus
CC	strains (disclosed). The chelating peptide operably linked to the
CC	PBP2A-27r proteins is useful for purifying PBPs.
XX	
SO	Sequence 2007 BP: 855 A; 272 C; 341 G; 539 T; 0 other:
XX	
Query Match	100.0%; Score 14; DB 19; Length 2007;
Best Local Similarity	100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GAAGGCTGCTTAC 14
DB	1094 GAAGCTGCTTAC 1081
RESULT 8	
ABA76993/C	
ID	ABA76993 standard; DNA; 2007 BP.
XX	
AC	ABA76993;
XX	
DT	28-JAN-2002 (first entry)
XX	
DE	Antibiotic resistance detection polynucleotide SEQ ID NO 169.
XX	
XX	Detection: bacterial species; animal; food; environment;
XX	antibiotic resistance: ds

```
XX OS Unidentified.
XX PN NZ501596-A.
XX PD 29-JUN-2001.
XX PF 12-SEP-1995; 95N2-0501596.
XX PR 12-SEP-1995; 95N2-0501596.
XX PA (IDI-) IDI INFECTIO DIAGNOSTIC INC.
XX PI Bergeron MG, Ouellette M, Roy PH.
XX DR WPI: 2001-615034/71.
XX PT Method for detecting target bacterial species in a sample, comprises
XX PT detecting the presence or amount of bacterial nucleic acid amplified by
XX PT a primer derived from bacterial DNA, specific for the target bacterial
XX PT species.
XX PS Claim 16; Page 159-160; 168pp; English.
XX CC The invention relates to detecting target bacterial species suspected to
XX CC be present in a sample, comprising contacting nucleic acids of target
XX CC bacterial species with an amplification primer pair derived from a
XX CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target
XX CC bacterial species but ubiquitous for different strains, amplifying the
XX CC nucleic acid and detecting the presence or amount of an amplified
XX CC sequence as an indication of the presence or amount of the target
XX CC bacterial species. The invention includes primers and probes
XX CC (ABA7662-ABA7694) against the target bacterial species, especially
XX CC E.coli, K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae,
XX CC S.aureus, S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes,
XX CC H.influenzae, M.catarhalis and/or group A Streptococci producing
XX CC exotoxin A gene spe A, suspected to be present in a sample which is
XX CC obtained from human patients, animals, environment or food, and which
XX CC consists of one or more bacterial colonies. Oligonucleotide
XX CC probes and primers complementary to the bacterial genes encoding
XX CC resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aacB,
XX CC aacC1, aacC2, aacC3, aacC4, mecA, vanA, vanX, vanY, aacA-aphD, vat,
XX CC vga, mraA, sul and/or int (ABA76985-ABA77001) are also useful to identify
XX CC commonly encountered and clinically important resistance genes. The
XX CC invention provides a rapid method of bacterial identification that can be
XX CC achieved, which reduces the time currently required for the
XX CC identification of pathogens in the clinical laboratory.
XX CC
XX Q Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
XX
XX Query Match 100.0%; Score 14; DB 22; Length 2007;
XX Best Local Similarity 100.0%; Pred. NO. 1.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAAGGTGTCCTTAC 14
XX DB 1094 GAAGGTGTCCTTAC 1081
XX
XX RESULT 9
XX ABN92247/c
XX ID ABN92247 standard; DNA; 2028 BP.
XX AC
XX AC ABN92247;
XX XX
XX DT 24-JUL-2002 (first entry)
XX DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.
XX DE Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX KW antibacterial; gene therapy; gene; ds.
XX XX
XX OS Staphylococcus epidermidis.
```

```
XX XX US6380370-B1.
XX PN 30-APR-2002.
XX PD 13-AUG-1998; 98US-0134001.
XX PF 14-AUG-1997; 97US-055779P.
XX PR 08-NOV-1997; 97US-064964P.
XX XX (GENO-) GENOME THERAPEUTICS CORP.
XX PA Doucette-Stamm LA, Bush D;
XX PI WPI: 2002-381255/41.
XX DR P-PSDB; ABP39702.
XX DR
XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
XX PT polypeptide, useful for diagnosing and treating bacterial infections.
XX XX Disclosure; SEQ ID 1710; 267pp; English.
XX PS
XX CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
XX CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
XX CC given in ABP3124 to ABP37960. The S. epidermidis sequences have
XX CC antibacterial activity and can be used in gene therapy. The sequences
XX CC can also be used in the diagnosis and treatment of bacterial infections,
XX CC particularly S. epidermidis infections. The sequences can be used to
XX CC screen for compounds able to interfere with the S. epidermidis life
XX CC cycle or inhibit S. epidermidis infection.
XX CC N.B. The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from the
XX CC USPTO web site.
XX CC
XX SQ Sequence 2028 BP; 861 A; 273 C; 346 G; 547 T; 1 other;
XX
XX Query Match 100.0%; Score 14; DB 24; Length 2028;
XX Best Local Similarity 100.0%; Pred. NO. 1.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAAGGTGTCCTTAC 14
XX DB 1115 GAAGGTGTCCTTAC 1102
XX
XX RESULT 10
XX AAQ35213/c
XX ID AAQ35213 standard; DNA; 2110 BP.
XX AC
XX AC AAQ35213;
XX XX
XX DT 06-JUN-1993 (first entry)
XX DE Sequence of the mec A gene.
XX DE
XX DE Methicillin-resistant staphylococci; detection; primer; PCR; ss.
XX KW Staphylococcus aureus.
XX OS
XX FH Key Location/Qualifiers
XX FT CDS 105..2110
XX FT /*tag= a
XX XX
XX PN EP527628-A.
XX PD 17-FEB-1993.
XX PD 10-AUG-1992; 92EP-0307307.
XX PF 13-AUG-1991; 91US-0744770.
XX PR (ELIL ) LILLY & CO ELI.
XX PA
XX XX
```



```

PI Skatrud PL, Unal S;
XX
DR WPI; 1993-054352/07.
DR P-PSDB; AAR30845.
XX
PT Detection of methicillin-resistant staphylococci - using
PT polymerase chain reaction method, and DNA primers, for rapid,
PT sensitive and accurate detection
XX
PS Disclosure: Pages 7-10; 16pp; English.
XX
CC The inventors claim a method for detecting methicillin-resistant
CC staphylococcal infections which involves the use of the PCR primed
CC by fragments of the Staphylococcus meca gene. More specifically, the
CC initial primers used are nucleotides 141-160 and the inverse
CC complement of nucleotides 1929-1952 of the S. aureus meca gene. The
CC interlor primers are nucleotides 568-593 and the inverse complement
CC of 1647-1670 of the S. aureus meca gene.
XX
SQ Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;

Query Match 100.0%; Score 14; DB 14; Length 2110;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGTCTTAC 14
DB 1198 GAAGGTGTCTTAC 1185
|||||
|||||

RESULT 11
AAQ25905/C
ID AAQ25905 standard; DNA: 2322 BP.
XX
AC AAQ25905;
XX
DT 18-JAN-1993 (first entry)
XX
DE PBP2'.
XX
KW Polymerase chain reaction; PCR; amplification; ss.
XX
OS Synthetic.
XX
FH Key location/Qualifiers
FT misc_binding 1581..1598
FT /*tag= a
FT /label= Probe_binding_site
FT
Y
JP04169200-A.
..X
PD 17-JUN-1992.
XX
PF 31-OCT-1990; 90JP-0296708.
XX
PR 31-OCT-1990; 90JP-0296708.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
DR WPI; 1992-253403/31.
XX
PT Detection of PBP2' gene for determ. of methicillin-resistance -
PT useful esp. for detection of methicillin-resistance
PT Staphylococcus aureus
XX
PS Disclosure; Fig 1; 9pp; Japanese.
XX
CC The sequence given is the PBP2' gene. This gene could be detected
CC by the primer sequences given in AAQ25897-904. Due to the results of
CC this amplification reaction resistance to methicillin in Staphylococcus
CC aureus could be determined.
XX
SQ Sequence 2322 BP; 940 A; 324 C; 389 G; 669 T; 0 other;

```

```

Query Match 100.0%; Score 14; DB 13; Length 2322;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGTCTTAC 14
DB 1100 GAAGGTGTCTTAC 1087
|||||
|||||

RESULT 12
AAT04538/C
ID AAT04538 standard; cDNA to mRNA; 2455 BP.
XX
AC AAT04538;
XX
DT 11-APR-1996 (first entry)
XX
DE Staphylococcus aureus meca protein coding sequence.
XX
KW methicillin-resistant Staphylococcus aureus; MRSA; 'meca' protein;
KW antibiotic resistance; ds.
XX
OS Staphylococcus aureus.
XX
FH Key location/Qualifiers
FT CDS 134..2146
FT /*tag= a
FT /product= mec_A_prl_ein
XX
PN JP07209294-A.
XX
PD 11-AUG-1995.
XX
PE 10-JAN-1994; 94JP-0012226.
XX
PR 10-JAN-1994; 94JP-0012226.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KAWA/) KAWANO M.
PA (MITU ) MITSUBISHI CHEM CORP.
XX
DR WPI; 1995-313917/41.
DR P-PSDB; AAR80036.
XX
XX
PT New 'mec A' protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
XX
PS Example 2; Page 8-10; 15pp; Japanese.
XX
CC The present sequence codes for the mec A protein. DNA coding for
CC the 'mec A' protein, which controls methicillin resistance in
CC methicillin-resistant Staph. aureus (MRSA), was obtained by PCR
CC amplification of the mec A sequence using primers AAT04537 and
CC AAT04539. The 'mec A' protein (mol. wt. 40000) is useful for
CC preparation of antiserum specific for MRSA, thereby allowing
CC methicillin-resistant and methicillin-sensitive strains to be
CC distinguished.
XX
SQ Sequence 2455 BP; 997 A; 344 C; 401 G; 713 T; 0 other;

Query Match 100.0%; Score 14; DB 16; Length 2455;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGTCTTAC 14
DB 1233 GAAGGTGTCTTAC 1220
|||||
|||||

RESULT 13
AAH01187/C
ID AAH01187 standard; DNA: 2456 BP.

```

XX AH01187;
 AC 24-JUL-2001 (first entry)
 XX
 DE Staphylococcus aureus nucleotide sequence SEQ ID NO:1178.
 XX
 XX Species specific; genus specific; family specific; probe; detection;
 KW identification; algal; archaeal; bacterial; fungal; parasitica;
 KW microorganism; diagnosis; translation elongation factor Tu; toxin;
 KW translation elongation factor G; RecA recombinase; resistance;
 KW catalytic subunit of proton-translocating ATPase; antimicrobial;
 KW vaccine; primer; ds.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200123604-A2.
 XX
 PD 05-APR-2001.
 XX
 XX 28-SEP-2000; 2000WO-CA01150.
 XX
 XX 28-SEP-1999; 99CA-2283458.
 XX
 XX 19-MAY-2000; 2000CA-2307010.
 XX
 PA (INFE-) INFECTION DIAGNOSTIC (IDI) INC.
 XX
 PI Bergeron MC, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX
 DR WPI; 2001-245006/25.
 XX
 PT Nucleic acid sequences are used to generate universal probes and
 PT primers which can be used to identify and detect the presence of algal,
 PT archaeal, bacterial, fungal and parasitica species in a test sample -
 XX
 PS Disclosure: Page 1048-1049; 1580pp: English.
 XX
 XX The present invention describes a method for generating a repertoire of
 CC nucleic acids of tuf, fts, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitica
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal
 CC and parasitica species, genus, family and group. A nucleic acid (I)
 CC obtained using the method of the invention can be used for the universal
 CC detection of any bacterium, fungus or parasite in a sample and for the
 CC detection of at least one antimicrobial agent resistance gene or at
 CC least one toxin gene. hexA nucleic acids are used for the specific and
 CC ubiquitous detection and for identification of Streptococcus pneumoniae.
 CC (I) can be used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
 CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
 CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
 CC provides faster results than substrate specificity tests as results can
 CC be determined in an hour and improved accuracy is also achieved.
 CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
 CC which are given in the exemplification of the present invention.
 XX
 XX Sequence 2456 BP; 1001 A; 344 C; 396 G; 715 T; 0 other;
 XX
 XX Query Match 100.0%; Score 14; DB 22; Length 2456;
 XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GAAGTGTGCTTAC 14
 DB 1234 GAAGTGTGCTTAC 1221

RESULT 14
 AAS93747
 ID AAS93747 standard; CDNA: 301 BP.
 XX
 XX AAS93747;
 AC
 XX 13-FEB-2002 (first entry)
 DE
 XX DNA encoding novel human diagnostic protein #29551.
 KW
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US08631.
 XX
 XX 31-MAR-2000; 2000US-0540217.
 XX
 XX 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 PI
 XX
 DR WPI; 2001-639362/73.
 XX
 DR P-PSDB: ABG29560.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnosis, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 1; SEQ ID NO 29551; 103pp: English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 XX Sequence 301 BP; 64 A; 67 C; 91 G; 79 T; 0 other;
 XX
 XX Query Match 92.9%; Score 13; DB 23; Length 301;
 XX Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 AAGTGTGCTTAC 14
 DB 132 AAGTGTGCTTAC 144

```
RESULT 15
AAK72181/c
ID AAK72181 standard; DNA: 422 BP.
XX
AC AAK72181;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26993.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
UP 17-JAN-2001; 2001WO-US01354.
XX
1 31-JAN-2000; 2000US-0179065.
2 04-FEB-2000; 2000US-0180628.
3 24-FEB-2000; 2000US-0184664.
4 02-MAR-2000; 2000US-0186350.
5 16-MAR-2000; 2000US-0189874.
6 17-MAR-2000; 2000US-0190076.
7 18-APR-2000; 2000US-0198123.
8 19-MAY-2000; 2000US-0205515.
9 07-JUN-2000; 2000US-0209467.
10 28-JUN-2000; 2000US-0214886.
11 30-JUN-2000; 2000US-0215135.
12 07-JUL-2000; 2000US-0216647.
13 07-JUL-2000; 2000US-0216880.
14 11-JUL-2000; 2000US-0217487.
15 11-JUL-2000; 2000US-0217486.
16 14-JUL-2000; 2000US-0218290.
17 26-JUL-2000; 2000US-0220963.
18 26-JUL-2000; 2000US-0220964.
19 14-AUG-2000; 2000US-0224518.
20 14-AUG-2000; 2000US-0224519.
21 14-AUG-2000; 2000US-0225213.
22 14-AUG-2000; 2000US-0225214.
23 14-AUG-2000; 2000US-0225266.
24 14-AUG-2000; 2000US-0225267.
25 14-AUG-2000; 2000US-0225268.
26 14-AUG-2000; 2000US-0225270.
27 14-AUG-2000; 2000US-0225447.
28 14-AUG-2000; 2000US-0225757.
29 14-AUG-2000; 2000US-0225758.
30 14-AUG-2000; 2000US-0225759.
31 18-AUG-2000; 2000US-0226279.
32 22-AUG-2000; 2000US-0226681.
33 22-AUG-2000; 2000US-0226868.
34 23-AUG-2000; 2000US-0227182.
35 23-AUG-2000; 2000US-02277009.
36 30-AUG-2000; 2000US-0228924.
37 01-SEP-2000; 2000US-0229287.
38 01-SEP-2000; 2000US-0229344.
39 01-SEP-2000; 2000US-0229345.
40 01-SEP-2000; 2000US-0229345.
41 05-SEP-2000; 2000US-0229509.
42 05-SEP-2000; 2000US-0229513.
43 06-SEP-2000; 2000US-0230437.
44 06-SEP-2000; 2000US-0230438.
45 08-SEP-2000; 2000US-0231242.
46 08-SEP-2000; 2000US-0231243.
47 08-SEP-2000; 2000US-0231244.
48 08-SEP-2000; 2000US-0231413.
49 08-SEP-2000; 2000US-0231414.
50 08-SEP-2000; 2000US-0232080.
51 08-SEP-2000; 2000US-0232081.
52 12-SEP-2000; 2000US-0231968.
```

```
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0234998.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 27-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
```

```

PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX
XX Disclosure: SEQ ID NO 26993; 3071bp + Sequence Listing; English.
XX
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases or haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention.
XX
XX
XX Sequence 422 BP; 75 A; 124 C; 135 G; 88 T; 0 other:
XX
XX
XX Query Match 92.9%; Score 13; DB 22; Length 422;
XX Best Local Similarity 100.0%; Pred. No. 4.5e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX / 1 GAAGGTGCTTA 13
XX | | | | | | | | | |
XX DB 419 GAAGGTGCTTA 407

```

Search completed: December 10, 2002, 17:32:30
 Job time : 94.2737 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 : Search time 433.631 Seconds

(Without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-23

Perfect score: 20

Sequence: 1 tttcttttattcttcggtta 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: gb_vl:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_mu:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pla:*
35: em_hlg_rod:*
36: em_hlg_mam:*
37: em_hlg_vit:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	20	100.0	20	6	AX306854
2	20	100.0	20	6	AX306864
3	20	100.0	467	6	A44526
4	20	100.0	1789	6	E09772
5	20	100.0	2007	6	AR089410
6	20	100.0	2007	6	AR093610
7	20	100.0	2322	6	SABBP
8	20	100.0	2322	6	E03736
9	20	100.0	2454	1	SEMECAPB
10	20	100.0	2455	6	E09771
11	20	100.0	2456	1	SAMECAPB
12	20	100.0	2456	6	AX110445
13	20	100.0	5596	1	SKBMCAC
14	20	100.0	6368	1	SSK3MBCA2
15	20	100.0	9047	1	SAMECAR11
16	20	100.0	21777	1	AB063173
17	20	100.0	26090	1	AB063172
18	20	100.0	39332	1	AB033763
19	20	100.0	58237	1	DB6934
20	20	100.0	68256	1	AB037671
21	20	100.0	290250	1	AP004822
22	20	100.0	298050	1	AP003129
23	20	100.0	349999	1	AP003358
24	18.4	92.0	2173	2	AC020510
25	18.4	92.0	8720	1	AF292711
26	18.4	92.0	9386	1	AE000791
27	18.4	92.0	13352	2	AC118882
28	18.4	92.0	165158	3	AC009912
29	18.4	92.0	166146	2	AC009732
30	18.4	92.0	167447	3	AC009459
31	18.4	92.0	172580	2	AC118425
32	18.4	92.0	313634	3	AE003454
33	17.4	87.0	664	9	HSASJ571
34	17.4	87.0	910	6	AX432674
35	17.4	87.0	1213	6	AX414123
36	17.4	87.0	1652	6	AX111451
37	17.4	87.0	2034	6	AX416437
38	17.4	87.0	2661	8	AF142717
39	17.4	87.0	3176	1	AF511037
40	17.4	87.0	10927	1	AE000262
41	17.4	87.0	11046	1	AE005390
42	17.4	87.0	14601	1	ECU68703
43	17.4	87.0	16575	5	M1CCCG
44	17.4	87.0	20476	1	D90810
45	17.4	87.0	37954	10	AF232228

ALIGNMENTS

RESULT 1
AX306854
LOCUS
DEFINITION
AX306854
ACCESSION
AX306854.1
GI:17894676
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.

REFERENCE
TAYLOR
JOURNAL
Taya, T., Ishiguro, T. and Saito, J.
Oligonucleotides and method for detection of meca gene of
methicillin-resistant *Staphylococcus aureus*
Patent: EP 1160333-A 13 05-DEC-2001;

FEATURES Tosoh Corporation (JP)
location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide capable of binding specifically to
meca gene or RNA derived from said gene"

BASE COUNT 2 a 3 c 2 g 13 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
|||||
1 TTCTTTTATCTTCGGTTA 20

RESULT 2
CUS AX306864 20 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 23 from Patent EP1160333.
ACCESSION AX306864
VERSION AX306864.1 GI:17894686
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Taya,T., Ishiguro,T. and Saito,J.
TITLE Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
JOURNAL Patent: EP 1160333-A 23 05-DEC-2001;
Tosoh Corporation (JP)
FEATURES location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 2 a 3 c 2 g 13 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
|||||
1 TTCTTTTATCTTCGGTTA 20

RESULT 3
A44526 467 bp DNA linear PAT 07-MAR-1997
LOCUS A44526
DEFINITION Sequence 2 from patent WO9513395.
ACCESSION A44526
VERSION A44526.1 GI:2299344
KEYWORDS
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 467)
AUTHORS Springer,W. and Endermann,R.
TITLE SPECIFIC GENE PROBES AND METHODS FOR QUANTITATIVE DETECTION OF
METHICILLIN-RESISTANT STAPHYLOCOCCI
JOURNAL Patent: WO 9513395-A 2 18-MAY-1995;
BAYER AG (DE)
COMMENT Other publication DE 4338119 950511.
FEATURES location/Qualifiers
source 1..467
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

BASE COUNT 187 a 73 c 85 g 122 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
|||||
143 TTCTTTTATCTTCGGTTA 124

RESULT 4
E09772 1789 bp RNA linear PAT 29-SEP-1997
LOCUS E09772
DEFINITION The base sequence of modified meca DNA.
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS JP 1995209294-A/2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 1789)
AUTHORS Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
TITLE NOVEL 'MECA' PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 2 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
COMMENT OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PE 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA,
PI SUGURO KAZUYA
PC C01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC
C12R1:19),
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key location/Qualifiers
FH FT source 1..1789
FT FT 1..1608 /organism="Staphylococcus aureus" FT CDS
FT 1..1789 /product="Modified meca".

FEATURES location/Qualifiers
source 1..1789
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

BASE COUNT 735 a 263 c 302 g 489 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1789;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
|||||
768 TTCTTTTATCTTCGGTTA 749

RESULT 5
AR089410 2007 bp DNA linear PAT 07-SEP-2000
LOCUS AR089410
DEFINITION Sequence 169 from patent US 5994066.
ACCESSION AR089410
VERSION AR089410.1 GI:10016167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)

AUTHORS Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
FEATURES Location/Qualifiers
 1..2007
 /organism="unknown"
BASH COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
 |||||||
Db 1167 TTCTTTTATCTTCGGTTA 1148

RESULT 6
LOCUS AR093610 2007 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 169 from patent US 6001564.
ACCESSION AR093610
VERSION AR093610.1 GI:10020359
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron,M.G., Ouellette,M. and Roy,P.H.
TITLE Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
FEATURES Location/Qualifiers
 1..2007
 /organism="unknown"
BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
 |||||||
Db 1167 TTCTTTTATCTTCGGTTA 1148

RESULT 7
SAPP/c 2322 bp DNA linear BCT 12-SEP-1993
LOCUS Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
ACCESSION Y00688
VERSION Y00688.1 GI:46628
KEYWORDS penicillin-binding protein.
SOURCE Staphylococcus aureus.
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2322)
AUTHORS Song,M.D., Machi,M., Doi,M., Ishino,F. and Matsubashi,M.
TITLE Evolution of an inducible penicillin-target protein in methicillin-resistant Staphylococcus aureus by gene fusion
JOURNAL FEBS Lett. 221 (1), 167-171 (1987)
MEDLINE 87304805
PUBMED 3305073
REFERENCE 2 (bases 1 to 2322)
AUTHORS Ryfel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,

TITLE Barberis-Maino,L., Kayser,F.H. and Berger-Bachl,B.
 Sequence comparison of mecA genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT Data kindly reviewed (13.1.88) by Matsubashi.
FEATURES Location/Qualifiers
 1..2322
 /organism="Staphylococcus aureus"
 /db_xref="taxon:1280"
 1..2013
 /note="penicillin-binding protein (PA 1-670)"
 /codon_start=1
 /transl_table=11
 /protein_id="CA68684.1"
 /db_xref="GI:46629"
 /db_xref="SWISS-PROT:P07944"
 /translation="MKKIRIVPLIVVVGQIYFYASKDEINNTIDAIEDKFKQVVKDSSYISKSDNGEVEENTERPILKIVNSIGVQDINIQDKRKVSKSKRRVLAQYKIKTNGNIDRNVOFNFKVEDGMMKIDMDHSYIIPQMKDOSIHILNLSKPGKILIDRNVEELANTGTHMRDLGIVPKNVSKKDYKALAKELISSEDIYNNKMKIKICYKMLPSHFPTVKKDEYISDPAKKRHILTNETESRNYPLGKATSHLSGYVGPINSEELKQKQYKGYKNDVIGKKGLEKLYDKKLQHDGRTVIVRVQDNSNTIAHTLLEKKKDGKDIQLTIDAKVOKSIVNNKNDYSGGTAIHPQTELLALVSTPSDYVPEPMYQMSNEEYKRLTEDKKEVLIANKPQITTPSGSTOKILTPAMIGLNKKTLDDKTSYKIDCKGQKDSMGCVNVTREYVNDNEILDKQAISSDNIIPFARVALHIGSKKPFEGMKLGVGEDIPSDYPPVAQISNKLIDNEILLADSGYGGCEIILNPQVILISYSALENNGNIINAPHILKPTKKVAKKN115KENINILNMGQOVNKKTKHEDYRSYANLIGSTAEKMKMGQETGRIGMFIISDKDNPMMALIVNKVDQKGMASVYNAKSGVYVDLYENKKNKTDIDE"

BASE COUNT 940 a 324 c 389 g 669 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 2322;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
 |||||||
Db 1173 TTCTTTTATCTTCGGTTA 1154

RESULT 8
LOCUS E03736 2322 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence of PBP2' gene for determination of methicillin resistance.
ACCESSION E03736
VERSION E03736.1 GI:2171951
KEYWORDS JP 1992169200-A/9.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2322)
AUTHORS Matsubashi,M., Nakamura,E., Teraoka,H., Wada,K., Minamide,W. and Murakami,K.
TITLE DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
JOURNAL Patent: JP 1992169200-A 9 17-JUN-1992;
COMMENT SHIONOGI & CO LTD
 OS (methicillin resistant)staphylococcus aureus
 PN JP 1992169200-A/9
 PD 17-JUN-1992
 PP 31-OCT-1990 JP 1990296708
 PI MATSUBASHI YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI, MINAMIDE WAKIO, MURAKAMI KAZUHIISA
 PC C1201/68, C12N15/11;
 CC strandedness: single;
 CC topology: linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Location/Qualifiers

FT misc:feature 1..2322
FT /note="PBP2' gene for determination of
FT methicillin
FT resistance".
FEATURES
source 1..2322
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 939 a 324 c 390 g 669 t
ORIGIN
Query Match 100.0%: Score 20; DB 6; Length 2322;
Best Local Similarity 100.0%: Pred. No. 2,5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTTTTATCTCGGTTA 20
|||||
Db 1173 TTCTTTTATCTCGGTTA 1154
TSUT 9
MECAPB/c 2454 bp DNA linear BCT 12-SEP-1993
LOCUS 5. epidermidis meca gene for PBP2' (penicillin binding protein 2').
DEFINITION X52592
ACCESSION X52592.1 GI:46993
VERSION meca gene; methicillin resistance; penicillin-binding protein;
KEYWORDS penicillin-binding protein 2'.
SOURCE Staphylococcus epidermidis.
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2448)
AUTHORS Ryffel,C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
REFERENCE 2 (bases 1 to 2454)
AUTHORS Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
TITLE Sequence comparison of meca genes from methicillin-resistant
Staphylococcus aureus and Staphylococcus epidermidis
JOURNAL Gene (1990) In press
REFERENCE 3 (bases 1 to 2454)
AUTHORS Ryffel,C.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
REFERENCE 4 (bases 1 to 2454)
AUTHORS Medical Microbiology, Gloristr 32, CH-8028 Zuerich, Switzerland
Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
TITLE Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52593-4> and <Y00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source 1..2454
/organism="Staphylococcus epidermidis"
/strain="WT5"
/db_xref="taxon:1282"
/clone="WT80/WT79"
80..85
/note="35 region"
101..105
/note="10 region"
130..134
/note="ribosome binding site"
141..2159
/note="primary transcript"
141..2147
CDS

/note="PBP2' (AA 1 - 668)"
/codon_start=1
/transl_table=1
/protein_id="CAA36828.1"
/db_xref="GI:46994"
/db_xref="SPTREMBL:054113"
/translation="MKKIKYPIPLIIIVVVGFGIYFVASKDEINNTIDATEDKNFKO
VYKDSYISKSDNCEVEKTEPRITKYSLSGYKDINIDRKIKKSKKKRVDQKTK
TNYGNIDRNVOFNFKEDGMKLDMDHSVLI1PGHOKQDSIH1ENI1KSPKCK1IDRNW
ELANTGTAIEIGIIVPKNVSKKDYAKIAKELS1SEBY1IKQMDKMWODDIPVPLKTVK
KMEY1LSDFAKFKPLTNTNTESSRNYPLQKATSHLGYVGP1NSEEL1KQEKYKQYDA
VIGKKLEKLYDKRKLQHEDEGYRAT1VDDNSMT1AHTLEKKKKGKD1OLT1IDAKVOK
S1YNNKMKDYGSGTA1HPQTELLALVSTPSYDYVPMYGGKSKGKDEP1LL
MKPQITSPSGSTOKILITAMIGLNTKTLDDKTSYK1IDGKGQKDKSGMGQYNTREYVN
GNID1KQALISSDNI1FFARVA1ELGSKKFKFGKRLCYGED1SDY1PPYNAQ1SNKL
DNEL1LADSGYGGCE1I1NPQV1I1SYSALENNGN1NAPH1L1KDTKKNVKKN11SKB
N1NLI1TDGMDQVANKTKH1EDI1YRSYAN1LGSCTAP1L1KKQGF1GCG1GWP1SYDKDN
PNNMA1IVKDVQDKGMASYNAK1SGVYDELYENGKKYDIDE"
441..448
/note="altaaac was ac in [1]"
/citation= [1]
old_sequence 641..643
/note="agc was ac in [1]"
old_sequence 652..653
/citation= [1]
old_sequence 731..733
/note="ta was tta in [1]"
old_sequence 780..781
/note="caa was ca in [1]"
/citation= [1]
old_sequence 780..781
/note="ct was ctt in [1]"
/citation= [1]
BASE COUNT 997 a 345 c 398 g 714 t
ORIGIN
Query Match 100.0%: Score 20; DB 1; Length 2454;
Best Local Similarity 100.0%: Pred. No. 2,4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTTTTATCTCGGTTA 20
|||||
Db 1307 TTCTTTTATCTCGGTTA 1288
RESULT 10 2455 bp RNA linear PAT 29-SEP-1997
E09771
LOCUS The base sequence of meca DNA.
DEFINITION E09771
ACCESSION E09771
VERSION E09771.1 GI:22026400
KEYWORDS JP 1995209294-A/1.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 2455)
AUTHORS Bacteria; Firmicutes; Bacillales; Staphylococcus.
TITLE Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
NOVEL MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
Patent: JP 1995209294-A 1 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/1
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53, C07K14/31, C12N1/21, C12N15/09, C12P21/02, C12N1/21, PC
C12R1:19)
PC (C12R1/02,C12R1:19):
CC strandedness: Double;
CC topology: Linear;

Query Match	100.0%	Score 20	DB 6	Length 2455
Host Local Similarity	100.0%	Prod. No.	2,4e+02	
Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0
0Y	1	TTCTTTTATCTTCGGTTA	20	
b	1306	TTCTTTTATCTTCGGTTA	1287	

NAMECAP/B/C	2456 bp	DNA	linear	BCT 12-SEP-1992
LOCUS	NAMECAPB			
DEFINITION	S. aureus mecA gene for PBP2' (penicillin binding protein 2).			
ACCESSION	X52593			
VERSION	X52593.1	GI:46610		
KEYWORDS	mecA gene; methicillin resistance; penicillin-binding protein; penicillin-binding protein 2 .			
SOURCE	Staphylococcus aureus .			
ORGANISM	Staphylococcus aureus .			
REFERENCE	Bacteria; Firmicutes; Bacillales; Staphylococcus .			
AUTHORS	1 (bases 1 to 2456)			
REFERENCE	Ryffel, C.			
AUTHORS	Direct Submission			
REFERENCE	Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland			
AUTHORS	2 (bases 1 to 2456)			
REFERENCE	Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E., Barbieri-Maino, L., Kayer, P. H. and Berger-Bachi, B.			
AUTHORS	Sequence comparison of mecA genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis			
TITLE	Gene 94 (1), 137-138 (1990)			
JOURNAL	Gene 94 (1), 137-138 (1990)			
MEDLINE	91033056			
PUBMED	2237446			
COMMENT	See also <X52592> <X52594> and <X00688> .			
FEATURES	Data kindly reviewed (23-JUL-1990) by C. Ryffel .			
SOURCE	Location/Qualifiers			
	1..2456			
	/organism="Staphylococcus aureus"			
	/strain="NCTC8325, isolate-BB270"			
	/db_xref="taxon:1280"			
	/clone_lib="EMBL-3"			
	80..85			
	/note=".35 region"			
	101..105			
	/note=".10 region"			
	130..134			
	/note=".ribosome binding site"			
	141..2153			
	/note=".primary transcript"			
	141..2147			
	/note="PBP2' (AA 1-668) "			
	/codon_start=1			
	/transl_table=11			
	/protein_id="CAA36829.1"			
	/db_xref="GI:46611"			
	/db_xref="SPRMBL:O53707"			
	/translation="MKIKIVLIVVVGFGIYFVAKRKEINNTIDALEDNKCKG VYKSSYTSKSDNGEVEKTEPPIITVNSLGVKIDNIDRKIKYKSKKKRDAQDIKIK ITNGSIDINVOFNFVKEDGMKMLDHSVILIPGQKDDSHIEMLKSRGKILDRNNN			
CDS	precursor_RNA			
	RBS			
	promoter			
	promoter			

BASE COUNT	1001 a	344 c	396 g	715 t	
ORIGIN					
Query Match	100.0%;	Score 20;	DB 1;	Length 2456;	
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;			
Matches 20:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1	TTCTTTTATCTTCGGTTA	20		
Db	1307	TTCTTTTATCTTCGGTTA	1288		
RESULT 12					
AX110445/c					
LOCUS	AX110445	2456 bp	DNA	linear	PAT 30-Apr-2001
DEFINITION	Sequence 1178 from Patent WO0123604.				
ACCESSION	AX110445				
VERSION	AX110445.1	GI:13926737			
KEYWORDS					
SOURCE	Staphylococcus aureus subsp. aureus NCIC 8325.				
ORGANISM	Staphylococcus aureus subsp. aureus NCIC 8325.				
REFERENCE	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
AUTHORS	1 (bases 1 to 2456) Bergeon, M.G., Boissinot, M., Huiletsky, A., m Nard, C., Ouellette, M., Picard, F.J., and Roy, P.H.				
TITLE	Highly conserved genes and their use to generate probes and primers for detection of microorganisms				
JOURNAL	Patent: WO 0123604-A 1178-05-APR-2001;				
FEATURES	Inteclo Diagnostic (1.D.1.) INC. (CA) location/Qualifiers 1..2456 /organism="Staphylococcus aureus subsp. aureus NCIC 8325" /db_xref="taxon:93061"				
BASE COUNT	1001 a	344 c	396 g	715 t	
ORIGIN					
Query Match	100.0%;	Score 20;	DB 6;	Length 2456;	
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;			
Matches 20:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1	TTCTTTTATCTTCGGTTA	20		
Db	1307	TTCTTTTATCTTCGGTTA	1288		
RESULT 13					
SSK8MECA/c					
LOCUS	SSK8MECA	5596 bp	DNA	linear	BCT 16-Jan-1998
DEFINITION	S.sciuri meca gene, strain K8 (ATCC700063).				
ACCESSION	Y13096				
VERSION	Y13096.1	GI:2791919			
KEYWORDS	meca gene; mecI gene; mecR1 gene; NTORF101; NTORF78; ORF142.				
SOURCE	Staphylococcus sciuri.				
ORGANISM	Staphylococcus sciuri				
REFERENCE	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
AUTHORS	1 (bases 1 to 5596) Wu, S., de Lencastre, H., and Tomasz, A.				
TITLE	Genetic organization of the meca region in methicillin-susceptible and methicillin-resistant strains of Staphylococcus sciuri				
JOURNAL	J. Bacteriol. 180 (2), 236-242 (1998)				
MEDLINE	98101461				
PUBMED	9440511				
REFERENCE	2 (bases 1 to 5596) Wu, S.				
AUTHORS					

TITLE	Direct Submission
JOURNAL	Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA
COMMENT FEATURES	Related sequences X53818, X56660, L14020, X52593, Y09223. location/Qualifiers
SOURCE	1. .5596 /organism="Staphylococcus sciuri" /strain="K8 (ATCC700063)" /sub_species="rodentius" /db_xref="taxon:1296"
gene	1. .236 /gene="NTOF78"
CDS	<1. .236 /gene="NTOF78" /codon_start=3 /transl_table=1 /protein_id="CAJ73550.1" /db_xref="GI:2791920" /db_xref="SPTRMBL:O54284" /translation="AFRLKPPCHTSKYLNLTLEODRHRIHKVTRTQSIINTAKNTLK GIEETALYKKNRSLDLYCFSPCHEISIMLAS" complement(485. .856) /gene="mecI" complement(485. .856) /gene="mecI" /codon_start=1 /transl_table=1 /product="MecI protein" /protein_id="CAJ73545.1" /db_xref="GI:2791921" /db_xref="SPTRMBL:O54285" /translation="MDNKTYEISSAEWEVMNIIMKKYASANYMIEELIQMKDKSPPT IRLTATRLRYKKGFIDRRKDNIKFOYSLSVEESDIKYTSKNFIKKVYKGGFNLSLVLPF VERKIDLSODEIEELRNILNKK" complement(join(856. .2613, 2620. .2626, 2638. .2643)) /gene="mecR1" complement(856. .2613) /gene="mecR1" /codon_start=1 /transl_table=1 /product="MecR1 protein" /protein_id="CAJ73546.1" /db_xref="GI:2791922" /translation="MLSSFLMLSTISSLITCYIFLVRMYIKYTQNIMSHKIWLVL VSPIPLIPLPFKLSNPFPFSKDMNNRVSDTTSSVHMLDCOSSVTKDLAINVOFFET SNIIYYMLILWFGSFLCILEPMIKAPNOIDYIKSSLESSYLNRLLKVCOSKMOPFY HITLTSYSDININPWFGLVQSOLIVPVVVFTNMKDELEYILLHELISHVSHDILPNQ LYVFRTKTFWNPALYISKTMMDNDCEKVCDRNVKLNLNHEHTRGESITKCSILKS OHINNAQYILGFRNSNTERVKYITALDSPFNKRNRIVAVTVGSISLIQLPALS AHVQDYETVWSYGRKLNLQALPYRGDFGVLYNERQASITYNEPSKORSPTSST YKILVALMAPDONILI,SLNHTEQDNWKHOYPKEWNODONLNSSMKSYVMNYEALNKH LRQBHVSVYLDILIEYGNEELSGOWENNESLKTSAILOYVNLKMKQHMHFPNKAII EKVANSMTLKOQDTYKVKVGCTGCIVNHKEANGFWGVETKIDNFYFAFHLAGEDANA NGEKAQDISERILTEMELI"
gene	complement(865. .869)
RBS	/gene="mecI" complement(865. .869) /gene="mecI" complement(2620. .2626) /gene="mecR1" complement(2638. .2643) /gene="mecR1"
-10_signal	2652. .2657 /gene="mecl"
gene	2652. .2657 /gene="mecl"
-35_signal	2652. .2657 /gene="mecl"
gene	complement(2663. .2668) /gene="mecl1" complement(2663. .2668) /gene="mecl1"
-35_signal	2676. .4719 /gene="mecl"
gene	2676. .2681 /gene="mecl"
-10_signal	

Query Match	100.0%	Score 20	DB 1	Length 5996
Best Local Similarity	100.0%	Pred. No. 2.2e+02		
Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy 1	TTCTTTTATCTTCGGTTA 20			
Db 3879	TTCTTTTATCTTCGGTTA 3860			
RESULT 14				
SSK3MECA2/c				
LOCUS	SSK3MECA2	6368 bp	DNA	
DEFINITION	S.sciuri meca2 gene, strain K3 (MM2).	linear	BCT 16-JAN-1998	
ACCESSION	Y13095			
VERSION	Y13095.1	GI:2791912		
KEYWORDS	CTOPF261 gene; meca2 gene; meci gene; mecr1 gene; NTORF101; ORF142.			
SOURCE	Staphylococcus sciuri			
ORGANISM	Staphylococcus sciuri			
RBS	/gene="meca" 2702..2707 /gene="meca" 2713..4719 /gene="meca" /codon_start=1 /transl_table=1 /product="Meca protein" /protein_id="CA73547.1" /db_xref="GI:2791923" /db_xref="SPTREMBL:054286" /translation="MKKIKIPLILIVVGRGIYFVAKDKKEININTJDAIEDNPFKQ VKKSSYISKSDNGEVEKTERPKIKYNSLQKDIINIDRKIKKSKKKRRDAQKIKIT TYNGSIDRNVQFNFVEKEDGMMKLDDHSVILPGMKDDSIHIEULKSERKILDRNN ELANGTAYEIGIVPKVNSKKDYKIAELSLSEDYIKQOMQMWQJDTVPILKTVN KMDLIDSPFAKKPHLITNETESRNPPLKAKSHLIGVGPINSEPLKQEKYKGDIDP V1GCKGLKLDYDKLQHEQDGRVTVNDNSNTIAHTLLEKKKDGKDIOLTIIDAKVO SYNNKKNDYSGSTAIHPQTGELLALVTPSYDYPPEMGKSNSEYKNTLEDKEPLIL NKFOITTSRGSSTOKLITAMIGLNNKTLTDKTSYKIDQGMQKDKSMGCYANTREYEV GNIDLKQALIESDNIFFARVALELSKKFEFGMKKLGVEDIPSDYPFYNAOISKNIN DNEILLADSGYGQGETLINIPQIILISTYALENNCINANPHLLKDTKNNVWKRNIISK NIILLTLDQGVYNNKTHKEDIYRSYANLIGKSGIAELKMKQGTGKRGIMPEISYDKD PNMMAIINVKDVQOKCMASYNAKISGKYVDELYENGGNKYDIDF" complement(4765)..5266) /gene="ORF142" complement(4765)..5193) /gene="ORF142" /transl_table=1 /codon_start=1 /protein_id="CA73548.1" /db_xref="GI:2791924" /db_xref="SPTREMBL:054520" /translation="MKYDPRITGCEPFKKSILHTEELIQYATTFEDQYMHIDKKAKR QSRKGIJASGMHTLISIFKLMWEGKTGEVFACTQNNVFKIPYPCNTLVIAHEAV ITNNKSIKKEGLVIVSLSTYNNENEIVFKGEVYALINNS" complement(5200)..5205) /gene="ORF142" complement(5238)..5243) /gene="ORF142" complement(5261)..5266) /gene="ORF142" complement(5290)..5596) /gene="NTORF101" complement(5280)..55596) /gene="NTORF101" /codon_start=2 /transl_table=1 /protein_id="CA73549.1" /db_xref="GI:2791925" /db_xref="SPTREMBL:054616" /translation="SFNVLVKILAEELIMPOYNRAVIFHTTSSRFHDWRFLLDYCNAKTIV NTEDAKILTKAVKVKVKEGVEELANVTYVTPARANQLANMWCVDIGLITPDNADKMYHLSQ"			

REFERENCE 1 (bases 1 to 6368)
Bacteria: Firmicutes; Bacillales; Staphylococcus.
AUTHORS Wu, S., de lencastre, H. and Tomasz, A.
TITLE Genetic organization of the mecA region in methicillin-susceptible
JOURNAL J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 98101461
PUBMED 9440511
REFERENCE 2 (bases 1 to 6368)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences U14020, X52593, Y09223.
FEATURES
source location/Qualifiers
1..6368
/organism="Staphylococcus sciuri"
/strain="K3 (MM2)"
/sub_species="rodentius"
/db_xref="taxon:1296"
complement(1..883)
/gene="CTORF261"
complement(<1..784)
/gene="CTORF261"
/codon_start=1
/transl_table=11
/protein_id="CAA73539.1"
/db_xref="GI:2791913"
/db_xref="SPTREMBL:O54280"
/translation="MENTLININDEKRYLAEIYNHNHISRTQISKNIEINKATISLL
NKLKYSLVNEVGSDSTKSGRKPIILLKNHLGYRISLDLYSSVEVMNFDGNY
IKHESYDLPEKVSLSIIKIHIDIEKLDYNGLLGVSISGVVDNEQHYLTF
HETEGISIAKKIEKITNVPVVEANMISALYERNMHNLSYNMLIALSIHKIGIAGL
IINOLYRGANGEGEIGKTLVSKVSDNVEIFHKIEDIFSQEA"
complement(791..797)
/gene="CTORF261"
complement(855..860)
/gene="CTORF261"
complement(878..883)
/gene="CTORF261"
complement(1257..1628)
/gene="mecI"
complement(1257..1628)
/gene="mecI"
/codon_start=1
/transl_table=11
/product="MecI protein"
/protein_id="CAA73540.1"
/db_xref="GI:2791914"
/db_xref="SPTREMBL:O54281"
/translation="MDNKIYESSAEWEVNNIIMKKYASANNILEIOMQRDMPKT
IKRLITRIYKKCFIDRKKDKIPQYISLVESDITKTKSNFINKKYKGGPNSLVLP
VEKEDLSQDEIEELRNLNK"
complement(1628..3385,3392..3398,3410..3415)
/gene="mecR1"
complement(1628..3385)
/gene="mecR1"
/codon_start=1
/transl_table=11
/product="MecR1 protein"
/protein_id="CAA73541.1"
/db_xref="GI:2791915"
/db_xref="SPTREMBL:O54282"
/translation="MLSSFLMLCIISLLTICVFLVRLMYIKYTONIMSKIMLIVL
VSTLPIIPYKISNPFSDKMMNRNRSPTTSVSHMLDQOQSVTDLAINNOFET
SNITTMILLVFGSLCLFYMKAPODIVIKSSLESSITLNERLVCOSKMDYFK
HITISYSSNDNPNVGLVKSQIVLPVVEIMNDKEIEYIIILHLSHVSHPDIQ
LYVFKMIFWENFALYISKTMNDCEKCDRNLKILNHEHRIYGESILKISILS
QHNINVAQYLLGFNSNIKERVYIALYDSMPNRRKRIYAVIVCSISLLIQPLS
AHVQODRETNVNSKILNOLAPYFKGDSFVLYNEROAYSIYNESPOYSORSPNT
KYIYIALMARFONLSLNHTEDQMDKHQYFPKEMNODONLSSMKYSVNNYENLNK
LRDEKYSYDLIEYGNESISCHNENYNNESIKISAEQVNLKDMQHNHFNKRI
EKVNSHTLKQDITKYVGTGIVNHEKANGFVGIVETKNTYIFATHLKEDNA

gene complement(1636..1640)
/gene="mecI"
complement(1636..1640)
/gene="mecI"
complement(3392..3398)
/gene="mecR1"
complement(3410..3415)
/gene="mecR1"
3424..3429
/gene="meca2"
3424..3429
/gene="meca2"
3424..3429
/gene="meca2"
complement(3433..3438)
/gene="mecR1"
complement(3433..3438)
/gene="mecR1"
3448..3453
/gene="meca2"
3474..3479
/gene="meca2"
3485..3491
/gene="meca2"
/codon_start=1
/transl_table=11
/product="Meca2 protein"
/protein_id="CAA73542.1"
/db_xref="GI:2791916"
/db_xref="SPTREMBL:O54283"
/translation="MKRIKIVPLIYVVVVGFIYFASKOKEINTIDAIGDNFKO
VYKSSYISDSNGEVEEMTEPRKITYNSLGVKDINODRKIKKYSKKKIKDRAV
TNGCNIDRNVFNKEDGMKILMDHSHVILIPGOKDOSIHINLASEKRIIDRNV
ELANTGAYEIGIYPAKVSCKDYKAIKELISDHYTKOOMDQWVDDTFVPLKTYK
KMDYISDFAKKFLITNETSRNPLEKATSHLGVGPINSEELKOKETKGYKDDA
VIGKKGLEKLYDKLQHEDEGRVITVDNSNTLAHTLIEKKKDGKDIOLTIDAKYOK
SIYNNMKNDGSGTAIHPOTGELLAVTSPSYDVPYPMGMSDEYKLTEDKEPPL
NKFOITTPSGSTOKILYAMIGLNKTLDDTSTYKIDGCKQKDSMGGYVVDREYVA
GNIDKOAIESDNIIPFARVALELGSKPFKGMKLGVDHIPSDFPYNAOISNKL
DNELLADSGGGEILLINPOLIISYSALENNGINAPVHLIDTKKKKKKNTISKE
NINLTGDMQVYKTKHEDIRSYANLIGKSGTAEIKMKOGETGRPIGNFISTDKON
PHLMALINVKDYPDKMASTNAKISGVYDELYENKKYDIDE"
complement(5537..5965)
/gene="ORF142"
complement(5537..5965)
/gene="ORF142"
/codon_start=1
/transl_table=11
/protein_id="CAA73543.1"
/db_xref="GI:2791917"
/db_xref="SPTREMBL:O54520"
/translation="MKYDDPVGTFPKTSILHTEPEIIQFATTFDPQYMHIDKKA
OSRFGIISGMHTLSISFKLWVEEGYGEVYAGTOMNNVFIKIPYYPONTIYVIAE
ITNKSITIKKNGIATVSLSTYNNEMELVFKEGYALINNS"
complement(5972..5977)
/gene="ORF142"
complement(6010..6015)
/gene="ORF142"
complement(6033..6038)
/gene="ORF142"
complement(6062..6368)
/gene="NTORF101"
complement(6062..6368)
/codon_start=2
/transl_table=11
/protein_id="CAA73544.1"
/db_xref="GI:2791918"
/db_xref="SPTREMBL:O54616"
/translation="SFNVVVLVLAEEIIMPQYNRAVIFHTTSFREDNRLLDYCNKIV
NTEBAKLTAKKVKVKEAGVELVTVNKPARANOLANMGVGDIFTDNDKRVHLISQ"

BASE COUNT

2230

a

998

c

884

g

2256

t

/translation-"MNFFRYKOFNKDVITVAVGYLYRYTLSTYROISETILREGVNVHH
STVYRWQOEYAPILYQIMKKKKKAYKMRIDETVITIKGKSYLYRAIDAGHTLDI
WLRKORDHNSAFAPIKRLIKOPCKPQXVITPOAPSTKAMAKVITAFKLPDCHCTSK
YLNNLIEDDHRIKVKTRVOSINTAKNTLKGIECTVADYKKNRSLQIYGFSPCHEI
SIMLAS"

BASE COUNT 3099 a 1469 c 1257 g 3222 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 9047;
Best local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTCGGTTA 20
|||||
DB 4638 TTCTTTTATCTCGGTTA 4619

Search completed: December 10, 2002, 20:17:03
Job time : 437.756 secs

PT mRNA -
 XX Claim 1; Page 17; 28pp; English.
 PS
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the meca gene (associated with methicillin resistance in
 CC Staphylococcus aureus) or its derived RNA. The invention also comprises
 CC a detection method employing an RNA amplification process, using RNA
 CC derived from the meca gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a
 CC change in the fluorescent property relative to that of a situation where
 CC a complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant S. aureus in
 CC clinical samples. They may also be used therapeutically to inhibit RNA
 CC reverse transcription or translation. These oligonucleotides permit
 CC rapid and very sensitive detection/identification of the meca gene, at a
 CC relatively low temperature without the need for heat denaturation of
 CC target RNA. The present sequence represents a methicillin resistant
 CC Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 2 G; 13 T; 0 other;
 Query Match 100.0%; Score 20; DB 24; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTCTTTTATCTCGGTTA 20
 DB 1 TTCTTTTATCTCGGTTA 20
 ID ABR85923 standard; DNA; 20 BP.
 XX ABR85923;
 AC 16-AUG-2002 (first entry)
 DT
 XX
 DE Methicillin resistant Staphylococcus aureus detection primer #23.
 XX
 KW Methicillin resistant Staphylococcus Aureus; MRSA; primer; ss;
 KW meca; probe.
 XX
 SC Staphylococcus aureus.
 EP1160333-A2.
 XX
 PD 05-DEC-2001.
 XX
 PF 29-MAY-2001; 2001EP-0112100.
 XX
 PR 29-MAY-2000; 2000JP-0163149.
 PR 09-JUN-2000; 2000JP-0179394.
 XX
 PA (TOXJ) TOSOH CORP.
 XX
 PI Taya T, Ishiguro T, Salto J;
 XX
 DR WPI: 2002-395832/43.
 XX
 PT New oligonucleotide specific for the meca methicillin-resistance gene,
 PT useful for cleavage, detection and amplification of the gene or related
 PT mRNA -
 XX
 PS Claim 5; Page 20; 28pp; English.
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the meca gene (associated with methicillin resistance in

CC Staphylococcus aureus) or its derived RNA. The invention also comprises
 CC a detection method employing an RNA amplification process, using RNA
 CC derived from the meca gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a
 CC change in the fluorescent property relative to that of a situation where
 CC a complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant S. aureus in
 CC clinical samples. They may also be used therapeutically to inhibit RNA
 CC reverse transcription or translation. These oligonucleotides permit
 CC rapid and very sensitive detection/identification of the meca gene, at a
 CC relatively low temperature without the need for heat denaturation of
 CC target RNA. The present sequence represents a methicillin resistant
 CC Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 2 G; 13 T; 0 other;
 Query Match 100.0%; Score 20; DB 24; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTCTTTTATCTCGGTTA 20
 DB 1 TTCTTTTATCTCGGTTA 20
 ID AAO86977/C
 XX AAO86977 standard; DNA; 467 BP.
 XX AAO86977;
 AC 16-JAN-1996 (first entry)
 DT
 XX
 DE Polynucleotide probe for methicillin resistant Staphylococcus aureus.
 XX
 KW MRSA; methicillin resistant Staphylococcus aureus; probe;
 KW hybridisation; meca; MRSE; Staphylococcus epidermis; ss.
 XX
 OS Staphylococcus aureus.
 XX
 PN DE4338119-A1.
 XX
 PD 11-MAY-1995.
 XX
 PE 08-NOV-1993; 93DE-4338119.
 XX
 PR 08-NOV-1993; 93DE-4338119.
 XX
 PA (FAHB) BAYER AG.
 XX
 PI Endermann R, Springer W;
 XX
 DR WPI: 1995-180108/24.
 XX
 PT Detection of methicillin resistant Staphylococcus - using an
 PT oligo:nucleotide derived from the meca gene
 XX
 PS Claim 2; Page 11; 14pp; German.
 XX
 CC An oligonucleotide probe having the 467 nucleotide sequence shown
 CC isolated from S. aureus, is capable of hybridising with the DNA or
 CC RNA of methicillin resistant S. aureus (MRSA). The probe is
 CC specifically derived from the meca gene of S. aureus and S. epidermidis.
 CC The meca gene product has no homology with known PBs
 CC (penicillin-binding proteins). The new probes allow for the rapid
 CC identification of all MRSE, indicating need for labour intensive in
 CC vitro cultivation and physiological assays.
 XX
 SQ Sequence 467 BP; 187 A; 73 C; 85 G; 122 T; 0 other;

```
Query Match      100.0%: Score 20; DB 16; Length 467;
Best Local Similarity 100.0%: Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTCGGTTA 20
    |||||||
Db 143 TTCTTTTATCTCGGTTA 124

RESULT 4
AAT04536/c
ID AAT04536 standard; cDNA to mRNA; 1789 BP.
XX
XX AAT04536;
AC
XX
XX 11-APR-1996 (first entry)
DT
XX
XX Staphylococcus aureus 'meca' protein coding sequence.
PT methicillin-resistant Staphylococcus aureus; MKSA; 'meca' protein;
KW antibiotic resistance; ds.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..1608
FT /*tag= a
FT /product= 'mec_A' protein
XX
XX JF07209294-A.
PN
XX
XX 11-AUG-1995.
PD
XX
XX 10-JAN-1994; 94JP-0012226.
PF
XX
XX 10-JAN-1994; 94JP-0012226.
PR
XX
XX 10-JAN-1994; 94JP-0012226.
PA (DENK-) DENKA SEIKEN KK.
PA (KAWA/) KAWANO M.
PA (MITU ) MITSUBISHI CHEM CORP.
XX
XX WPI: 1995-313917/41.
DR P-PSDB; AAR80035.
XX
XX New 'mec A' protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
PT
XX
XX Claim 5; Page 11-13; 15pp; Japanese.
AX
CC The present sequence codes for the 'mec A' protein which controls
CC methicillin resistance in methicillin-resistant Staph. aureus. The
CC 'mec A' protein (mol. wt. 40000) is useful for preparation of
CC antiserum specific for MRSA, thereby allowing methicillin-resistant
CC and methicillin-sensitive strains to be distinguished. The coding
CC sequence was obtained by PCR amplification of the mec A sequence
CC (see AAT04538) using primers AAT04537 and AAT04539.
CC N.B. in the sequence listing of the patent specification, the
CC sequence length is stated to be 1785 bp.
XX
XX
SQ Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;

Query Match      100.0%: Score 20; DB 16; Length 1789;
Best Local Similarity 100.0%: Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTCGGTTA 20
    |||||||
Db 768 TTCTTTTATCTCGGTTA 749

RESULT 5
AAQ28399/c
```

```
ID AAQ28599 standard; DNA; 2007 BP.
XX
XX AAQ28599;
AC
XX
XX 19-FEB-1993 (first entry)
DT
XX
XX Encodes penicillin binding protein PBP2a-27R.
DE
XX
XX Penicillin; antibiotic; bacteria; methicillin; staphylococci;
KW soluble; chelating peptide; MRS infection; methicillin resistant;
KW strain.
XX
XX Staphylococcus aureus strain 27R.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..2007
FT /*tag= a
FT
XX
XX EP505151-A.
PN
XX
XX 23-SEP-1992.
PD
XX
XX 18-MAR-1992; 92EP-0302298.
PF
XX
XX 19-MAR-1991; 91US-0672704.
PR
XX
XX (ELIL ) LILLY & CO E.L.I.
PA
XX
XX Blaszcak LC, Skatrud PL, Smith MC, Wu CYE;
PI WPI: 1992-318034/39.
XX
XX Polynucleotide cpd. encoding PBP 2a-27R protein or its deriv. -
PT contains PBP isolated from Staphylococcus aureus and is used to
PT treat methicillin resistant staphylococci
XX
XX Disclosure: Page 14; 101pp; English.
XX
XX This sequence encodes a PBP2a penicillin binding protein isolated
CC from S. aureus strain 27R. A cDNA library was constructed from
CC S. aureus DNA in lambda phage EMBL3. Packaging extracts from this were
CC then used to infect E. coli Cj236. Plaques were screened for the
CC presence of the mecA-27R gene by a probe produced by PCR amplification
CC of the mecA gene using primers Q28600.1. Positive plaques were purified
CC and digested with HindIII, and this fragment digested with XbaI and
CC cloned into M13mp18 and M13mp19 for sequencing.
CC
XX
XX Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
SQ

Query Match      100.0%: Score 20; DB 13; Length 2007;
Best Local Similarity 100.0%: Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTCGGTTA 20
    |||||||
Db 1167 TTCTTTTATCTCGGTTA 1148

RESULT 6
AAT28568/c
ID AAT28568 standard; DNA; 2007 BP.
XX
XX AAT28568;
AC
XX
XX 01-APR-1997 (first entry)
DT
XX
XX Bacterial antibiotic resistance gene, mecA, probe.
DE
XX
XX Detection: probe; amplification primer; bacterial pathogen; pneumonia;
KW Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
KW Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
KW Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
KW Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
KW
```


KM		penicillin binding protein; PBPA-27A; meca-27R gene;
KW		penicillin resistance; antibiotic; assay; purification; ss.
XX		
OS		Staphylococcus aureus.
XX		
PX		EP875578-A2.
PD		
XX		04-NOV-1998.
PF		18-MAR-1992; 92EP-0302298.
PR		19-MAR-1991; 91US-0672704.
PA	(ELIL) LILLY & CO ELI.	
PL	Biasczak LC, Skatrud PL, Smith MC, Wu CE;	
DR	WPI: 1998-559443/48.	
DR	P-PDSB; AAM81149.	
XX		
PT	New Staphylococcus aureus soluble penicillin-binding proteins and	
PT	their derivatives - useful for screening for compounds effective	
PT	against methicillin resistant organisms	
PS	Disclosure: Page 14-16; 97pp: English.	
CC	This meca-27R gene encodes penicillin binding protein 2A (PBPA-27R)	
CC	responsible for the methicillin resistance of Staphylococcus aureus	
CC	strain 27R. The invention provides new PBPs of formula Sp-I-PBP2As,	
CC	where: Sp is 0 or a signal peptide (preferably from the ampc, ompA or	
CC	Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see	
CC	AAM81151-58) of formula (His)x(A-Y)(His)z and A=an amino acid,	
CC	x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above,	
CC	polypeptide where each monomer unit is the same or different; Pro	
CC	is proline, n = 0 or 1; and PBP2As is soluble PBPA-27R protein (see	
CC	AAM81159-62). Also claimed are polynucleotides encoding specific	
CC	soluble PBPA compounds. The new PBPA-27R proteins are useful for	
CC	assaying for agents useful as antibiotics against methicillin	
CC	resistant Staphylococcus strains by creating a kinetically inert	
CC	complex between a support-immobilised transition ion and a modified	
CC	soluble PBPA protein comprising a chelating agent, which screens	
CC	for agents which bind to PBPA proteins (disclosed).	
CC	transmembrane association region, and so are useful for x-ray	
CC	crystallography studies of the protein, assisting in the design of	
CC	antibiotic compounds against methicillin resistant Staphylococcus	
CC	strains (disclosed).	
CC	The chelating peptide operably linked to the	
CC	PBPA-27R proteins is useful for purifying PBPs.	
SQ	Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other:	
	Query Match	
	Best Local Similarity 100.0%; Score 20; DH 19; Length 2007;	
	Matches 20; Conservative 0; Pred.No. 35;	
OY	1 TTCTTTTATTCGCGCTTA 20	
DJ	TTTTTTTTTTTT	
	1167 TTTCTTTTATCTTGCGCTTA 1148	
	TTTTTTTTTTTT	
	ABAT6993/C	
XX	ABA76993 standard; DNA; 2007 BP.	
AC	ABA76993;	
DT	28-JAN-2002 (first entry)	
XX		
XE	Antibiotic resistance detection polymucleotide SEQ ID NO 169.	
XX		

XX OS Unidentified.
 XX PN NZ501596-A.
 XX PD 29-JUN-2001.
 XX PF 12-SEP-1995; 95NZ-0501596.
 XX PR 12-SEP-1995; 95NZ-0501596.
 XX PA (ID11-) ID1 INFECTION DIAGNOSTIC INC.
 XX PI Bergeron MG, Ouellette M, Roy PH;
 XX DR WPI: 2001-615034/71.
 XX PS
 PT Method for detecting target bacterial species in a sample, comprises
 PT detecting the presence or amount of bacterial nucleic acid amplified by
 PT a primer derived from bacterial DNA, specific for the target bacterial
 PT species -
 XX
 PS Claim 16; Page 159-160; 168pp; English.
 CC The invention relates to detecting target bacterial species suspected to
 CC be present in a sample, comprising contacting nucleic acids of target
 CC bacterial species with an amplification primer pair derived from a
 CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target
 CC bacterial species but ubiquitous for different strains, amplifying the
 CC nucleic acid and detecting the presence or amount of an amplified
 CC sequence as an indication of the presence or amount of the target
 CC bacterial species. The invention includes primers and probes
 CC (ABA76862-ABA76984) against the target bacterial species, especially
 CC E.coli, K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae,
 CC S.aureus, S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes,
 CC H.influenzae, M.catalis and/or group A Streptococci producing
 CC exotoxin A gene spe A, suspected to be present in a sample which is
 CC obtained from human patients, animals, environment or food, and which
 CC consists of one or more bacterial colonies. Oligonucleotide
 CC probes and primers complementary to the bacterial genes encoding
 CC resistance to antibiotics such as bla(tem), bla(tob), bla(shv), aadB,
 CC aacC1, aacC2, aacC3, aacC4, mecA, vanA, vanX, aacA-aphD, vat,
 CC vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify
 CC commonly encountered and clinically important resistance genes. The
 CC invention provides a rapid method of bacterial identification that can be
 CC achieved, which reduces the time currently required for the
 CC identification of pathogens in the clinical laboratory.
 CC
 XX
 SQ Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
 Query Match 100.0%; Score 20; DB 22; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TTCTTTTATCTTCGCTTA 20
 Db 1167 TTCTTTTATCTTCGCTTA 1148
 XX
 RESULT 9
 ID ABA92247/c
 XX ABA92247 standard; DNA; 2028 BP.
 XX AC ABA92247;
 XX
 DT 24-JUL-2002 (first entry)
 XX
 DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.
 XX
 KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 XX antibacterial; gene therapy; gene; ds.
 OS Staphylococcus epidermidis.

XX PN US6380370-B1.
 XX PD 30-APR-2002.
 XX PF 13-AUG-1998; 98US-0134001.
 XX PR 14-AUG-1997; 97US-055779P.
 XX PR 08-NOV-1997; 97US-064964P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Doucette-Stamm LA, Bush D;
 XX DR WPI: 2002-381255/41.
 XX DR P-PSDB: ABP39702.
 XX PS
 PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
 PT polypeptide, useful for diagnosing and treating bacterial infections -
 XX
 PS Disclosure: SEQ ID 1710; 267pp; English.
 CC ABA990538 to ABA93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABA935124 to ABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences
 CC can also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life
 CC cycle or inhibit S. epidermidis infection.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO web site.
 CC
 XX
 SQ Sequence 2028 BP; 861 A; 273 C; 346 G; 547 T; 1 other;
 Query Match 100.0%; Score 20; DB 24; Length 2028;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TTCTTTTATCTTCGCTTA 20
 Db 1188 TTCTTTTATCTTCGCTTA 1169
 XX
 RESULT 10
 ID ABA935213/c
 XX ABA935213 standard; DNA; 2110 BP.
 XX AC ABA935213;
 XX
 DT 06-JUN-1993 (first entry)
 XX
 DE Sequence of the msc A gene.
 XX
 KW Methicillin-resistant staphylococci; detection; primer; PCR; ss.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key location/Qualifiers
 FT CDS 105..2110
 FT /*tag= a
 XX
 PN EP527628-A.
 XX
 PD 17-FEB-1993.
 XX
 PF 10-AUG-1992; 92EP-0307307.
 XX
 PR 13-AUG-1991; 91US-0744770.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX

PI Skatrud PL, Unal S;
 XX
 DR WPI: 1993-054352/07.
 DR P-PSDB; AAR30845.
 XX
 PT
 PT Detection of methicillin-resistant staphylococci - using
 PT sensitive and accurate detection
 XX
 PS Disclosure; Pages 7-10; 16pp; English.
 XX
 CC The inventors claim a method for detecting methicillin-resistant
 CC staphylococcal infections which involves the use of the PCR primed
 CC by fragments of the staphylococcus meca gene. More specifically, the
 CC initial primers used are nucleotides 141-160 and the inverse
 CC complement of nucleotides 1929-1952 of the S. aureus meca gene.
 CC The interior primers are nucleotides 568-593 and the inverse complement
 CC of 1647-1670 of the S. aureus meca gene.
 XX
 SO Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;
 Query Match 100.0%; Score 20; DB 14; Length 2110;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TTCTTTTATCTTCGGTTA 20
 DB 1271 TTCTTTTATCTTCGGTTA 1252

RESULT 11
 AAQ25905/c
 ID AAQ25905 standard; DNA; 2322 BP.
 XX
 AC AAQ25905;
 XX
 DT 18-JAN-1993 (first entry)
 XX
 DE PBP2'.
 XX
 KM Polymerase chain reaction; PCR; amplification; ss.
 OS Synthetic.
 XX
 FH Key location/Qualifiers
 FT misc_binding 1581..1598
 FT /tag= a
 FT /Label= Probe_binding_site
 XX
 PN JP04169200-A.
 PD
 XX 17-JUN-1992.
 XX
 PF 31-OCT-1990; 90JP-0296708.
 31-OCT-1990; 90JP-0296708.
 (SHIO) SHIONOGI & CO LTD.
 WPI: 1992-253403/31.
 Detection of PBP2' gene for determ. of methicillin-resistance -
 PT useful esp. for detection of methicillin-resistance -
 PT Staphylococcus aureus
 XX
 PS Disclosure; Fig 1; 9pp; Japanese.
 CC The sequence given is the PBP2' gene. This gene could be detected
 CC by the primer sequences given in AAQ25897-904. Due to the results of
 CC this amplification reaction resistance to methicillin in Staphylococcus
 CC aureus could be determined.
 XX
 SO Sequence 2322 BP; 940 A; 324 C; 389 G; 669 T; 0 other;

Query Match 100.0%; Score 20; DB 13; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TTCTTTTATCTTCGGTTA 20
 DB 1173 TTCTTTTATCTTCGGTTA 1154

RESULT 12
 AAT04538/c
 ID AAT04538 standard; CDNA to mRNA; 2455 BP.
 XX
 AC AAT04538;
 XX
 DT 11-APR-1996 (first entry)
 XX
 DE Staphylococcus aureus meca protein coding sequence.
 XX
 KM methicillin-resistant Staphylococcus aureus; MRSA; 'meca protein';
 KW antibiotic resistance; ds.
 XX
 OS Staphylococcus aureus.

FH Key location/Qualifiers
 FT CDS 134..2146
 FT /tag= a
 FT /Product= mec_A-protein
 XX
 PN JP07209294-A.
 PD
 XX 11-AUG-1995.
 XX
 PE 10-JAN-1994; 94JP-0012226.
 XX
 PR 10-JAN-1994; 94JP-0012226.
 XX

PA (DENK-) DENKA SEIKEN KK.
 PA (KAWA/) KAWANO M.
 PA (MITU) MITSUBISHI CHEM CORP.
 XX
 DR WPI: 1995-313917/41.
 DR P-PSDB; AAR80036.
 XX

PT New 'mec A protein and DNA encoding it - used for the detection of
 PT methicillin-resistant Staphylococcus aureus
 XX

PS Example 2; Page 8-10; 15pp; Japanese.

CC The present sequence codes for the mec A protein. DNA coding for
 CC the 'mec A protein, which controls methicillin resistance in
 CC methicillin-resistant Staph. aureus (MRSA), was obtained by PCR
 CC AAT04539. The 'mec A sequence using primers AAT04537 and
 CC preparation of antiserum specific for MRSA, thereby allowing
 CC methicillin-resistant and methicillin-sensitive strains to be
 CC distinguished.
 XX

SO Sequence 2455 BP; 997 A; 344 C; 401 G; 713 T; 0 other;
 Query Match 100.0%; Score 20; DB 16; Length 2455;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
 DB 1306 TTCTTTTATCTTCGGTTA 1287

RESULT 13
 AAH01187/c
 ID AAH01187 standard; DNA; 2456 BP.

```

XX AC AAH01187;
XX DT
XX DE Staphylococcus aureus nucleotide sequence SEQ ID NO:1178.
XX ST
XX KW Species specific; genus specific; family specific; probe; detection;
XX KW Identification; algal; archaeal; bacterial; fungal; parasitic;
XX KW microorganism; diagnosis; translation elongation factor Tu; toxin;
XX KW translation elongation factor G; RecA recombinase; resistance;
XX KW catalytic subunit of proton-translocating ATPase; antimicrobial;
XX KW vaccine; primer; ds.
XX OS Staphylococcus aureus.
XX PN
XX MO200123604-A2.
XX 05-APR-2001.
XX 28-SEP-2000; 2000MO-CN01150.
XX PR 28-SEP-1999; 99CA-2283458.
XX PR 19-MAY-2000; 2000CA-2307010.
XX PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
XX PI Picard FJ, Roy PH;
XX DR WPI; 2001-245006/25.
XX PT Nucleic acid sequences are used to generate universal probes and
XX PT primers which can be used to identify and detect the presence of algal,
XX PT archaeal, bacterial, fungal and parasitological species in a test sample -
XX PS disclosure; Page 1048-1049; 1580pp; English.
XX CC The present invention describes a method for generating a repository of
XX CC nucleic acids of tuf, fus, atpd and/or recA genes from which probes
XX CC and/or primers are derived. The method comprises amplifying the nucleic
XX CC acids of determined algal, archaeal, bacterial, fungal and parasitological
XX CC species with a combination of defined primer pairs. The method can be
XX CC used for producing probes and/or primers for detecting one or more
XX CC related microorganisms e.g. algae, archaea, bacteria, fungi and
XX CC parasites, for universal detection and for specific, bacterial, fungal
XX CC detection and identification of an algal, archaeal, bacterial, fungal
XX CC and parasitological species, genus, family and group. A nucleic acid (I)
XX CC obtained using the method of the invention can be used for the universal
XX CC detection of any bacterium, fungus or parasite in a sample and for the
XX CC detection of at least one antimicrobial agent resistance gene or at
XX CC least one toxin gene. hexa nucleic acids are used for the specific and
XX CC ubiquitous detection and for identification of Streptococcus pneumoniae.
XX CC (I) can be used to design a therapeutic agent which is effective against
XX CC microorganisms. Microbial species or genus or family or phylum or group
XX CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
XX CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
XX CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp.,
XX CC Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests
XX CC provides faster results than substrate specificity tests as results can
XX CC be determined in an hour and improved accuracy is also achieved.
XX CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
XX CC which are given in the exemplification of the present invention.
XX SQ
SQ Sequence 2456 BP; 1001 A; 344 C; 396 G; 715 T; 0 other;
Query Match 100.0%; Score 20; DB 22; Length 2456;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTTTTATCTTCGCTTA 20
DB 1307 TTCTTTTATCTTCGCTTA 1288

```

```

RESULT 14
AAAX20260/C
ID AAAX20260 standard; DNA: 9542 BP.
XX AC
XX DE AAAX20260;
XX ST
XX KW 04-MAY-1999 (first entry)
XX DE Borrelia burgdorferi polynucleotide sequence #13.
XX KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
XX KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
XX KW infection; diagnosis; characterisation; detection; ds.
XX OS Borrelia burgdorferi.
XX PN
XX MO9858943-A1.
XX PD
XX 30-DEC-1998.
XX PF 18-JUN-1998; 98MO-US12764.
XX PR 03-SEP-1997; 97US-0057483.
XX PR 20-JUN-1997; 97US-0050359.
XX PR 22-JUL-1997; 97US-0053344.
XX PR 22-JUL-1997; 97US-0053377.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (MED1-) MEDIMUNE INC.
XX PI Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO;
XX PI White OR;
XX DR WPI; 1999-081217/07.
XX CC New isolated Borrelia burgdorferi nucleic acids - used to develop
XX CC products for the detection, diagnosis, characterisation, prevention
XX CC and therapy of infections, particularly Lyme disease
XX PS Claim 1; Page 920-925; 1128pp; English.
XX CC AAAX20248 to AAAX20402 represent polynucleotide sequences isolated from
XX CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for
XX CC the detection, diagnosis, characterisation, prevention and therapy of
XX CC Bb infections, e.g. Lyme disease. They can also be used for the
XX CC production of biosynthetic products, e.g. enzymes. Borrelia belongs
XX CC to a family of motile, spiral-shaped bacteria called Spirochetes.
XX CC Spirochetes are pathogenic in humans and Borrelia causes epidemic and
XX CC endemic relapsing fever, and Lyme borreliosis, more commonly known as
XX CC Lyme disease.
XX SQ
SQ Sequence 9542 BP; 3812 A; 1160 C; 1113 G; 3457 T; 0 other;
Query Match 92.0%; Score 18.4; DB 20; Length 9542;
Best Local Similarity 95.08; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTCTTTTATCTTCGCTTA 20
DB 4253 TTCTTTTATCTTCGCTTA 4234

```

```

RESULT 15
ABK73798/C
ID ABK73798 standard; DNA: 910 BP.
XX AC
XX DE ABK73798;
XX ST
XX KW 13-AUG-2002 (first entry)
XX DT
XX DE Bacillus licheniformis genomic sequence tag (GSTR) #1089.

```

XX Differential gene expression; genomic sequenced tag; GST;
 KW altered culture condition; environmental stress;
 KW physiological provocation; ds.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO200229113-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31437.
 XX
 PR 06-OCT-2000; 2000US-0680598.
 PR 27-MAR-2001; 2001US-279526P.
 XX
 PA (NOVO) NOVOZYMES BIOTECH INC.
 XX (NOVO) NOVOZYMES AS.
 PI Berka R, Clausen IG;
 DR WPI; 2002-416684/44.
 XX
 PT Monitoring differential expression of several genes in first Bacillus
 PT cell relative to expression of same genes in one or more second
 PP sequenced tag array -
 XX
 PS Claim 4; SEQ ID NO 1089; 200pp; English.
 XX
 CC The invention describes a method of monitoring differential expression of
 CC genes in a first Bacillus cell relative to expression of the genes in
 CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
 CC isolated from Bacillus cells to a substrate containing array of Bacillus
 CC genomic sequenced tags (GST), examining the array, and determining
 CC a spot in the array. The method is useful for measuring the expression of
 CC genes in a first Bacillus cell relative to expression of the same genes
 CC in one or more second Bacillus cells. The method is useful for monitoring
 CC global expression of several genes from a Bacillus cell, discovering new
 CC genes, identifying possible functions of unknown open reading frames and
 CC monitoring gene copy number variation and stability. Monitoring changes
 CC in expression of genes may be used to provide a representation of the way
 CC in which Bacillus cells adapt to changes in culture conditions, changes
 CC environmental stress or other physiological provocation. Extensive
 CC follow-up characterisation is unnecessary, when one spot on an array
 CC equals one gene or one open reading frame, since sequence information is
 CC available. This sequence represents a genomic sequence tag (GST) used in
 CC the method of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 910 BP; 248 A; 217 C; 262 G; 183 T; 0 other;

Query Match 87.0%; Score 17.4; DB 24; Length 910;
 Best local Similarity 94.7%; Pred. No. 3.8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTCTTTTATCTTCGCTT 19
 | |||||
 DB 552 TCCTTTTATCTTCGCTT 534

Search completed: December 10, 2002, 17:32:38
 Job time : 133.391 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 : Search time 36.2905 Seconds
(Without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-22

Perfect score: 28

Sequence: 1 aaagaaaaaagatgcgaagaatattcaa 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCY_NEM_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEM_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCYUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEM_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEM_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	10	US-09-865-579A-22
2	28	100.0	39	10	US-09-865-579A-28
3	28	100.0	2007	10	US-09-452-599-169
4	20.6	73.6	2429	10	US-09-764-864-69
5	20.6	73.6	368004	10	US-09-949-854-3
6	20.2	72.1	180557	12	US-10-003-806-6
7	20.2	72.1	180557	12	US-10-003-806-9
8	20	71.4	429	10	US-09-960-352-2449
9	20	71.4	1665	9	US-09-938-842A-3442
10	19.6	70.0	143	10	US-09-974-300-3560
11	19.6	70.0	173	10	US-09-923-876-946
12	19.6	70.0	189	10	US-09-878-574-7719
13	19.6	70.0	254	10	US-09-878-574-5615
14	19.6	70.0	260	10	US-09-878-574-8576
15	19.6	70.0	264	10	US-09-878-574-10488
16	19.6	70.0	266	10	US-09-878-574-10469
17	19.6	70.0	360	10	US-09-878-574-2202
18	19.6	70.0	389	10	US-09-878-574-2715
19	19.6	70.0	393	10	US-09-878-574-3731

20	19.6	70.0	413	10	US-09-878-574-3703	Sequence 3703, Ap
21	19.6	70.0	2153	10	US-09-917-800A-1599	Sequence 1599, Ap
22	19.6	70.0	57130	10	US-09-835-081-3	Sequence 3, Appl1
23	19.2	68.6	16484	10	US-09-070-927A-158	Sequence 158, App
24	19	67.9	281	10	US-09-867-701-8891	Sequence 8891, Ap
25	19	67.9	311	9	US-10-046-935-1802	Sequence 1802, Ap
26	19	67.9	311	9	US-09-878-178-1802	Sequence 1802, Ap
27	19	67.9	340	10	US-09-777-564-272	Sequence 272, App
28	19	67.9	346	10	US-09-878-574-2152	Sequence 2152, Ap
29	19	67.9	380	10	US-09-964-824A-2149	Sequence 349, App
30	19	67.9	380	10	US-09-880-107-1135	Sequence 1135, Ap
31	19	67.9	389	10	US-09-960-352-7839	Sequence 7839, Ap
32	19	67.9	391	10	US-09-867-701-9233	Sequence 9233, Ap
33	19	67.9	569	10	US-09-777-564-463	Sequence 463, App
34	19	67.9	2290	10	US-09-764-864-332	Sequence 332, App
35	19	67.9	3694	10	US-09-764-864-329	Sequence 329, App
36	19	67.9	397658	10	US-09-813-320-3	Sequence 3, Appl1
37	18.8	67.1	330	10	US-09-878-574-615	Sequence 615, App
38	18.8	67.1	29607	10	US-09-764-877-3626	Sequence 3626, Ap
39	18.6	66.4	446	10	US-09-974-300-5765	Sequence 5765, Ap
40	18.6	66.4	897	10	US-09-070-927A-845	Sequence 845, App
41	18.6	66.4	2000	9	US-09-938-842A-4638	Sequence 4638, Ap
42	18.6	66.4	2000	9	US-09-938-842A-4638	Sequence 4638, Ap
43	18.6	66.4	6156	10	US-09-842-256-1	Sequence 1, Appl1
44	18.6	66.4	21129	10	US-09-764-869-1734	Sequence 1734, Ap
45	18.4	65.7	242	10	US-09-867-701-286	Sequence 286, App

ALIGNMENTS

RESULT 1
US-09-865-579A-22
Sequence 22, Application US/09865579A
Patent NO. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865, 579A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-865-579A-22
Query Match 100.0% Score 28; DB 10; Length 28;
Best local Similarity 100.0%; Pred. No. 0.077;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AAAGAAAAGTGCAGAAATATTCAA 28
Db 1 AAAGAAAAGTGCAGAAATATTCAA 28
RESULT 2
US-09-865-579A-28/c
Sequence 28, Application US/09865579A
Patent NO. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Toshiki

```
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 28
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-865-579A-28
```

```
Query Match          100.0%; Score 28; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 AAAGAAAAAGATGCCAAGATATTCAA 28
Db 33 AAAGAAAAAGATGCCAAGATATTCAA 6
```

```
RESULT 3
US-09-452-599-169
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Hergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169
```

```
Query Match          100.0%; Score 28; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 AAAGAAAAAGATGCCAAGATATTCAA 28
Db 948 AAAGAAAAAGATGCCAAGATATTCAA 975
```

```
RESULT 4
US-09-764-864-69
; Sequence 69, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
```

```
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 69
; LENGTH: 2429
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2299)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2359)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2362)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2386)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-69
```

```
Query Match          73.6%; Score 20.6; DB 10; Length 2429;
Best Local Similarity 85.2%; Pred. No. 65;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 AAAGAAAAAGATGCCAAGATATTCA 27
Db 1570 AAAGAAAAAGATGCCAAGATATTCA 1596
```

```
RESULT 5
US-09-949-654-3
; Sequence 3, Application US/09949654
; Patent No. US20020127644A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000817
; CURRENT APPLICATION NUMBER: US/09/949,654
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/231,572
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 368004
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(368004)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-654-3
```

```
Query Match          73.6%; Score 20.6; DB 10; Length 368004;
Best Local Similarity 85.2%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 AAAGAAAAAGATGCCAAGATATTCA 27
Db 39518 AAAGAAAAAGATGCCAAGATATTCA 39544
```

```
RESULT 6
US-10-003-806-6
; Sequence 6, Application US/10003806
; Patent No. US20020119929A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Bishop, Colin E.
; APPLICANT: Agoulalik, Alexander I.
; APPLICANT: Zhu, Qichao
; TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
; FILE REFERENCE: P02066US1/10024824
; CURRENT APPLICATION NUMBER: US/10/003,806
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,872
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 180557
; TYPE: DNA
; ORGANISM: Human
US-10-003-806-6
```

```
Query Match 72.1%; Score 20.2; DB 12; Length 180557;
Best Local Similarity 88.0%; Pred. NO. 1.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 AAAGAAAAAGATGCCAAGATATT 25
|||||
DB 46438 AAAGTAAAAAGATGACAAAAATATT 46462
```

```
RESULT 7
US-10-003-806-9
; Sequence 9, Application US/10003806
; Patent No. US2002011929A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Colin E.
; APPLICANT: Agoulalik, Alexander I.
; APPLICANT: Zhu, Qichao
; TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
; FILE REFERENCE: P02066US1/10024824
; CURRENT APPLICATION NUMBER: US/10/003,806
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,872
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 180557
; TYPE: DNA
; ORGANISM: Human
US-10-003-806-9
```

```
Query Match 72.1%; Score 20.2; DB 12; Length 180557;
Best Local Similarity 88.0%; Pred. NO. 1.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 AAAGAAAAAGATGCCAAGATATT 25
|||||
DB 46438 AAAGTAAAAAGATGACAAAAATATT 46462
```

```
RESULT 8
US-09-960-352-2449/C
; Sequence 2449, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengding
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
```

```
; SEQ ID NO 2449
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 11-L1B3058-031-Q1-K1-C11
US-09-960-352-2449
```

```
Query Match 71.4%; Score 20; DB 10; Length 429;
Best Local Similarity 82.1%; Pred. NO. 81;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 AAAGAAAAAGATGCCAAGATATTCAA 28
|||||
DB 145 AAAGAAAGTATGTGCCAAAGTCTTCAA 118
```

```
RESULT 9
US-09-938-842A-3442
; Sequence 3442, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: S01P1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3442
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3442
```

```
Query Match 71.4%; Score 20; DB 9; Length 1665;
Best Local Similarity 82.1%; Pred. NO. 1e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 AAAGAAAAAGATGCCAAGATATTCAA 28
|||||
DB 1001 AAAGAAAAATATGGAAATAGATTAAA 1028
```

```
RESULT 10
US-09-974-300-3560
; Sequence 3560, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3560
; LENGTH: 143
; TYPE: DNA
```


ORGANISM: *Bacillus licheniformis*
US-09-974-300-3560

Query Match	70.0%	Score 19.6	DB 10	Length 143
Best local Similarity	84.6%	Pred. No. 95		
Matches 22	Conservative 0	Mismatches 4	Indels 0	Gaps 0

```

Qy      1  AAGAAAAAAGATGGCAAGATATTTC 26
         ||| |||| | | ||||| |||| |
Db      6  AAATAAAAACGACGGCAAGATATTGC 31

```

RESULT 11

```

US-09-923-876-946
; Sequence 946, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalitadi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 946
; LENGTH: 173
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700157851H1
; US-09-923-876-946

```

Query Match	70.0%	Score 19.6	DB 10	Length 173
Best Local Similarity	84.6%	Pred. Nc. 98		
Matches 22	Conservative 0	Mismatches 4	Indels 0	Gaps 0

QY 3 AGAAAAAGATGGCAAGATATTCAA 28
 ||||| | | | | | | | |
 Db 14 AGAAAAAGAGACAGAGATTATAA 39

RESULT 12

```

1--09-878-574-7719
2Sequence 7719, Application US/09878574
3Patent No. US20020110548A1
4
5GENERAL INFORMATION:
6
7APPLICANT: Byrum, Joseph R.
8APPLICANT: La Rosa, Thomas J.
9APPLICANT: Thompson, Michael D.
10TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
11TITLE OF INVENTION: Plants
12FILE REFERENCE: 38-21(15401)B
13CURRENT APPLICATION NUMBER: US/09/878,574
14CURRENT FILING DATE: 2001-12-21
15PRIOR APPLICATION NUMBER: 09/333,535
16PRIOR FILING DATE: 1999-06-14
17NUMBER OF SEQ ID NOS: 15775
18SEQ ID NO 7719
19LENGTH: 189
20
21TYPE: DNA
22
23ORGANISM: glycine max
24
25OTHER INFORMATION: Clone ID: 701100249H1
26--09-878-574-7719

```

Query Match	Score	DB	Length
Best Local Similarity	19.6;	10;	189;
	84.68;	Pred. No. 99;	

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY      1 AAAGAAAAAGATGGCAAGATATTC 26
          ||| | ||| ||| ||| |||
Db      89 AAAGTATAAGATGGCAGAGACATTC 114

```

RESULT 13

```

US-09-878-574-5615
: Sequence 5615, Application US/09878574
: Patent No. US20020110548A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Byrum, Joseph R.
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Thompson, Michael D.
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(15401)B
: CURRENT APPLICATION NUMBER: US/09/878,574
: CURRENT FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 09/333,535
: PRIOR FILING DATE: 1999-06-14
: NUMBER OF SEQ ID NOS: 15775
: SEQ ID NO 5615
:
: LENGTH: 254
:
: TYPE: DNA
:
: ORGANISM: Glycine max
:
: OTHER INFORMATION: Clone ID: 701091173H1
US-09-878-574-5615

```

Query Match	70.0%;	Score 19.6;	DB 10;	Length 254;
Best Local Similarity	84.6%;	Pred. No. 1e+02;		
Matches 22;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1	AAAGAAAAACATGGCAAGATATTC	26
Db	98	AAAGTATAAAGATGGCAGAGACATTC	123

RESULT 14

```

US-09-878-574-8576
: Sequence 8576, Application US/09878574
: Patent No. US20020110548A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Byrum, Joseph R.
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Thompson, Michael D.
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(15401)B
: CURRENT APPLICATION NUMBER: US/09/878,574
: CURRENT FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 09/333,535
: PRIOR FILING DATE: 1999-06-14
: NUMBER OF SEQ ID NOS: 15775
: SEQ ID NO 8576
: LENGTH: 260
:
: TYPE: DNA
:
: ORGANISM: Glycine max
:
: OTHER INFORMATION: Clone ID: 701101393H1
:
US-09-878-574-8576

```

Query Match	70.08;	Score 19.6;	DB 10;	Length 260;
Best Local Similarity	84.68;	Pred. NO. 1e+02;		
Matches 22;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

QY 1 AAAGAAAAAGATGGCAAGATATTC 26
||| | ||||| ||| |||
Db 78 AAAGTATAAAGATGGCAGACACATTC 103

RESULT 15
US-09-878-574-10488

```
; Sequence 10488, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ. ID NOS: 15775
; SEQ. ID NO 10488
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700966730H1
; US-09-878-574-10488

Query Match      70.0%; Score 19.6; DB 10; Length 264;
Best Local Similarity 84.6%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1  AAAGCAAAAGATCGCAAGATATTTC 26
      ||| | ||||| ||| ||| |||
Db      84  AAAGTATTAAGATGCGAGAGCATTTTC 109
```

Search completed: December 11, 2002, 06:09:17
Job time : 149.29 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 ; Search time 1435.66 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-22

Sequence: 1 aagaagaaagatgcgaagatattca 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_estrc:*
9: qb_estl1:*
10: qb_estl2:*
11: qb_estl3:*
12: qb_estl4:*
13: qb_estl5:*
14: qb_estl6:*
15: em_estfun:*
16: em_estlom:*
17: qb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.2	82.9	613	17	BH009254 ef26a02.x
2	23.2	82.9	707	17	BH532191 BCGP68TF
3	23.2	82.9	921	17	CNS06Y01 AL421343 T7 end of
4	22.8	81.4	618	10	AW255568 M6604 pep
5	22.2	79.3	360	17	AQ283551 RPT111-77
6	21.6	77.1	353	14	BH875833 BH875833

7	21.6	77.1	375	10	BH841882	BH841882
8	21.6	77.1	443	14	W89911	W89911.mf76c12.r1
9	21.6	77.1	470	13	B146683	B146683.1e25908.y
10	21.6	77.1	507	9	A1430420	A1430420.mf76c12.y
11	21.6	77.1	589	17	A2216057	A2216057.sheared.D
12	21.6	77.1	621	17	AQ487311	AQ487311.RPCT-11-2
13	21.6	77.1	636	10	BH642313	BH642313.BH642313
14	21.6	77.1	639	10	BH660787	BH660787.BH660787
15	21.6	77.1	685	17	BH029119	BH029119.RPCT-24-3
16	21.6	77.1	690	9	A1526147	A1526147.pc3-2.D06
17	21.6	77.1	716	17	BH029113	BH029113.RPCT-24-3
18	21.6	77.1	749	13	B1660259	B1660259.603302656
19	21.6	77.1	793	17	AG108121	AG108121.pan.trog1
20	21.6	77.1	876	14	B0895101	B0895101.AGPMCOURT
21	21.2	75.7	235	12	BE171087	BE171087.PCT2036.M
22	21.2	75.7	550	9	A1820785	A1820785.y161c02.y
23	21.2	75.7	572	9	A1668612	A1668612.y161c02.x
24	21.2	75.7	581	17	AQ425329	AQ425329.CITB1-E1-
25	21.2	75.7	726	17	AG125961	AG125961.pan.trog1
26	21.2	75.7	882	17	BH138799	BH138799.ENTNE31TF
27	21.2	75.7	1040	17	BH162219	BH162219.ENTOX25TF
28	20.8	74.3	433	17	A2150645	A2150645.SP.0039.B
29	20.8	74.3	509	17	AQ558792	AQ558792.HS.2067.B
30	20.8	74.3	927	17	BH135840	BH135840.ENTOV83TR
31	20.6	73.6	343	9	A1018760	A1018760.ov28h05.x
32	20.6	73.6	369	10	AW970299	AW970299.EST382380
33	20.6	73.6	374	12	AL757658	AL757658.Arabidops
34	20.6	73.6	374	12	BG602883	BG602883.EST501973
35	20.6	73.6	388	9	A1124708	A1124708.am61a02.x
36	20.6	73.6	415	10	BE552194	BE552194.hy04c06.x
37	20.6	73.6	418	10	AW232707	AW232707.t124911.x
38	20.6	73.6	447	10	BH730538	BH730538.HS.30538
39	20.6	73.6	480	17	AQ203600	AQ203600.HS.3103.B
40	20.6	73.6	485	9	AA797561	AA797561.vw25b03.r
41	20.6	73.6	494	9	A1650954	A1650954.wa96a11.x
42	20.6	73.6	516	12	BG741432	BG741432.602632214
43	20.6	73.6	606	12	BM159980	BM159980.EST562503
44	20.6	73.6	616	12	BG064533	BG064533.H3020H02-
45	20.6	73.6	632	12	BG077948	BG077948.H3020H02-

ALIGNMENTS

RESULT 1
BH009254
LOCUS ef26a02.x1 TO1000 Brassica oleracea genomic clone ef26a02 5', DNA
DEFINITION
ACCESSION BH009254
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 613)
Katarl,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J., Ballia
,V., Bell,M., Cunnus,D.M., King,L., Kirchoff,K., Kuit,R., Miller
,B., Nascento,L., Preston,R., Rodriguez,S., Santos,L., Shah,R.,
Vil,M.D., Zutavern,T., Bal,H., Dedhia,N. and McCombie,W.R.
Whole Genome Shotgun Reads from Brassica oleracea
Unpublished (2001)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@csbl.org
Plate: ef26 row: a column: 02
Seq primer: -21ttwduiv

```

Class: Shotgun
High quality sequence stop: 613.
Location/Qualifiers
FEATURES
  source
    1..613
    /organism="Brassica oleracea"
    /db_xref="taxon:3712"
    /clone_ef26a02"
    /clone_lib="TO1000"
    /note="Vector: M13 for .x reads, pZero-2 for .b and .g
reads; Site_1: ECoRV; DNA prepared as whole genome shotgun
library from young, green leaves. May contain some plastid
DNA; DNA provided by Dr. Tom Osborn, University of
Wisconsin-Madison, Department of Agronomy."
BASE COUNT
  175 a 121 c 128 g 189 t
ORIGIN
  Query Match      82.9%: Score 23.2: DB 17: Length 613:
  Best Local Similarity 89.3%: Pred. No. 9.6e+02:
  Matches 25: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

v 1 AAGAGAAAAGATGCCAAGATATTCAA 28
  ||||| ||||| ||||| |||||
  ..b 106 AAGAGAAAAGATGCCAAGACTTCAA 133

RESULT 2
LOCUS BH532191 707 bp DNA linear GSS 14-DEC-2001
DEFINITION BOGXP68TF BOGP Brassica oleracea genomic clone BOGXP68, DNA
sequence.
ACCESSION BH532191
VERSION BH532191.1 GI:17753725
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 707)
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSS: BOGXP68TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
FEATURES
  source
    1..707
    /organism="Brassica oleracea"
    /strain="TO1000DH3"
    /db_xref="taxon:3712"
    /clone="BOGXP68"
    /clone_lib="BOGP"
    /note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT
  187 a 139 c 147 g 234 t
ORIGIN
  Query Match      82.9%: Score 23.2: DB 17: Length 707:
  Best Local Similarity 89.3%: Pred. No. 9.4e+02:
  Matches 25: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

OY 1 AAGAGAAAAGATGCCAAGATATTCAA 28
  ||||| ||||| ||||| |||||
  Db 37 AAGAGAAAAGATGCCAAGACTTCAA 64

```

```

RESULT 3
LOCUS CNS06Y01/c 921 bp DNA linear GSS 06-JUL-2001
DEFINITION T7 end of clone AY0AA011H08 of library AY0AA from strain CBS 6340
of Kluyveromyces thermotolerans, genomic survey sequence.
ACCESSION AL421343
VERSION AL421343.1 GI:12204542
KEYWORDS GSS.
SOURCE Kluyveromyces thermotolerans.
ORGANISM Kluyveromyces thermotolerans
Fukuyota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
1 (bases 1 to 921)
Soucié,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S.,
de-Monigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Olier-Kalogeropoulos,O., Porter,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
REFERENCE
  PUBMED 20584711
  FEMS Lett. 487 (1), 3-12 (2000)
  11152876
  2 (bases 1 to 921)
  Malpertuy,A., Llorente,B., Blandin,G., Artiguenave,F., Wincker,P.
  and Dujon,B.
  Genomic exploration of the hemiascomycetous yeasts: 10.
  Kluyveromyces thermotolerans
  FEMS Lett. 487 (1), 61-65 (2000)
  11152885
  3 (bases 1 to 921)
  Genoscope.
  Direct Submission
  Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
  2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
  seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
  This GSS is part of a random genomic sequencing program of thirteen
  yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
  exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
  Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
  lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
  angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
  Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
  5 kb were prepared and both extremities were sequenced. See
  keywords for description of this sequence and for the sequence of
  the other extremity of this insert.
  Location/Qualifiers
FEATURES
  source
    1..921
    /organism="Kluyveromyces thermotolerans"
    /strain="CBS 6340"
    /db_xref="taxon:4916"
    /clone="AY0AA011H08"
    /clone_lib="AY0AA"
    /note="end : 77"
    <18..>329
    /note="similar to Saccharomyces cerevisiae ORF YDL015c [
similarity to rat synaptic glycoprotein SC2 ]"
    /evidence-not-experimental
    complement(426..>919)
    /note="similar to Saccharomyces cerevisiae ORF YDL017w [
CDC7 ; protein kinase ]
1 putative frimesshift(s)"
    /evidence-not-experimental
misc-feature
  237 a 212 c 189 g 278 t 5 others
BASE COUNT
  237 a 212 c 189 g 278 t 5 others
ORIGIN
  Query Match      82.9%: Score 23.2: DB 17: Length 921:
  Best Local Similarity 89.3%: Pred. No. 9e+02:
  Matches 25: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

OY 1 AAGAGAAAAGATGCCAAGATATTCAA 28

```

```

Db      240 AAGAAAGACAGCGCAATATATTCAA 213
||||| ||| ||||| |||||
RESULT 4
LOCUS   AM255568/c                      618 bp  mRNA  linear  EST 23-AUG-2000
DEFINITION M604 peppermint glandular trichome Mentha x piperita cDNA, mRNA
sequence.
ACCESSION AM255568
VERSION   AM255568.1  GI:7244820
KEYWORDS EST.
SOURCE    peppermint.
ORGANISM  Mentha x piperita
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Asteridae; euasterids I; Lamiales; Lamiaceae; Mentha.
REFERENCE
AUTHORS  Lange, B.M., Wildung, M.R., Stauber, E.J., Sanchez, C., Pouchnik, D. and
          Crocrau, R.
          Probing essential oil biosynthesis and secretion by functional
          evaluation of expressed sequence tags from mint glandular trichomes
          Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000)
JOURNAL  2018392
MEDLINE  Contact: Lange, B.M.
COMMENT   Institute of Biological Chemistry/Washington State University
          Pullman, WA
          Email: lange-m@mail.wsu.edu.
          Location/Qualifiers
            1..618
              /organism="Mentha x piperita"
              /cultivar="Black Mitcham"
              /db_xref="taxon:34256"
              /clone_id="peppermint glandular trichome"
              /rname="peppermint glandular trichomes"
              /cell_type="secretory"
              /note="Vector: lambda ZAPII"
BASE COUNT  182 a 129 c 120 g 187 t
ORIGIN
Query Match      81.4%; Score 22.8; DB 10; Length 618;
Best Local Similarity 92.3%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 AAGAAAAAGATGCGCAAGATATTC 26
||||| ||||| ||||| ||||| ||
Db      552 AAGAAAAAGATGCGCAAGATATTC 527

RESULT 5
LOCUS   AQ283551                      360 bp  DNA  linear  GSS 27-APR-1999
DEFINITION RPC11-77B19.TV RPC1-11 Homo sapiens genomic clone RPC1-11-77B19,
          DNA sequence.
ACCESSION AQ283551
VERSION   AQ283551.1  GI:3909946
KEYWORDS GSS.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS  Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
          Berry, K., Granger, D., Sub, E., Mible, C., de Jong, P. and Venter, J.C.
          Use of human BAC End Sequences for Sequence-Ready Map Building
          Unpublished (1998)
JOURNAL  Other_GSSs: RPC11-77B19.TV
COMMENT   Contact: Mark Adams
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208

```

```

Email: mdadams@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC end.

FEATURES
source      Location/Qualifiers
            1..360
              /organism="Homo sapiens"
              /db_xref="GDB:7529226"
              /db_xref="taxon:9606"
              /clone="RPC1-11-77B19"
              /clone_id="RPC1-11"
              /sex="Male"
              /cell_type="lymphocytes"
              /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
              RPC11 Human Male BAC library"
BASE COUNT  156 a 49 c 58 g 97 t
ORIGIN
Query Match      79.3%; Score 22.2; DB 17; Length 360;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 AAGAAAAAGATGCGCAAGATATTCAA 28
||||| ||||| ||||| ||||| ||
Db      211 AAGAAAAATATCGCAAGCAATTCAA 237

RESULT 6
LOCUS   BM875833/c                      353 bp  mRNA  linear  EST 07-MAR-2002
DEFINITION i186d03.x1 Kaestner ngn3 - - subtracted Mus musculus cDNA 3', mRNA
sequence.
ACCESSION BM875833
VERSION   BM875833.1  GI:19243499
KEYWORDS EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS  Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
          Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
          Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Hirstain, A.,
          Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
          /M., Gibbons, M., McCann, R., Cole, K., Tsagarisvili, K., Williams, T.,
          Jackson, X. and Bowers, Y.
          Endocrine Pancreas Consortium
          Unpublished (2000)
          Other_ESTs: i186d03.y1
          Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
          Harvard University, Howard Hughes Medical Institute
          Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
          MA 02138
          Tel: 617-495-1812
          Fax: 617-495-8557
          Email: dmelton@biohp.harvard.edu
          Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
          2000) Library was constructed by Catherine Lee DNA sequencing by:
          Washington University Genome Sequencing Center For information on
          obtaining a clone please contact: Dr. Marie Scarce
          (mscarce@mail.med.upenn.edu)
          Seq primer: -400p from G1bco
          High quality sequence stop: 343.
          Location/Qualifiers
            1..353
              /organism="Mus musculus"
              /strain="129/Sv x C57"

```

```

/db_xref="taxon:10090"
/clone_lib="Kaestner ngn3 - - subtracted"
/sex="not known"
/tissue_type="pancreas"
/dev_stage="E14.5"
/lab_host="DH12S"
/note="Vector: pSPORT1 (GIBCO); Site_1: Not I; Site_2: Sal
I; Both wildtype (target) and ngn3-/- (driver) cDNA
libraries were amplified. The ssDNA from the wildtype cDNA
library was prepared by infecting with M1307 and blocked
with 5'GCGGCCGCT(15) oligo before hybridization. Sail
digested dsDNA from the ngn3-/- cDNA library was used to
synthesize biotinylated RNA with T7 RNA polymerase.
Subtractive hybridization was performed at 42°C in 80%
formamide, 100 mM HEPES pH 7.5, 2mM EDTA and 0.2% SDS.
Streptavidin was used to remove clones common between the
two libraries. After repair of the subtracted ssDNA with
5'GCGGCCGCT(15) oligo using Taq polymerase and Vent
polymerase, the subtracted cDNA library was digested with
SpeI and electroporated into DH12S cells (LTI)."
```

AGE COUNT 88 a 76 c 67 g 122 t

IGIN

Query Match 77.1% Score 21.6; DB 14; Length 353;
Best Local Similarity 85.7% Pred. No. 3.3e+03;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AAGAGAAAAAGATGCAAGATATTCA 28
||| ||||| ||||| ||||| ||
Db 347 AAAAAAAGGTGCAGATATTATAA 320

RESULT 7
BB841882

LOCUS BB841882 RIKEN full-length enriched, 6 days neonate spleen Mus
DEFINITION BB841882 musculus cDNA clone FA30002F24 5', mRNA sequence.
ACCESSION BB841882
VERSION BB841882.1 GI:17042613
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 375)
Akimura,T., Arai,K., Carinci,P., Furuno,M., Hangaki,T.,
Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K., Ishii
,T., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
,Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
,A., Takahashi,F., Takaku-Akehata,S., Tanaka,T., Tomaru,A., Toya,T.,
Watabiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)

TITLE Unpublished (2001)
JOURNAL Contact: Yoshitide Hayashizaki
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
url:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagii,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

```

Hayashizaki,Y.  

RIKEN integrated sequence analysis (RISA) system--384-format  

sequencing pipeline with 384 multicapillary sequencer. Genome Res.  

10 (11), 1757-1771 (2000)  

Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara  

,Y. and Hayashizaki,Y.  

Computer-based methods for the mouse full-length cDNA  

encyclopedia: real-time sequence clustering for construction of a  

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  

Please visit our web site (http://genome.gsc.riken.go.jp) for  

further details.  

e mouse tissues.
```

FEATURES
source

location/Qualifiers
1. 375
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="FA30002F24"
/clone_lib="RIKEN full-length enriched, 6 days neonate
spleen"
/tissue_type="spleen"
/dev_stage="6 days neonate"
/note="Vector: pSPORT1; Site_1: Sail; Site_2: NotI; This
clone is among a rearranged set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5 embryos
and E12.5 female mesonephros/gonad) and one newborn
ovary cDNA library. Average insert size 1.5 kb. All
source libraries are cloned unidirectionally with oligo(dT
)-NOT primers. References include: (1) Genome-wide
expression profiling of mid-gestation placenta and embryo
using a 15,000 mouse developmental cDNA microarray, 2000,
Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
Large-scale cDNA analysis reveals phased gene expression
patterns during preimplantation mouse development, 2000,
Development, 127: 1737-1749; (3) Genome-wide mapping of
unselected transcripts from extraembryonic tissue of
7.5-day mouse embryos reveals enrichment in the t-complex
and under-representation on the X chromosome, 1998, Hum
Mol Genet 7: 1967-1978."

BASE COUNT 113 a 81 c 86 g 95 t

ORIGIN

Query Match 77.1% Score 21.6; DB 10; Length 375;
Best Local Similarity 85.7% Pred. No. 3.2e+03;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AAGAGAAAAAGATGCAAGATATTCA 28
||| ||||| ||||| ||||| ||
Db 247 AAAAAAAGGTGCAGATATTATAA 274

RESULT 8
WB89911

LOCUS WB89911 443 bp mRNA linear EST 12-SEP-1996
DEFINITION m776c12.r1 Soares mouse embryo NBM713.5 14.5 Mus musculus cDNA
ACCESSION WB89911
VERSION WB89911.1 GI:1538992
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 443)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelning,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HIMI Mouse EST Project
Unpublished (1996)


```

FEATURES
  source          POLYA-No.
                  Location/Qualifiers
1..507
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:420214"
/clone_lib="Soares mouse embryo NBMEL3.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTGAGATGGAGCGCGCGAATTTTATTTTATTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Benito Soares and
M. Fatima Bonaldo."
BASE COUNT      146 a 128 c 147 g 85 t 1 others
ORIGIN

Query Match      77.1% Score 21.6; DB 9; Length 507;
Best Local Similarity 85.7%; Pred. No. 3.1e+03;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAGCAAAAGATGCGCAAGATATTCAA 28
DB 319 AAGCAAAAGAGAGCGAGATGATCAA 346

RESULT 11
LOCUS      A2216057      589 bp      DNA      linear      GSS 09-JUN-2000
DEFINITION Sheared DNA-56F11.TR Sheared DNA Trypanosoma brucei genomic clone
ACCESSION  A2216057
VERSION    A2216057.1 GI:8433857
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei.
ORGANISM   Trypanosoma brucei.
            Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
            1 (bases 1 to 589)
            El-Sayed,N., Zhao,S., Gill,S., Suh,E., Malek,J., Fujii,C.,
            Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
            Fraser,C. and Adams,M.
            Determination of clone end sequences from Trypanosoma brucei GUTat
            10.1 sheared DNA library
            Unpublished (1999)
            Other GSS: Sheared DNA-56F11.TF
            Contact: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: neisayed@tigr.org
            Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
            DNA library constructed at TIGR. Clones will be available for
            distribution through Research Genetics, Alabama, USA. Sheared DNA
            end sequences search page: http://www.tigr.org/tldb/mdb/tldb/.
            Seq primer: M13-Reverse
            Class: Shotgun.
FEATURES
  source          Location/Qualifiers
1..589
/organism="Trypanosoma brucei"
/strain="TREU927/4 CUTat 10.1"

```

```

/clone="Sheared DNA-56F11"
/clone_lib="Sheared DNA"
/notes="Vector: pUC18; Site_1: SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Barrell, Oxford University
press, 1999)."
BASE COUNT      152 a 101 c 108 g 228 t
ORIGIN

Query Match      77.1% Score 21.6; DB 17; Length 589;
Best Local Similarity 85.7%; Pred. No. 3e+03;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAGCAAAAGATGCGCAAGATATTCAA 28
DB 337 AAAAAAAGATGATMAAGATATCAA 310

RESULT 12
LOCUS      AQ487311      621 bp      DNA      linear      GSS 24-APR-1999
DEFINITION RPCI-11-245E21.TV RPCI-11 Homo sapiens genomic clone RPCI-11-245E21
ACCESSION  AQ487311
VERSION    AQ487311.1 GI:4673185
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 621)
            Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter
            ,J.C.
            Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
            Unpublished (1997)
            Other GSS: RPCI-11-245E21.TJ
            Contact: Shaying Zhao, William Niernan, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genel cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES
  source          Location/Qualifiers
1..621
/organism="Homo sapiens"
/db_xref="GDB:7593812"
/db_xref="taxon:9606"
/clone="RPCI-11-245E21"
/clone_lib="RPCI-11"
/sex="Male"
/notes="Lympocytes"
/notes="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT      175 a 112 c 105 g 229 t
ORIGIN

```


Hayashizaki, Y.
 RIKEN Integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
 , Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedias: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
 , K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome, 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.

FEATURES

source

location/Qualifiers

1..639
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="D63005H02"
 /clone.lib="RIKEN full-length enriched, 0 day neonate
 kidney"
 /tissue_type="kidney"
 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Fnyclopedias
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer 15'
 GAGACAGACAGCCGCCACACCTCGAGTTTCTTTTCTTNN 3', cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence 15'
 CAGACAGAGATTTCGACTTATTATAATTATCCCCCCCCCC 3'. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 pBluescript KS(+) after bulk excision from lambda FLC I."

BASE COUNT 187 a 155 c 131 g 166 t
 ORIGIN

Query Match 77.1%; Score 21.6; DB 10; Length 639;
 Best Local Similarity 85.7%; Pred. No. 2.9e+03;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 AAGAGAAAAAGATGCGAAGATATTCAA 28
 ||| ||||| ||||| ||||| ||||| ||
 18 AAAAAAAAAAGCTGCCAATATTATAA 45

RESULT 15
 BH029119 685 bp DNA linear GSS 17-JUL-2001
 LOCUS RPCI-24-336F4.TV RPCI-24 Mus musculus genomic clone RPCI-24-336F4,
 DEFINITION DNA sequence.
 ACCESSION BH029119
 VERSION BH029119.1 GI:14796446
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 685)
 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akimov, B., Levins, M.,
 Tsegay, G., Goert, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,
 Russell, D., de Jong, P. and Fraser, C. M.
 Mouse BAC End Sequences from Library RPCI-24
 Unpublished (1999)
 TITLE JOURNAL
 COMMENT Other_GSSs: RPCI-24-336F4.TV

Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@ligr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (piet@ligr.org). Clones may be purchased from BACPAC
 Resources (<http://www.chori.org/bacpac/orderingframe.html>). BAC end
 page: http://www.ligr.org/lbd/bac-ends/mouse/bac_end_intro.html
 Plate: 336 row: F column: 4
 Seq primer: 17
 Class: BAC ends.

FEATURES

source

location/Qualifiers

1..685
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-336F4"
 /clone.lib="RPCI-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pIABAC1; Site_1: BamHI; Site_2: BamHI;
 RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
 library was cloned in the pIABAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

BASE COUNT 283 a 159 c 93 g 150 t
 ORIGIN

Query Match 77.1%; Score 21.6; DB 17; Length 685;
 Best Local Similarity 85.7%; Pred. No. 2.9e+03;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

0Y 1 AAGAGAAAAAGATGCGAAGATATTCAA 28
 ||| ||||| ||||| ||||| ||||| ||
 DB 221 AAAAAAAAAAGCTGCCAATATTATAA 248

Search completed: December 10, 2002, 22:50:05
 Job time : 1440.66 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 : Search time 717.832 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-19
Perfect score: 14
Sequence: 1 gaaggtgcttac 14

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	14	100.0	134	17	AZ506708 1M0348C03
C 2	14	100.0	215	3	AV221833 AV221833
C 3	14	100.0	266	17	AZ906716 RPCI-24-1
C 4	14	100.0	383	9	AL699442 DKFZ66860
C 5	14	100.0	404	10	BR457319 US49910.Y
C 6	14	100.0	417	14	BQ457284 ke37b11.Y

Result	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45								
LOCUS	AZ506708	134 bp	DNA	linear	GSS	05-OCT-2000																																															
DEFINITION	1M0348C03F Mouse 10kb plasmid UUGCM library Mus musculus genomic																																																				
ACCESSION	AZ506708																																																				
VERSION	AZ506708.1																																																				
KEYWORDS	GSS.																																																				
SOURCE	house mouse.																																																				
ORGANISM	Mus musculus																																																				
REFERENCE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.																																																				
AUTHORS	Mouse whole genome scaffolding with paired end reads from 10kb																																																				
TITLE	Plasmid inserts																																																				
JOURNAL	Unpublished (2000)																																																				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00																																																				

ALIGNMENTS

RESULT 1
LOCUS AZ506708 134 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0348C03F Mouse 10kb plasmid UUGCM library Mus musculus genomic
ACCESSION AZ506708
VERSION AZ506708.1 GI:10688024
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
TITLE Plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0348 row: C column: 03
 Seq primer: CGTTCGTAACGACGCGCAGT
 Class: Plasmid ends
 High quality sequence stop: 134.

FEATURES
source

1. 134
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6j"
 /db_xref="taxon:10090"
 /clone="MGC1M0348C03"
 /clone_1ib="Mouse 10kb plasmid UUC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; purified genomic DNA from M. musculus C57BL/6j (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b/AH129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 36 a 31 c 28 g 39 t
 ORIGIN

Query Match 100.0%; Score 14; DB 17; Length 134;
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGTGCTGCTTAC 14
 Db 59 GAAGTGCTGCTTAC 46

RESULT 2 215 bp mRNA linear EST 14-NOV-2001
 AV221833 RIKEN full-length enriched, adult male brain Mus musculus
 LOCUS AV221833
 DEFINITION cDNA clone 3526402016 3' similar to U58280 Mus musculus second
 largest subunit of RNA polymerase I (RP42) mRNA, mRNA sequence.

ACCESSION AV221833.1 GI:6171010
 VERSION AV221833
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 215)
 AUTHORS Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
 Fukushima, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
 Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai,
 C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
 Owa, C., Ozawa, Y., Saito, H., Sano, M., Saito, K., Shibata, K., Shibata,
 Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H.,
 Suzuki, H., Takahashi, F., Tateno, M., Tomioka, N., Tsunoda, Y.,
 Watanabe, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,
 Yoshiki, A., Yoshino, M., Yamamoto, M., and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs (Kono, H., et al. 1999)
 JOURNAL Unpublished (1999)

COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Sasaki, N., Izawa, M., Watanabe, M., Okazaki, Y., Yoneeda, Y.,
 Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki,
 Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
 Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES
source

Location/Qualifiers
 1. 215
 /organism="Mus musculus"
 /strain="C57BL/6j"
 /db_xref="taxon:10090"
 /clone="3526402016"
 /clone_1ib="RIKEN full-length enriched, adult male brain"
 /sex="male"
 /tissue_type="brain"
 /dev_stage="adult"
 /lab_host="DH10B"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGACCTCTTTTCTTTTCTTTTCTTTN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence 15'
 GAGAGAGAGATTCGAGTTTAATTAATTAATCCCCCCCCC 3'}. cDNA
 was cloned into the XhoI and BamHI sites. Vector: a
 modified pBluescript KS(+) after bulk excision from Lambda
 phage 1."

BASE COUNT 58 a 36 c 49 g 72 t
 ORIGIN

Query Match 100.0%; Score 14; DB 9; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGTGCTGCTTAC 14
 Db 12 GAAGTGCTGCTTAC 25

RESULT 3 266 bp DNA linear GSS 05-MAR-2001
 AV206716 RPI-24-164B11.TV RPI-24 Mus musculus genomic clone RPI-24-164B11
 LOCUS AV206716
 DEFINITION RPI-24-164B11.TV RPI-24 Mus musculus genomic clone RPI-24-164B11
 , DNA sequence.

ACCESSION AV206716.1 GI:13225661
 VERSION AV206716
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 266)

AUTHORS

Zhao, S., Niernman, M., Malek, J., Shatsman, S., Aktinect, B., Levins, M.,
 Regge, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebregorgis, E.,
 Russell, D., de Jong, P. and Fraser, C.M.

TITLE

Mouse BAC End Sequences from Library RPCI-24

JOURNAL

Unpublished (1999)

Other GSSs: RPCI-24-164B11.TJ

COMMENT

Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org). Clones may be purchased from BACPAC
 Resources (<http://www.choi.org/bacpac/orderingframe.html>). BAC end
 page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
 Plate: 164 row: B column: 11
 Seq primer: 47
 Class: BAC ends.

FEATURES

Location/Qualifiers

1..266

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-164B11"

/clone_lib="RPCI-24"

/sex="Male"

/cell_type="Spleen/Brain"

/note="Vector: pTAKAC1; Site_1: BamHI; Site_2: BamHI;
 RPCI-24 Mouse BAC library produced by Pieter de Jong. The
 library was cloned in the pTAKAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

BASE COUNT

56 a 48 c 84 g 78 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 14; DB 17; Length 266;
 Pred. No. 1.2e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14

|||||

Db 60 GAAGTGTGCTTAC 73

RESULT 4

LOCUS

Al699442 383 bp mRNA linear EST 21-MAR-2002

DEFINITION

DKFZp68601113.F1 686 (synonym: hlc3) Homo sapiens cDNA clone

ACCESSION

DKFZp68601113

VERSION

Al699442

KEYWORDS

Al699442.1 GI:19619982

SOURCE

EST.

ORGANISM

human.

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

Ottensweider, B., Obermaier, B., Mewes, M., Mewes, H.W., Weill, B. and
 Wiemann, S.

TITLE

EST (Ottensweider, B., Obermaier, B., Mewes, H.W., Weill, B. and Wiemann
 , S.)

JOURNAL

Unpublished (2001)

COMMENT

Contact: Ottensweider B

MIPS

Am Klopferplatz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de

Sequenced by Medigenomix (Martinsried/Germany) within the cDNA

sequencing consortium of the German Genome Project. No sl sequence

available.

This clone (DKFZp68601113) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clonezrpd.de.

FEATURES

source

1..383

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="DKFZp68601113"

/issue_lib="686 (synonym: hlc3)"

/issue_type="human skeletal muscle"

/dev_stage="adult"

/lab_host="DH10B"

/note="Vector: pTIP1Ex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

BASE COUNT

125 a 60 c 104 g 94 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 14; DB 9; Length 383;
 Pred. No. 1.5e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14

|||||

Db 285 GAAGTGTGCTTAC 298

RESULT 5

LOCUS

BE457319 404 bp mRNA linear EST 26-JUL-2000

DEFINITION

us49g10.y1 Perkins LRH Mus musculus cDNA clone IMAGE:3215778 5',
 mRNA sequence.

ACCESSION

BE457319

VERSION

BE457319.1 GI:9479333

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Marr, M., Hillier, L., Kucaba, T., Martini, J., Beck, C., Wylie, T.,
 Underwood, K., Stepien, M., Theising, B., Allen, M., Hovers, Y., Nelson
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
 E., Kohn, S., Shin, T., Jackson, V., Cardenas, M., McCann, R.,
 Waterson, R. and Wilson, R.

TITLE

The WashU-NCI Mouse EST Project 1999

JOURNAL

Unpublished (1999)

COMMENT

Contact: Marr, M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LBNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:1065926

Seq primer: -400P from Gibco

High quality sequence stop: 347.

Location/Qualifiers

1..404

/organism="Mus musculus"

/strain="BALB/c"

/db_xref="taxon:10090"

/clone="IMAGE:3215778"

/clone_lib="Perkins LRH"

/sex="female"

/issue_type="primary sorted bone marrow cells"

/dev_stage="adult"

/lab_host="DH10B (phage-resistant)"

/note="Vector: pZL1; Site_1: SalI; Site_2: EagI; cDNA made
 by oligo-dT priming. Library amplified by stretch PCR.
 Subtraction method: Bonaldo, et al., Genome Research
 6:791. Library constructed by Dr. Archibald Perkins (Yale

```

BASE COUNT      116 a      84 c      80 g      124 t
ORIGIN
Query Match      100.0%; Score 14; DB 10; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAGGTGCTTAC 14
    |||||||
Db 15 GAAGGTGCTTAC 2

RESULT 6
LOCUS      B0457284      417 bp      mRNA      linear      EST 29-MAY-2002
DEFINITION ke3b11.y1 Dirofilaria immitis adult PAMP1 v1 Dirofilaria immitis
            cDNA 5' similar to WP:CE24447 Y54E10A.3 thiorodoxin-like protein ;
            mRNA sequence.
ACCESSION   B0457284
VERSION     B0457284.1 GI:21260396
KEYWORDS    EST.
SOURCE      Dirofilaria immitis.
ORGANISM    Dirofilaria immitis
REFERENCE    1 (bases 1 to 417)
AUTHORS      McCarter,J., Clifton,S., Chiappelli,B., Pape,D., Martin,J., Wylie,T.,
            Danle,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
            Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagaris,V., R.,
            Ronko,I., Kennedy,S., Magillie,L., Beck,C., Underwood,K., Steptoe
            ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
            Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
            Wilson,R.
TITLE        The Washington Univ. Nematode EST Project, 1999
JOURNAL      Unpublished (1999)
COMMENT      Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: estewatson.wustl.edu
FEATURES
     source
     1..417
     Location/Qualifiers
         /organism="Dirofilaria immitis"
         /db_xref="taxon:6287"
         /clone_lib="Dirofilaria immitis adult PAMP1 v1"
         /dev_stage="adult"
         /lab_host="DH10B"
         /note="Vector: PAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
            The library was constructed by Claire Murphy and Dr. James McCarter
            at Washington University, St. Louis. Adult nematodes were harvested
            from infected dogs by Dr. Prema Arasu of North Carolina State
            University, Raleigh, NC (Prema.Arasu@ncsu.edu) Total RNA was
            isolated by Merry McIaird of Divergence, Inc., St. Louis, MO. DNA
            Sequencing by: Washington University Genome Sequencing Center
            Seq primer: -40RP from Gibco.
BASE COUNT      134 a      79 c      90 g      114 t
ORIGIN
Query Match      100.0%; Score 14; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;

```

```

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAGGTGCTTAC 14
    |||||||
Db 192 GAAGGTGCTTAC 205

RESULT 7
LOCUS      AL368921      457 bp      mRNA      linear      EST 03-AUG-2000
DEFINITION MUBA27F09R1 MUBA Medicago truncatula cDNA clone MUBA27F09 T7, mRNA
            sequence.
ACCESSION   AL368921
VERSION     AL368921.1 GI:9668674
KEYWORDS    EST.
SOURCE      barrel medic.
ORGANISM    Medicago truncatula
REFERENCE    1 (bases 1 to 457)
AUTHORS      Journel,E., P., Crespeau,H., van-Tuinen,D., Guzy,J., Jallion,O.,
            Niebel,A., Carreau,V., Chataigner,O., Kahn,D., Ghanmazzi-Pearson
            ,V. and Gamas,P.
TITLE        Medicago truncatula ESTs from nitrogen-starved roots
JOURNAL      Unpublished (2000)
COMMENT      Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Contact : Pascal Gamas and Etienne-Pascal Journel, Laboratoire de
            Biologie Moleculaire des Relations Plantes-Microorganismes,
            CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
            Mt-est@jouy.inra.fr Website :
            http://sequence.jouy.inra.fr/Mtruncatula.html).
FEATURES
     source
     1..457
     Location/Qualifiers
         /organism="Medicago truncatula"
         /cultivar="Jemalong"
         /db_xref="taxon:3880"
         /clone_lib="MUBA27F09"
         /clone_lib="MUBA"
         /tissue_type="root tips"
         /dev_stage="harvested after 3 days of N-starvation"
         /note="Vector: pBluescript PSK; Site 1: EcoRI; Site 2:
            XhoI; Plants were grown in an aeroponic chamber for 14
            days on nitrogen-rich medium followed by 3 days on N-free
            medium. RNA was extracted from root tips (1-3 cm). cDNA
            was prepared from polyA+ enriched RNA. The cDNA was
            directionally ligated into uni-2apxR vector from
            Stralagene and packaged using Gigapack Gold packaging
            extracts. Plasmids containing cDNA inserts were
            mass-excised from phage stocks using Exsist helper phage
            and propagated in S01K cells. Clone ordering and
            sequencing was performed by the Centre National de
            Sequencage (Genoscope, Evry, France)."
BASE COUNT      143 a      97 c      89 g      128 t
ORIGIN
Query Match      100.0%; Score 14; DB 9; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAGGTGCTTAC 14
    |||||||
Db 72 GAAGGTGCTTAC 85

RESULT 8
LOCUS      AQ930007      615 bp      DNA      linear      GSS 21-DEC-1999
DEFINITION RPCI-23-283F20.r1 RPCI-23 Mus musculus genomic clone RPCI-23-283F20

```

, DNA sequence.
 ACCESSION AQ930007 GI:6618937
 VERSION AQ930007.1
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 615)
 REFERENCE Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S., Akiret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 TITLE JOURNAL COMMENT
 Other-GSSs: RPCI-23-283F20.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pietor de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 283 row: F column: 20
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1. .615
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-283F20"
 /clone_1lb="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1; EcoRI: Site 2; EcoRI: Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 171 a 148 c 126 g 170 t
 r t c g a
 Query Match 100.0%; Score 14; DB 17; Length 615;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAAGCTGTGCTTAC 14
 ||||||||||||
 Db 360 GAAGGTGTGCTTAC 347
 RESULT 9
 ACCESSION AQ930007 GI:6618937
 VERSION AQ930007.1
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 617)
 REFERENCE Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S., Akiret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 TITLE JOURNAL COMMENT
 Other-GSSs: RPCI-23-2308.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pietor de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 23 row: 0 column: 8
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1. .617
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-2308"
 /clone_1lb="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1; EcoRI: Site 2; EcoRI: Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 166 a 153 c 124 g 174 t
 r t c g a
 Query Match 100.0%; Score 14; DB 17; Length 617;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAAGCTGTGCTTAC 14
 ||||||||||||
 Db 343 GAAGGTGTGCTTAC 330
 RESULT 10
 ACCESSION AQ930007 GI:6618937
 VERSION AQ930007.1
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 649)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 TITLE JOURNAL COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 TITLE JOURNAL COMMENT
 Other-GSSs: RPCI-23-2308.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pietor de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 23 row: 0 column: 8
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1. .617
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-2308"
 /clone_1lb="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1; EcoRI: Site 2; EcoRI: Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 166 a 153 c 124 g 174 t
 r t c g a
 Query Match 100.0%; Score 14; DB 17; Length 617;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAAGCTGTGCTTAC 14
 ||||||||||||
 Db 343 GAAGGTGTGCTTAC 330
 RESULT 10
 ACCESSION AQ930007 GI:6618937
 VERSION AQ930007.1
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 649)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 TITLE JOURNAL COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0161 row: K column: 10
Seq primer: CGTGTAAACGACGCGCCAGT
Class: Plasmid ends
High quality sequence stop: 649.
location/Qualifiers
1..649

FEATURES
source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0161K10"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (911473211419b|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
216 a 129 c 93 g 211 t

ORIGIN

Query Match 100.0%; Score 14; DB 17; Length 649;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTTAC 14
|||||

Db 274 GAAGCTGCTTAC 287

30UT 11
.351941
LOCUS
DEFINITION BG351941 666 bp mRNA linear EST 01-MAR-2001
134G06 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
sequence.
ACCESSION BG351941
VERSION BG351941.1 GI:13180683
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; eunasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 666)
Nielsen, K.L., Crookshanks, M., Emmersen, J. and Welinder, K.G.
EST-sequencing of mature potato tuber (Var. Kuras)
Unpublished (2000)
JOURNAL
COMMENT
Contact: Karen G. Welinder
Institut for Biologiologi
Aalborg Universitet
Sohnsgaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk

Sequenced from the 5' end.
High quality sequence stop: 666
POLYA=NO.

FEATURES
source

Location/Qualifiers
1..666
/organism="Solanum tuberosum"
/cultivar="Field grown Kuras"
/db_xref="taxon:4113"
/clone_lib="Mature tuber lambda ZAP"
/tissue_type="Tuber"
/note="Vector: lambda ZAP"

BASE COUNT
189 a 97 c 184 g 196 t

ORIGIN

Query Match 100.0%; Score 14; DB 12; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTTAC 14
|||||

Db 77 GAAGCTGCTTAC 90

RESULT 12
BG753057 746 bp mRNA linear EST 15-MAY-2001
LOCUS 602732326F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4875606 5',
DEFINITION mRNA sequence.
ACCESSION BG753057
VERSION BG753057.1 GI:14063710
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 746)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI, at:
http://image.llnl.gov
Plate: LNCMI757 row: d column: 07

High quality sequence stop: 742.
location/Qualifiers

FEATURES
source

1..746
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4875606"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. !"

BASE COUNT
223 a 159 c 191 g 173 t

ORIGIN

Query Match 100.0%; Score 14; DB 12; Length 746;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 14
 |||||||
 Db 701 GAAGGTGCTTAC 714

RESULT 13
 B1180700/c
 LOCUS
 DEFINITION LRR218 LMH (lin Rhodamine and Hoechst dye) Mus musculus cDNA clone
 B1180700
 VERSION B1180700
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Fungi: Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Ma, X.Y., Husaln, T., Peng, H., Lin, S., Lu, B.F., Tuck, D., Milronenko, O.,
 Johnson, S., Krause, D. and Perkins, A.
 Development of a murine myeloid cDNA microarray using a subtracted
 cDNA library
 Unpublished (2001)
 JOURNAL Contact: Hui Peng, MD, & PhD.
 Dr. Archibald Perkins' Lab
 Yale University School of Medicine
 310 Cedar Street, LH 305, New Haven, CT 06520, USA
 Tel: 203-764-9977
 Email: hui.peng@yale.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: M13AK as 3' primer, T7 as 5' primer.

FEATURES
 source
 1..752
 /location="Qualifiers
 /organism="Mus musculus"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="321729(5.)"
 /clone.lib="LMH (lin Rhodamine and Hoechst dye)"
 /sex="Female"
 /tissue-type="Primary sorted bone marrow cells"
 /dev-stage="Adult"
 /lab_host="DH10B (phage-resistant)"
 /note="Vector: pZL1; Site 1: Salt site; Site 2: EagI site;
 LRM library was constructed from cDNA of primary bone
 marrow cells depicted of lineage-committed cells and
 enriched for primitive cells by FACS sorting for cells
 with low level staining with rhodamine123 and Hoechst
 33342 dyes. cDNA from 5000 cells derived from 30 mice,
 5000 cells were directionally cloned into Salt-EagI
 restriction site of the (Ziplox (Gibco BRL). The ligated
 cDNA fragments were transformed into DH10B host cells.
 The original library had an initial plating complexity of
 1.44X10⁷ clones."

BASE COUNT 177 a 95 c 106 g 142 t 232 others
 ORIGIN

Query Match 100.0%; Score 14; DB 13; Length 752;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 14
 |||||||
 Db 18 GAAGGTGCTTAC 5

RESULT 14
 CNS02819
 LOCUS
 DEFINITION Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
 244A19 of library G from Tetraodon nigroviridis, genomic survey
 sequence.
 ACCESSION AL185382

VERSION AL185382.1 GI:7823486
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodon.

REFERENCE
 1 (bases 1 to 765)
 Roest-Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
 Bernot, A., Fitzames, C., Wncker, P., Brotlier, P., Quetier, F.,
 Saurin, W. and Weissenbach, J.
 Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence

TITLE Unpublished
 JOURNAL 2 (bases 1 to 765)
 Roest-Crollius, H., Jallion, O., Dasilva, C., Fitzames, C., Fisher, C.,
 Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
 Weissenbach, J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis

TITLE Unpublished
 JOURNAL 3 (bases 1 to 765)
 Roest-Crollius, H., Jallion, O., Dasilva, C., Fitzames, C., Fisher, C.,
 Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
 Weissenbach, J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis

REFERENCE
 3 (bases 1 to 765)
 Roest-Crollius, H., Jallion, O., Dasilva, C., Fitzames, C., Fisher, C.,
 Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
 Weissenbach, J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis

TITLE Submitted (12-APR-2000)
 JOURNAL Direct Submission
 Genoscope.
 This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetraodon.
 Location/Qualifiers
 1..765
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:9983"
 /clone="244A19"
 /clone.lib="G"
 /note="Genoscope sequence ID : C0AG244A10SP1-end :
 pUC-ori"

BASE COUNT 224 a 185 c 177 g 178 t 1 others
 ORIGIN

Query Match 100.0%; Score 14; DB 17; Length 765;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 14
 |||||||
 Db 503 GAAGGTGCTTAC 516

RESULT 15
 B0137473/c
 LOCUS B0137473
 DEFINITION NF012D06NRF1000 Nodulated root Medicago truncatula cDNA clone
 B0137473
 VERSION B0137473
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.

REFERENCE
 1 (bases 1 to 776)
 Watson, B.S., Shin, H.-S., Lopez-Meyer, M., Scott, A.D., Harris, A.R.,
 Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May
 G.D. and Palva, N.L.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula nodulated root library
 Unpublished (2000)
 JOURNAL Contact: Palva NL
 COMMENT Plant Biology Division

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380

Email: alpaiva@noble.org
Insert length: 776 Std Error: 0.00
Plate: 012 Row: D Column: 06
Seq primer: TCACACAGCAACACGCTATGAC.

FEATURES

Source
1. .776
Location/Qualifiers
/organism="Medicago truncatula"
/db_xref="taxon:380"
/clone="NF012D06NR"
/clone_id="Nodulated root"
/issue_type="root"
/dev_stage="Pooled developmental"
/note="Vector: lambda Zap; Four-week old Rhizobium
meliloti-inoculated Medicago truncatula roots, containing
a mixture of young and old roots and nodules."
a mixture of young and old roots and nodules.
11 others

BASH COUNT

238 a 188 c 177 g 162 t 11 others

IGIN

Query Match

Best local similarity 100.0%; Score 14; DB 14; Length 776;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTCGCTTAC 14
|||||

Db 366 GAAGGTGCTTAC 353

Search completed: December 10, 2002, 22:49:51
Job time : 722.832 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 455.313 Seconds

(Without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579a-20

Perfect score: 21

Sequence: 1 tttcttcttctctataatg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inu:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pin:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	21	6	AX306851	AX306851 Sequence
2	21	100.0	21	6	AX306861	AX306861 Sequence
3	21	100.0	39	6	AX306868	AX306868 Sequence
4	21	100.0	1789	6	E09772	E09772 The base se
5	21	100.0	2007	6	AR089410	AR089410 Sequence
6	21	100.0	2007	6	AR093610	AR093610 Sequence
7	21	100.0	2322	1	SAPAP	Y00688 Staphylococ
8	21	100.0	2322	6	E03736	E03736 DNA sequenc
9	21	100.0	2454	1	SEMECAPB	X52592 S. epidermi
10	21	100.0	2455	6	E09771	E09771 The base se
11	21	100.0	2456	6	SAMECAPB	X52593 S. aureus m
12	21	100.0	5068	6	AX110445	AX110445 Sequence
13	21	100.0	5068	1	SSK1MECA	Y09223 S. sciuri me
14	21	100.0	5596	1	SSK8MECA	Y13096 S. sciuri me
15	21	100.0	6368	1	SSK3MECA2	Y13095 S. sciuri me
16	21	100.0	9047	1	SAMECAR1	Y14051 Staphylococ
17	21	100.0	21777	1	AB063173	AB063173 Staphyloc
18	21	100.0	26090	1	AB063172	AB063172 Staphyloc
19	21	100.0	39332	1	AB033763	AB033763 Staphyloc
20	21	100.0	58237	1	D86934	D86934 Staphylococ
21	21	100.0	68256	1	AB037671	AH037671 Staphyloc
22	21	100.0	290250	1	AP004822	AP004822 Staphyloc
23	21	100.0	298050	1	AP003129	AP003129 Staphyloc
24	21	100.0	349999	1	AP003358	AP003358 Staphyloc
25	20	95.2	157223	9	AC099664	AC099664 Homo sapi
26	20	95.2	183978	2	AC024967	AC024967 Homo sapi
27	19.4	92.4	6684	1	SSK11MECA	AL499610 Human DNA
28	19.4	92.4	64986	9	AL499610	AL499610 Human DNA
29	19.4	92.4	74119	9	AL731777	AL731777 Human DNA
30	19.4	92.4	130110	9	AL731777	AL731777 Human DNA
31	19.4	92.4	132906	2	AC111352	AC111352 Rattus no
32	19.4	92.4	135160	9	AC016894	AC016894 Homo sapi
33	19.4	92.4	135450	9	AC112131	AC112131 Homo sapi
34	19.4	92.4	138245	8	AC027662	AC027662 Oryza sat
35	19.4	92.4	139035	2	AC108917	AC108917 Mus muscu
36	19.4	92.4	141854	2	AC021595	AC021595 Homo sapi
37	19.4	92.4	148517	2	AC011147	AC011147 Homo sapi
38	19.4	92.4	152449	2	AC080175	AC080175 Homo sapi
39	19.4	92.4	154001	9	AC083904	AC083904 Homo sapi
40	19.4	92.4	160174	2	AP005103	AP005103 Oryza sat
41	19.4	92.4	160664	2	AC102419	AC102419 Mus muscu
42	19.4	92.4	171695	9	AC012337	AC012337 Homo sapi
43	19.4	92.4	177964	9	AC016705	AC016705 Homo sapi
44	19.4	92.4	180672	9	AC011451	AC011451 Homo sapi
45	19.4	92.4	186120	2	AC125910	AC125910 Rattus no

ALIGNMENTS

RESULT 1
AX306851
LOCUS AX306851
DEFINITION Sequence 10 from Patent EP1160333.
ACCESSION AX306851
VERSION AX306851.1 GI:117894673
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1
Taya, T., Ishiguro, T. and Saito, J.
Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
Patent: EP 1160333-A 10 05-DEC-2001;
JOURNAL

```
FEATURES             Tosoh Corporation (JP)
                      Location/Qualifiers
                      1..21
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
                        /note="Oligonucleotide capable of binding specifically to
                        meca gene or RNA derived from said gene"
BASE COUNT           3 a      3 c      1 g      14 t
ORIGIN
Query Match          100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTCTTTTCTCTATTATG 21
    ||||||||||||||||
Db 1 TTTCTTTTCTCTATTATG 21

RESULT 2
ACUS X306861
DEFINITION Sequence 20 from Patent EP1160333.
ACCESSION AX306861
VERSION AX306861.1 GI:17894683
KEYWORDS
SOURCE synthetic construct.
          artificial sequences.
REFERENCE
AUTHORS Taya,T., Ishiguro,T. and Saito,J.
TITLE Oligonucleotides and method for detection of meca gene of
        methicillin-resistant Staphylococcus aureus
        Patent: EP 1160333-A 20 05-DEC-2001;
JOURNAL Tosoh Corporation (JP)
FEATURES
          source
            1..21
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Primer"
BASE COUNT           3 a      3 c      1 g      14 t
ORIGIN
Query Match          100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTCTTTTCTCTATTATG 21
    ||||||||||||||||
    1 TTTCTTTTCTCTATTATG 21

RESULT 3
ACUS X306868
LOCUS AX306868 39 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 27 from Patent EP1160333.
ACCESSION AX306868
VERSION AX306868.1 GI:17894690
KEYWORDS
SOURCE synthetic construct.
          synthetic construct.
          artificial sequences.
REFERENCE
AUTHORS Taya,T., Ishiguro,T. and Saito,J.
TITLE Oligonucleotides and method for detection of meca gene of
        methicillin-resistant Staphylococcus aureus
        Patent: EP 1160333-A 27 05-DEC-2001;
JOURNAL Tosoh Corporation (JP)
FEATURES
          source
            1..39
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Probe"

FEATURES             Tosoh Corporation (JP)
                      Location/Qualifiers
                      1..21
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
                        /note="Probe"
BASE COUNT           6 a      5 c      6 g      22 t
ORIGIN
Query Match          100.0%; Score 21; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTCTTTTCTCTATTATG 21
    ||||||||||||||||
Db 1 TTTCTTTTCTCTATTATG 21

RESULT 4
ACUS E09772/C
DEFINITION The base sequence of modified meca DNA.
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS JP 1995209294-A/2.
SOURCE Staphylococcus aureus.
          Staphylococcus aureus.
          Staphylococcus aureus.
          Bacteria: Firmicutes; Bacillales; Staphylococcus.
          1 (bases 1 to 1789)
REFERENCE Kono,M., Hiramatsu,K., Sasazaki,M., Noguchi,M. and Suguro,K.
AUTHORS NOVEL "MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
TITLE METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
        Patent: JP 1995209294-A 2 11-AUG-1995;
JOURNAL KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
          OS Staphylococcus aureus
          PN JP 1995209294-A/2
          PD 11-AUG-1995
          PF 10-JAN-1994 JP 1994012226
          PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
          MASAHISA,
          PI SOGURO KAZUYA
          PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC
          C12R1:19),
          PC (C12P21/02,C12R1:19);
          CC Stranded-ss: Double;
          CC Topology: Linear;
          FH Key
          FT source
          FT 1..1789 /organism="Staphylococcus aureus" FT CDS
          FT 1..1608 /product="Modified meca".
FEATURES
          source
            1..1789
              /organism="Staphylococcus aureus"
              /db_xref="taxon:1280"
BASE COUNT           735 a    263 c    302 g    489 t
ORIGIN
Query Match          100.0%; Score 21; DB 6; Length 1789;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTCTTTTCTCTATTATG 21
    ||||||||||||||||
Db 556 TTTCTTTTCTCTATTATG 536

RESULT 5
ACUS AR089410/C
LOCUS AR089410 2007 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 169 from patent US 5994066.
ACCESSION AR089410
VERSION AR089410.1 GI:10016167
KEYWORDS
SOURCE unknown.
          unknown.
          unclassified.
REFERENCE 1 (bases 1 to 2007)
```

AUTHORS Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..2007
BASP COUNT 855 a 270 c 341 g 541 t
ORIGIN
Query Match 100.0%; Score 21; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTTCTTTTCTCTATTATG 21
DB 955 TTTTCTTTTCTCTATTATG 935
FEATURES
LOCUS AR093610 2007 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 169 from patent US 6001564.
ACCESSION AR093610
VERSION AR093610.1 GI:10020359
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron,M.G., Ouellette,M. and Roy,P.H.
TITLE Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..2007
BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN
Query Match 100.0%; Score 21; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 TTTTCTTTTCTCTATTATG 21
DB 955 TTTTCTTTTCTCTATTATG 935
RESULT 7
SABP/c 2322 bp DNA linear BCT 12-SEP-1993
LOCUS Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
ACCESSION Y00688.1 GI:46628
VERSION Y00688
KEYWORDS penicillin-binding protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 2322)
AUTHORS Song,M.D., Machi,M., Dol,M., Ishino,F. and Matsunashi,M.
TITLE Evolution of an inducible penicillin-target protein in methicillin-resistant Staphylococcus aureus by gene fusion
JOURNAL FEBS Lett. 221 (1), 167-171 (1987)
MEDLINE 87304805
PUBMED 3305073
REFERENCE 2 (bases 1 to 2322)
AUTHORS Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,

TITLE Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
Sequence comparison of mecA genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT Data kindly reviewed (13.1.88) by Matsunashi.
FEATURES Location/Qualifiers
source 1..2322
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"
1..2013
/note="penicillin-binding protein (AA 1-670)"
/codon_start=1
/transl_table=1
/protein_id="CAA68684.1"
/db_xref="GI:46629"
/db_xref="SWISS-PROT:P07944"
/translation="MKIKIYPLILIVVVGFGIYFVASKDEINNTIDATEDKKNFQ
VYKDSYISKDNCEVEEMERPIKINISLGKVDINIDRKIKKYSKKKRVDAQYKIK
TRYGNIDRNVQPNFYKEDGKKLIDHSYIIPGMKDSIHENIKSERGKILDRNV
ETANTGTHRLGIVPKVNSKDYKAIAKELISDY INKKMKGKMI PSFHKTVK
KMDXELSDFAKKFHLTTNETESRNPGLKATSHLGVGPINSEELKQEKGYKDA
VYKKGLEKLYDKLQHEGYRVTIVRVDDNSNTIAHLIERKKDKGDIQLTIDAKV
OKSIYNNKNDYSGTAIHPOTGELLAVSTPSYDVYFPYGMSEENKLTEDKEP
LNKFOITTPSGSTOKILYAMIGLNKTLIDPSTYKIDGKGMOKDSMGGVVTVREV
VNGNDIKQALIESNDNIFPARVALPLGSKKKEKMKKIGVCHDI PSQYPIYNAOISNK
NIDNELIADSGYCGEILINPVOLISTYSALENNNGINNAHRLIKYTNKKYKKKIIIS
KENILNDGMQOVVNAKTHKEDIYRSVNLGKSGTALAKMGQGTGIGFISYDK
DNPMMMAINVDVODKGASVNAISIKYVDYELNGNKRYIDE"
BASE COUNT 940 a 324 c 389 g 669 t
ORIGIN
Query Match 100.0%; Score 21; DB 1; Length 2322;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTTCTTTTCTCTATTATG 21
DB 961 TTTTCTTTTCTCTATTATG 941
RESULT 8
E03736/c 2322 bp DNA linear PAT 29-SEP-1997
LOCUS DNA sequence of PBP2' gene for determination of methicillin resistance.
DEFINITION
ACCESSION E03736
VERSION E03736.1 GI:2171951
KEYWORDS JP 1992169200-A/9.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2322)
AUTHORS Watanabe,Y., Nakamura,E., Teraoka,H., Wada,K., Minamide,W. and Murakami,K.
TITLE Detection of PBP 2' GENE AND JUDGMENT OF METHICILLIN RESISTANCE
JOURNAL SHIONOGI & CO LTD
COMMENT OS (methicillin resistant)staphylococcus aureus
PN JP 1992169200-A/9
PD 17-JUN-1992
PF 31-OCT-1990 JP 1990296708
PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI,
PI MINAMIDE MAKIO, MURAKAMI KAZUHISA
PC C1201/68, C12N15/11;
CC strandness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers

FEATURES	FT	misc-feature	1..2322	
source	FT		/note="PBP2' gene for determination of P ^T methicillin resistance'.	
Location/Qualifiers			1..2322	
/organism="unidentified"			/db_xref="taxon:32644"	
BASE COUNT		939 a	324 c	390 g 669 t
ORIGIN				
Query Match		100.0%;	Score 21;	DB 6; Length 2322;
Best Local Similarity		100.0%;	Pred. No. 3.8e+02;	
Matches	21;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	TTTTCTTTTCTCTATTATG	21	
Db	961	TTTTCTCTTTCTCTATTATG	941	
RESULT 9				
MECAPB/C				
LOCUS		SEMECAPB	2454 bp	DNA linear BCT 12-SEP-1993
DEFINITION		S. epidermididis meca gene for PBP2'		(penicillin binding protein 2').
ACCESSION		X52592		
VERSION		X52592.1	GI:46993	
KEYWORDS		meca gene; methicillin resistance; penicillin-binding protein; penicillin-binding protein 2'.		
SOURCE		Staphylococcus epidermidis.		
ORGANISM		Staphylococcus epidermidis		
REFERENCE		Bacteria; Firmicutes; Bacillales; Staphylococcus.		
AUTHORS		1 (bases 1 to 2448)		
TITLE		Ryffel,C.		
JOURNAL		Direct Submission		
REFERENCE		Submitted (05-APR-1990)		Ryffel C., University of Zuerich, Instl of Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
AUTHORS		2 (bases 1 to 2454)		
TITLE		Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,		
JOURNAL		Barberis-Maino,L., Kayser,F.H. and Berger-Baechli,B.		
REFERENCE		Sequence comparison of meca genes from methicillin-resistant		
AUTHORS		Staphylococcus aureus and Staphylococcus epidermidis		
TITLE		Gene (1990) In press		
JOURNAL		3 (bases 1 to 2454)		
REFERENCE		Ryffel,C.		
AUTHORS		Direct Submission		
TITLE		Submitted (23-JUL-1990)		Ryffel C., University of Zuerich, Instl of Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
JOURNAL		4 (bases 1 to 2454)		
REFERENCE		Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,		
AUTHORS		Barberis-Maino,L., Kayser,F.H. and Berger-Baechli,B.		
TITLE		Sequence comparison of meca genes isolated from		
JOURNAL		methicillin-resistant Staphylococcus aureus and Staphylococcus		
REFERENCE		epidermidis		
AUTHORS		Gene 94 (1), 137-138 (1990)		
TITLE		91033056		
JOURNAL		2227446		
MEDLINE		See also <X52593-4> and <X00688>		
PUBMED		Data kindly reviewed (23-JUL-1990) by C. Ryffel.		
COMMENT		Location/Qualifiers		
FEATURES		1..2454		
source		/organism="Staphylococcus epidermidis"		
		/strain="WT55"		
		/db_xref="taxon:1282"		
		/clone="WT80/WT9"		
		80..85		
		/note="35 region"		
		101..105		
		/note="10 region"		
		130..134		
		/note="ribosome binding site"		
		141..2159		
		/note="primary transcript"		
		141..2147		
		CDS		

	/note="rBP2' (AA 1 - 668) "
	/codon_start=1
	/transl_table=1
	/protein_id="CA36828.1"
	/db_xref="GI:46994"
	/translation="MKKIKIIVPILIIIVVVGCGIYFASAKDKLINNTIDAIEPKNFKO VYKRSYSISKSDNCEVFMTFRPIKITVNSIGYKDINIDDKIKVSKKKKKVDQYKIK ITNGINIRNOVFNFKEGMMKLDMDSVIIPEGOKDOSIHTEMLSEKRLIDRNV ELANTGAIEIGEIVKPNVSKRDVKAIKEKLSIEDSYIKQODNMWODDFVLPTKY KMDEYLDPFAKKPHLTTNETESRNYPGKAATSHLEGVGPINSELKOKFYKGKDDA VICGGJGLEKIYDKKLQHHDGYRAVIIVDENSENTIAHTLIIEKKKKGKDIQLTIKAVOK SIYNMKNMGOSGTALIPHOTGELLALVSPTSYDYVPYMGMSNPETVKKIIEDEKPEPLI NKHOITSPGSTOKIITAMICGNKKTLDDKTPSYKIDCKGMOKXSGCVWVTFEYVN GNIDLKOAIESSDNIFFARVALBELGSKRFEKKKLLGVGEDIFSDIFYNAOISNNKL DNELLDGSGEGCELINFPVOILSITSALENNONTINAPHLKDTKNNKKNKTISE NINLTGOGMOOVNKKTHKEDIYRSYANLIGKSTGAELKMKOGLETGRQIGMFISYDKDN PNMMAINVKDVODCKMASYNAKISGVYDPLVENCNKKYDIDE"
old_sequence	441..448
	/note="atcaaac was ac in [1]"
	/citation=[1]
old_sequence	641..643
	/note="agc was ac in [1]"
	/citation=[1]
old_sequence	652..653
	/note="ta was tta in [1]"
	/citation=[1]
old_sequence	731..733
	/note="caa was ca in [1]"
	/citation=[1]
old_sequence	780..781
	/note="ct was ctt in [1]"
	/citation=[1]
BASE COUNT	997 a 345 c 398 g 714 L
ORIGIN	
Query Match	100.0%; Score 21; DB 1; Length 2454;
Best Local Similarity	100.0%; Pred. No. 3,7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy 1 TTTCTTTTCTCATTAATG 21 	
Db 1095 TTTTCTTTTCTCTATTAAAG 1075	
RESULT 10	
E09771/c	
LOCUS	E09771 2455 bp RNA linear PAT 29-SEP-1997
DEFINITION	The base sequence of meca DNA.
ACCESSION	E09771
VERSION	E09771.1 GI:22026400
KEYWORDS	JP 1995209294-A/1.
SOURCE	Staphylococcus aureus.
ORGANISM	Staphylococcus aureus
REFERENCE	Bacteria: Firmicutes; Bacillales; Staphylococcus.
AUTHORS	1 (bases 1 to 2455);
TITLE	Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K. NOVEL "MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS Patent: JP 1995209294-A 11-AUG-1995; KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD OS Staphylococcus aureus PN JP 1995209294-A/1
JOURNAL	PD 11-AUG-1995 PF 10-JAN-1994 JP 1994012226 PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA, PI SUGURO KAZUYA PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,(C12N1/21, PC C12N1:19)' CC (C12P21/02,C12P1:19); CC strandedness: Double; CC topology: Linear;

```

FH      key      location/Qualifiers
FH      source      1. .2455
FT      134. .2146 /organism='Staphylococcus aureus' FT CDS
FT      /product='meca protein'.
FEATURES
source      1.2455
            /organism='Staphylococcus aureus'
            /db_xref='taxon:1280'
BASE COUNT      997 a 344 c 401 g 713 t
ORIGIN
Query Match      100.0%; Score 21; DB 6; Length 2455;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTTCTTTTCTCTATTATG 21
        |||
b      1094 TTTTCTTTTCTCTATTATG 1074

```

```

RESULT 11
SAMBCAP/c      2456 bp      DNA      linear      BCT 12-SEP-1993
LOCUS      S. aureus meca gene for PBP2' (penicillin binding protein 2').
DEFINITION      X52593
ACCESSION      X52593.1 GI:46610
VERSION      meca gene: methicillin resistance; penicillin-binding protein;
KEYWORDS      penicillin-binding protein 2.
SOURCE      Staphylococcus aureus.
ORGANISM      Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE      1 (bases 1 to 2456)
AUTHORS      Ryffel, C.
TITLE      Direct Submission
JOURNAL      Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
REFERENCE      Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
AUTHORS      2 (bases 1 to 2456)
            Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P.E.,
            Barberis-Maino, L., Kayser, F.H. and Berger-Bachl, B.
            Sequence comparison of meca genes isolated from
            methicillin-resistant Staphylococcus aureus and Staphylococcus
            epidermidis
            Gene 94 (1), 137-138 (1990)
JOURNAL      91033056
MEDLINE      222746
COMMENT      See also <X52592>, <X52594> and <Y00688>.
            Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source      1.2456
            /organism='Staphylococcus aureus'
            /strain='NCTC8325, isolate-BB270'
            /db_xref='taxon:1280'
            /clone_11b='EMBL-3'
            80. .85
            /note='-.35 region'
            101. .105
            /note='-.10 region'
            130. .134
            /note='ribosome binding site'
            141. .2153
            /note='primary transcript'
            141. .2147
            /note='PBP2' (NA 1-668)'
            /codon_start=1
            /transl_table=1
            /protein_id='CAA36829.1'
            /db_xref='gi:46611'
            /db_xref='SPTREMBL:053707'
            /translation='MKIKIIVPLILIVVVGSGIYFVASKDEINNTDAIDKDKFKO
            VYKSSYSKSNQNGEVEMTHRIKIKYNSLQVADINIQDKIKKVSNNKKRVDAQYRIK
            TNYGNIDRNVOFNFVKGDMKLDMDHSVILIPGOKODSIHTENLSEKGIIDRNNV

```

```

ELANCTHMRIGIVPKNSKKDYKKAIAKELISIEDY INNKMIK IGYKMI PSHPRKTVK
KDEYISDPAKKPHLTNTETESRNPLEKATSHILCYVCP INSEIKOKRYKQKIDA
VIGKGLEKLYDKKLOHEDGYRVTIVDDSNSTIAHTLIEKKKDGKDILDTIDAKVOK
SIYNNKKNDYSGSTAIHPQGTGLAVSPSPDYPPMGSMNEEYNNKLTETKEPELL
NKFOITTSFGSTQKILITAMIGLNKNTLDRKTSYKIGDGKQKDSMGVNVRYEVVN
GNIDLKQALISSDNIIPFAHVALLGSKFKFKGKIKIGVCHD IPSDYPIYNAOISNNI.
DNEILLADSGYGGGELLINPVOLLSIYSALENNGNINAHILLKDPYNNKYNKNIISKI
NINLIDMGQOYVNNKTHKEDIYKSYANLIGKSTALIKKQCHSCHQICWPISYDKDN
PNMMAINVKDQVODKGMASYSYMAISGVYDELYENGNKKYDIDE'
BASE COUNT      1001 a 344 c 396 g 715 t
ORIGIN
Query Match      100.0%; Score 21; DB 1; Length 2456;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTTCTTTTCTCTATTATG 21
        |||
Db      1095 TTTTCTTTTCTCTATTATG 1075

```

```

RESULT 12
AX110445/c      2456 bp      DNA      linear      PAT 30-APR-2001
LOCUS      Sequence 1178 from Patent WO0123604.
DEFINITION      AX110445
ACCESSION      AX110445
VERSION      AX110445.1 GI:13926737
KEYWORDS
SOURCE      Staphylococcus subsp. aureus NCTC 8325.
ORGANISM      Staphylococcus aureus subsp. aureus NCTC 8325.
REFERENCE      Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS      1 (bases 1 to 2456)
            Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
            Picard, F.J. and Roy, P.H.
            Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
            Patent: WO 0123604-A 1178 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source      1.2456
            /organism='Staphylococcus aureus subsp. aureus NCTC 8325'
            /db_xref='taxon:93061'
            /db_xref='taxon:93061'
BASE COUNT      1001 a 344 c 396 g 715 t
ORIGIN
Query Match      100.0%; Score 21; DB 6; Length 2456;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTTCTTTTCTCTATTATG 21
        |||
Db      1095 TTTTCTTTTCTCTATTATG 1075

```

```

RESULT 13
SSKIMECA/c      5068 bp      DNA      linear      BCT 07-MAY-1997
LOCUS      S.sciuri meca gene & ORF's 450, 145 & 179.
DEFINITION      Y09223
ACCESSION      Y09223.1 GI:2073520
VERSION      meca gene.
KEYWORDS      Staphylococcus sciuri.
SOURCE      Staphylococcus sciuri.
ORGANISM      Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE      1 (bases 1 to 5068)
AUTHORS      Wu, S., Piscitelli, C., de Lencastre, H. and Tomasz, A.
TITLE      Tracking the evolutionary origin of the methicillin resistance
            gene: cloning and sequencing of a homologue of meca from a
            methicillin-susceptible strain of Staphylococcus sciuri
            Michb. Drug Res. 2, 435-441 (1996)
REFERENCE      2 (bases 1 to 5068)
JOURNAL      Wu, S.
AUTHORS      Direct Submission

```

JOURNAL Submitted (05-NOV-1996) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
REFERENCE 3 (bases 1 to 5068)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
COMMENT On May 8, 1997 this sequence version replaced gi:1769448.
FEATURES
source location/Qualifiers
1..5068
/organism="Staphylococcus sciuri"
/strain="ATCC29062"
/sub-species="sciuri"
/db_xref="taxon:1296"
complement(<1..1351)
/note="ORF450"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="CAA70424.1"
/db_xref="GI:2073521"
/db_xref="SPTREMBL:O05983"
/translation="MIPSOAKRLIGPKKKKELONKISNTKALATLSSPALSSVAV
GPEQILIVSYLGAIAMAYTPITAFITLITLVISROYIAYPHGGAGYTSKIN
LGEKMSILAGSLVDYITLYAVSISSTDLVAFPSTLEKRLINCLITILILN
LKGLESATVISTPVIETFLQIMLVASWKAATGAEPOITISVGSVGYTFLL
LKAFSSGASLTGVEAISNSYKSPDAKNAVATLLAMGSILOPMLVGWYTFPG
IMPORETTVLSQAKQVGESEVIFYPFOGAVVLLILIAANGTAPFLAAMAKDKY
MPMHFTVAGDRLGYSNSITILIGVLAIFLIGFNKTNLPLVAVGVIFPTLQOLM
MIKWIKKPKMKKKLAINFLTGIVITFTIFMILLITMKMPHWPILFIPVILMFVRI
*
RBS complement(1358..1362)
/note="ORF450"
complement(1413..1418)
/note="ORF450"
complement(1437..1442)
/note="ORF450"
1559..3640
/gene="meca"
1559..1564
/gene="meca"
1581..1586
/gene="meca"
1628..1634
/gene="meca"
1640..3640
/gene="mea"
/codon_start=1
/transl_table=11
/product="MecA protein"
/protein_id="CAA70425.1"
/db_xref="GI:1769449"
/db_xref="SPTREMBL:P96018"
/translation="MKRLIATVITVAVSGVFVASKDKKINETIDAEKKNVQV
FKNSTYQKNDNGEVEMTDRPIKIYDSLVKVDINIKRIDIKKYSKKNKQVAKKELOT
NYGKINDVAGTINFKEDDKMLDNQNAIIPGMKKNSINTEPLKSRGILDNNE
LATGTGTHVGATVPNNVSTSDYKAIAKLLDSEYIKQOTEDWVKDDIYPLKTVD
MNODLKNFVKYHLTQETESRQPLEEATHLHGGYPTNSEELKOKAKRGYKDDI
VGGKIGELVDKDLONKDGVRVTLIDNNNVIDTLIEKKIKDCKDILTDAROKSI
YNNMKDDVSGTAHPOTGELLAVSPSYDVYFPNMGDEDEKRLTEDDEPLK
FOITTSFGSTOKITITAMIGLNKTKLDKSTIKINGKQMKDSKSGDNVIRVEVND
IDKQALLESSDNITFAFVALELSKKEBEKMKRGVEDIPSDYFYNAAISNNLND
ELLADSGYGOGELLINPVOILSYSALENKGNVNAHVLDKRNKWKNNITSOENT
KLITDGMQOVGNKTHREDIYRSYANLVGKSGTALMKKOCETGOOLGMPISYDKDNH
IMAINVNDVODGMASYNAKISGKYVDLIDNCKKTYRIDK"
4011..4016
/note="ORF145"
4034..4039
/note="ORF145"
4063..4067
/note="ORF145"
4074..4511
/note="ORF145"
CDS
-35_signal
-10_signal
RBS
CDS

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="CAA70426.1"
/db_xref="GI:2073522"
/db_xref="SPTREMBL:O05984"
/translation="MDYNNMKLANCVSNVSLFAOFYEKELKSGLTYSQVLL
SLMEILKHTOLVINNNLSNTLTPLKRLRLEOSGAWTTRKSDQDKRQLVSLQKCK
DOKQPIYDAISRCSEDMNDLIYKQTDIMQLEATILRKQINK"
4476..4481
/note="ORF179"
4500..4505
/note="ORF179"
4520..4524
/note="ORF179"
4532..45068
/note="similar to MADH-ferredoxin oxidoreductase of
S. erythraea & glutathione reductase of N. labacum"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="CAA70423.1"
/db_xref="GI:2073523"
/db_xref="SPTREMBL:O05985"
/db_xref="SPTREMBL:O05985"
/translation="MKREDDVFISGHAAMHATLTKHAGKVAIIEKDTIAGCTNY
GCNKKILLEGYEVLEASHVPOIIESDOLHVNNKNNLMQYKAVINPLSTLKMFEQ
OGIEVIMGACGLVAHVTVDEGCTPIQAKENIVIAIGQSNKIDIHGSAI/THDSRDIPL
DKMNSITFIAGIISIEP"
BASE COUNT 1887 a 837 c 833 g 1511 t
ORIGIN
Query Match 100.0%; Score 21; DB 1; Length 5068;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TTTCTTTTCTTATTATG 21
|||||
Db 2588 TTTCTTTTCTTATTATG 2568
RESULT 14
SSK8MECA 5596 bp DNA linear BCT 16-JAN-1998
LOCUS S_sciuri meca gene, strain K8 (ATCC700063).
DEFINITION Y13096
ACCESSION Y13096
VERSION Y13096.1 GI:2791919
KEYWORDS meca gene; mecI gene; mecR1 gene; NTORF101; NTORF78; ORF142.
SOURCE Staphylococcus sciuri.
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 5596)
Wu, S., de Lencastre, H. and Tomasz, A.
Genetic organization of the meca region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 96101461
PUBMED 9440511
REFERENCE 2 (bases 1 to 5596)
Wu, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences X53818, X54660, L14020, X52593, Y09223.
FEATURES
source location/Qualifiers
1..5596
/organism="Staphylococcus sciuri"
/strain="K8 (ATCC700063)"
/sub-species="rodentius"
/db_xref="taxon:1296"
1..236
/gene="NTORF78"
<1..236
/gene="NTORF78"

[illegible]

	gene	E L A T G A V P E G I Y P K R N V S K D K Y A I K A I K E L S I S P D Y I K O O M D N M Y D O P F V L K T Y K K M D E Y I S D F A K K F I L T T N E B S E R N T P L E K A T S H I L G V G I T N S E L K O K E Y K G K D D A V I C K R G L E K Y D K R L Q H E D G Y R V T I V D N S N T I A H T I E K R K D G K D I Q J T I I A K V O K S I Y A N N K N D Y G S T A I H P O T G E I L A L V S P S Y D V P P M Y C M S N E Y N K I L E D K K E P L L N K F P T T S P G S T O T I L T A M I G I L N N K T L D D T S Y K J I D K G M Q K I S W C Y V A V T R E Y V N G N I D K O A I E S S D I F F A R V A L E I G S K F E K G M K I G V G E D I P S D Y P Y A O I S N K L D N E I L L A D S G Y G O G E I L I N P O L I S T A L E N G N I N A P U L I K D T R K Y V K N I S K E N I L I T D G M Q V A K T I K E D I Y R S Y A N L I G S G T A E L K M G Q E T G R I G M F I S Y D K D N P N M M A I I N V K D V O D K M A S Y N A K I S G A V Y D L Y E N G K K K D I I D "					
CDS		/gene="ORF142"	complement(4765..5266)				
		/codon_start=1					
		/transl_table=1					
		/protein_id="CAA3548.1"					
		/db_xref="GI:2791924"					
		/db_xref="SPTRMBL:O54520"					
		/translation="MKYDDFLVGTFETKSLSHITEEELIOFATTPDPYUHIKENAE					
		OSRKGILASGMHTLSIPFKLMVEEGYGEYVAAGTOMNVKRIRIKPYRGNTLYIAIE					
		IYNKKSLIKENGCIATVTSLSYNNEMBEIVFGAYVALINNS"					
RBS		complement(5200..5203)					
		/gene="ORF142"					
-10_signal		complement(5238..5243)					
		/gene="ORF142"					
-35_signal		complement(5261..5266)					
		/gene="ORF142"					
gene		complement(5290..5596)					
		/gene="NTORF101"					
CDS		complement(5290..5596)					
		/gene="NTORF101"					
		/codon_start=2					
		/transl_table=1					
		/protein_id="CA473549.1"					
		/db_xref="GI:2791925"					
		/db_xref="SPTRMBL:O54616"					
		/translation="SEFNVLVKLAEEIIMPYNRNAVIFHTTSFREDMRTLLDYCNNAKV					
		NTEBAKLTAKKVVKEAGVELNWTVNKNKPARANQLANMGVDGIFTDNADKRVHLSSO"					
BASE COUNT	1991 a	836 c	821 g	1928 t			
ORIGIN							
Query Match	100.0%	Score 21:	DB 1:	Length 5596:			
Best Local Similarity	100.0%	Pred. No. 3.	Le+02;				
Matches 21: Conservative	0:	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1	TTTTCTTTTCCTCATTAATC	21				
Dd	3667	TTTTCTTTTCCTATTAAATG	3667				
RESULT 15							
SSK3MECA2/c							
LOCUS	SSK3MECA2	6368 bp	DNA	linear	HCT 16-JAN-1998		
DEFINITION	S. sciuri meca2 gene, strain K3 (MM2).						
VERSION	V13095						
KEYWORDS	X13095.1 GI:2791912						
ORGANISM	CTORF261 gene; meca2 gene; mec1 gene; mec1 gene; NTORF101; ORF142. Staphylococcus sciuri Staphylococcus sciuri Bacteria; Firmicutes; Bacillales; Staphylococcus. 1 (bases 1 to 6368) Wu,S., de Lencastre,H. and Tomasz,A. Genetic organization of the meca region in methicillin-susceptible and methicillin-resistant strains of Staphylococcus sciuri J. Bacteriol. 180 (2), 236-242 (1998)						
JOURNAL MEDLINE PUBMED	98101461						
REFERENCE	2 (bases 1 to 6368)						
AUTHORS	Wu,S.						
TITLE	Direct Submission						
JOURNAL	Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA						
COMMENT	Related sequences U14020, X52593, Y09223						

```
FEATURES
source      1..6368
             /organism="Staphylococcus sciuri"
             /strain="K3 (MM2)"
             /sub_species="Todenlius"
             /db_xref="taxon:1296"
             complement(1..883)
             /gene="Ctorp261"
             complement(<1..784)
             /gene="Ctorp261"
             /codon_start=1
             /transl_table=11
             /protein_id="CAA73539.1"
             /db_xref="GI:2791913"
             /db_xref="SPTREMBL:O54280"
             /translation="MENILNINDEKRVLEIYNHINI SRQISKNLEFNKATISSIL
             NKLKKSILVNEGEDSTKSGRKPILLKVNHLITGYFSLDITSSVEVMYFEGNV
             IKHESYDI.PDEKVVSI.LSI.IKKHIDIQEKIDYNGCLGVSVIHGVVNDMEQVTVI.PF
             HETFCISIAKRIKEITNVVVENKLANLSALERNFNHLSYNNLIALSIHKGICAGL
             11NNOLYKANCAGEIGKTLVSKVSDNVEI.FHKIEDI.FSOEA"
             complement(791..797)
             /gene="Ctorf261"
             complement(855..860)
             /gene="Ctorh261"
             complement(878..883)
             /gene="Ctorp261"
             complement(1257..1628)
             /gene="mec1"
             complement(1257..1628)
             /gene="mec1"
             /codon_start=1
             /transl_table=11
             /product="Mec1 protein"
             /protein_id="CAA73540.1"
             /db_xref="GI:2791914"
             /db_xref="SPTREMBL:O54281"
             /translation="MDNKYEISSAEWEVMNIIMKKYASANNILEIOMQDMSPT
             IPTILIRLYKKGFIIDKKDKNIFQYYSIVEESDIYKTSKNINIKVYGGFNSIYLVN
             VEKEDLSQDEIEELNINLKK"
             complement(1628..3385,3392..3398,3410..3415)
             /gene="mecr1"
             complement(1628..3385)
             /gene="mecr1"
             /codon_start=1
             /transl_table=11
             /product="Mecr1 protein"
             /protein_id="CAA73541.1"
             /db_xref="GI:2791915"
             /db_xref="SPTREMBL:O54282"
             /translation="MSSPIMICIISSILITICVPLI.VEMLYIKYTONIMSHKIMU.IVL
             VSTLPIPEYKISNFTSKDMNRNVSIDTSSVSHMDGOOSVTKDLAINVOEET
             SNITMYLLIWFEGSLCLFYMKAFROIIVYKSSLESSTYNEELKVCQSMQYRK
             HTTISXSSNIDNPMYEGLYKQIYLPYVVEIEMDKETETIILHELSHVSHDLIFNO
             IIVYKMI.FWNPALYISKTMNDNCEKVCNVLILNRHRI.RYGESILSKSLKLS
             OHINNAOYLILGFENSKI.RERYKIALYDSMPKPRNKRIVAYIVCSISLLOAPILS
             AHVODKJETVNSYKILNQIAPYFKGPDGSEVLVNERQAVSIYNESPESKQYSPNST
             KYIYALAFQDNLSLNTHEQOMDKHQYPEKEMQDONLSMSKYSVMWYENKHI
             LRODEKSYLDLIEYGENEISGENENYENESSIKISAIQOVNLIKMKQHNHFDKAI
             EKVENSMILKOKDITKGVYKGTGTGI.VNKEANGWVGVYETKNDNTYYFATHLKGDNA
             NCKEKOQISERIKMELI"
             complement(1636..1640)
             /gene="mec1"
             complement(1636..1640)
             /gene="mec1"
             complement(1636..1640)
             /gene="mec1"
             complement(3392..3398)
             /gene="mecr1"
             complement(3410..3415)
             /gene="mecr1"
             3424..3429
             /gene="meca2"
             3424..3429
             /gene="meca2"
             complement(3433..3438)
             /gene="meca2"
             complement(3433..3438)
```

```
-35_signal      /gene="mecr1"
                 complement(3433..3438)
gene            /gene="mecr1"
                 3448..3491
-10_signal      /gene="meca2"
                 3448..3453
RBS             /gene="meca2"
                 3474..3479
CDS             /gene="meca2"
                 3485..5491
                 /gene="meca2"
                 /codon_start=1
                 /transl_table=11
                 /product="MecA2 protein"
                 /protein_id="CAA73542.1"
                 /db_xref="GI:2791916"
                 /db_xref="SPTREMBL:O54283"
                 /translation="MKKIKI.VPLI.IVVVVGCIYVYASKIK.EI.NNT.IDAIDCKNFKQ
                 VYKDSYSISKSDNCEVEEMTERP.IK.IYNSIGVKDI.NI.OPK.IKYSKNKRKYDAQYK.IK
                 TNVGNIDRNVOPNFVPEKEDOMMKLMDHSY.IIPGMOKDOS.IHLENLKSRRK.IIDRNV
                 ELANTGTAYEIGIVPKVNSKKDYKAI.IAKELSTSEDIYIKOQMDQNMVODDFEVLKTVK
                 KMDYLSPFAK.FH.LTNETESRNP.IKELSTSHLLGYGPIINSEELKQKEYKGYKDDA
                 VIKKGLKELDKKIQHEDGIVNTTVDDNSNTIANTLLEKRRKDGKDIQLTIDAKVOK
                 SIYNNMKNDYSGTA.IHPQTCFLAI.VSTPSYDVY.PMYGMSNEYNKI.TEDKKRPIL
                 NKFO.ITTSFGTQK.II."AMI.GLNKTI.IADKTSYK.IIDGCMQWDKSMGCVNTRYEVN
                 GN.IDLKQAI.ESSDNI.FFARVALEIGSKFEEKMKI.GYGPDI.PSDYPPYNAQ.I.SKNL
                 DNEILADSGYGGEGILINPVO.ILSITSALBNNGNINAPHLIKOTKKNVKKNIISKE
                 NINILTDGQGVNKTIKEDIYRSYAN.IGKSGTALMKKGEGRP.IGMPI.SYDKDN
                 PILMAIIVKDPD.KGMSYNKIKSGKYVDELYENGNKKYDIDE"
                 complement(5537..6038)
                 /gene="ORF142"
                 complement(5537..5965)
                 /gene="ORF142"
                 /codon_start=1
                 /transl_table=11
                 /protein_id="CAA73543.1"
                 /db_xref="GI:2791917"
                 /db_xref="SPTREMBL:O54520"
                 /translation="MKYDDFIVGETFKTSLIITEEITOFATTFDDPYMHIDREKAE
                 QSREFGI.IASGMHTLSISFKLWDEGKGEEVAVAGTOMNNV.KFIKPYPGMTLVIAE
                 ITNKSIRKENGLVLSIYSENEIEIVFKGEVTLINNS"
                 complement(5972..5977)
                 /gene="ORF142"
                 complement(6010..6015)
                 /gene="ORF142"
                 complement(6033..6038)
                 /gene="ORF142"
                 complement(6062..6368)
                 /gene="NTORP101"
                 complement(6062..>6368)
                 /gene="NTORP101"
                 /codon_start=2
                 /transl_table=11
                 /protein_id="CAA73544.1"
                 /db_xref="GI:2791918"
                 /db_xref="SPTREMBL:O544616"
                 /translation="SFNVVLVILKEIIPYVNRVAYIFHTTSFRDNRITLDYCAKIY
                 NTEDAKIKAVKRYKREGEIYNTVTVKPARANDLANMGVDGIFTDNADKMHLSQ"
                 ORIGIN
BASE COUNT      2230 a      998 c      864 g      2236 t
Query Match      100.0%; Score 21; DB 1; Length 6368;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTCTTTTTCCTATTAATG 21
   |||||||
DB 4439 TTTTCTTTTTCCTATTAATG 4419
Search completed: December 10, 2002, 20:16:49
Job time : 459.438 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 : Search time 303.542 Seconds
(without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-19
Perfect score: 14
Sequence: 1 gaagagtgcttac 14

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBank:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pt:*
10: gb_ro:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sy:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rod:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlg_hum:*
40: em_hlg_mus:*
41: em_hlg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	14	100.0	14 6 AX306858	AX306858 Sequence
2	14	100.0	14 6 AX306860	AX306860 Sequence
3	14	100.0	467 6 A44526	A44526 Sequence 2
4	14	100.0	720 6 HSA336539	AJ336539 Homo sapi
5	14	100.0	1789 6 E09772	E09772 The base se
6	14	100.0	2007 6 AR089410	AR089410 Sequence
7	14	100.0	2007 6 AR093610	AR093610 Sequence
8	14	100.0	2322 6 SAPBP	Y00688 Staphylococ
9	14	100.0	2322 6 E03736	E03736 DNA sequenc
10	14	100.0	2454 6 SEMECAPB	X52592 S. epidermi
11	14	100.0	2455 6 E09771	E09771 The base se
12	14	100.0	2456 6 SAMECAPB	X52593 S. aureus m
13	14	100.0	2456 6 AX110445	AX110445 Sequence
14	14	100.0	5596 1 SSKBMECA	Y13095 S. sciuri me
15	14	100.0	6368 1 SSKBMECA2	Y14051 Staphylococ
16	14	100.0	9047 1 SAMECAPB	AE000716 Aquillex a
17	14	100.0	14567 1 AE000716	AE000716 Aquillex a
18	14	100.0	21777 1 AB063173	AB063173 Staphyloc
19	14	100.0	26090 1 AB063172	AB063172 Staphyloc
20	14	100.0	39332 1 AB033763	AB033763 Staphyloc
21	14	100.0	42689 8 SPC330	AI031603 S. pombe c
22	14	100.0	58237 1 D86934	D86934 Staphylococ
23	14	100.0	62311 9 AL157716	AL157716 Human DNA
24	14	100.0	63672 2 AC114608	AC114608 Mus muscu
25	14	100.0	68256 1 AB037671	AB037671 Staphyloc
26	14	100.0	80301 2 AC097768	AC097768 Rattus no
27	14	100.0	81650 8 NCB9815	AL451014 Neurospor
28	14	100.0	95155 9 AC078950	AC078950 Homo sapi
29	14	100.0	110000 9 AF440620_2	Continuation (3 of
30	14	100.0	126427 9 AL161424	AL161424 Human DNA
31	14	100.0	133387 2 AP004061	AP004061 Oryza sat
32	14	100.0	135270 2 AC105669	AC105669 Rattus no
33	14	100.0	147599 2 AC126088	AC126088 Rattus no
34	14	100.0	155803 9 AC090799	AC090799 Homo sapi
35	14	100.0	161095 2 AP005647	AP005647 Oryza sat
36	14	100.0	169323 2 AC125229	AC125229 Mus muscu
37	14	100.0	172612 2 AC110523	AC110523 Mus muscu
38	14	100.0	175485 2 AC111539	AC111539 Rattus no
39	14	100.0	183502 2 AC117454	AC117454 Homo sapi
40	14	100.0	184245 2 AC097819	AC097819 Rattus no
41	14	100.0	184315 2 AC073482	AC073482 Homo sapi
42	14	100.0	187730 2 AL845355	AL845355 Mus muscu
43	14	100.0	190612 2 AC129093	AC129093 Mus muscu
44	14	100.0	191669 9 HS403H13	AI513412 Homo sapi
45	14	100.0	201564 10 AL662909	AL662909 Mouse DNA

ALIGNMENTS

RESULT 1
AX306858
LOCUS AX306858
DEFINITION Sequence 17 from Patent EP1160333.
ACCESSION AX306858
VERSION AX306858.1 GI:17894680
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
Taya, T., Ishiguro, T. and Saito, J.
Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
Patent: EP 1160333-A 17 05-DEC-2001;

```

FEATURES          Tosoh Corporation (JP)
source            Location/Qualifiers
1. 14
   /organism="synthetic construct"
   /db_xref="taxon:32630"
   /note="Oligonucleotide capable of binding specifically to
   meca gene or RNA derived from said gene"
BASE COUNT      3 a      2 c      5 g      4 t
ORIGIN
Query Match      100.0%; Score 14; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
    |||||||
Db 1 GAAGTGTGCTTAC 14

RESULT 2
LOCUS AX306860 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 19 from Patent EPL160333.
ACCESSION AX306860
VERSION AX306860.1 GI:17894682
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Tayu, T., Ishiguro, T. and Saito, J.
AUTHORS
TITLE Oligonucleotides and method for detection of meca gene of
JOURNAL methicillin-resistant Staphylococcus aureus
Tosoh Corporation (JP)
LOCATION/Qualifiers
1. 14
   /organism="synthetic construct"
   /db_xref="taxon:32630"
   /note="Primer"
BASE COUNT      3 a      2 c      5 g      4 t
ORIGIN
Query Match      100.0%; Score 14; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
    |||||||
1 GAAGTGTGCTTAC 14

RESULT 3
LOCUS A44526 467 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 2 from Patent WO9513395.
ACCESSION A44526
VERSION A44526.1 GI:2299344
KEYWORDS
SOURCE
ORGANISM
Staphylococcus aureus.
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
1 (bases 1 to 467)
AUTHORS Springer, W. and Endermann, R.
TITLE SPECIFIC GENE PROBES AND METHODS FOR QUANTITATIVE DETECTION OF
METHICILLIN-RESISTANT STAPHYLOCOCCI
JOURNAL Patent: WO 9513395-A 2 18-MAY-1995;
Bayer AG (DE)
Other publication DE 4338119 950511.
COMMENT
source Location/Qualifiers
1. 467
   /organism="Staphylococcus aureus"
   /db_xref="taxon:1280"

```

```

BASE COUNT      187 a      73 c      85 g      122 t
ORIGIN
Query Match      100.0%; Score 14; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
    |||||||
Db 70 GAAGTGTGCTTAC 57

RESULT 4
LOCUS HSA336539 720 bp DNA linear PRI 18-JUL-2002
DEFINITION HSA336539 Homo sapiens genomic sequence surrounding NCI site, clone
NRI-PF5C.
ACCESSION AJ336539
VERSION AJ336539.1 GI:15880957
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 720)
AUTHORS Kutsenko, A.S., Glatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I.,
Kisselev, L.L., Masserman, M., Mahlestedt, C. and Zbarovsky, E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 2231767
PUBMED 12136098
REFERENCE
2 (bases 1 to 720)
AUTHORS Zbarovsky, E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumoriobiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES
source Location/Qualifiers
1. 720
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="NRI-PF5C"
BASE COUNT      113 a      203 c      211 g      193 t
ORIGIN
Query Match      100.0%; Score 14; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
    |||||||
Db 457 GAAGTGTGCTTAC 470

RESULT 5
LOCUS E09772 1789 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of modified meca DNA.
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS JP 1995209294-A/2.
SOURCE
ORGANISM
Staphylococcus aureus.
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
1 (bases 1 to 1789)
AUTHORS Kono, M., Hiramatsu, K., Sasazu, M., Noguchi, M. and Suguro, K.
TITLE NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 2 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD

```

COMMENT OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PP 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC C12R1.19)
PC (C12P21/02,C12R1.19);
CC strandedness: Double;
CC topology: Linear;
FH Key location/Qualifiers
FT source 1..1789
FT 1..1608 /organism='Staphylococcus aureus' FT CDS
FEATURES
source location/Qualifiers
1..1789 /organism='Staphylococcus aureus'
/db_xref='taxon:1280'
BASE COUNT 735 a 263 c 302 g 489 t
ORIGIN

Query Match 100.0%; Score 14; DB 6; Length 1789;
Host Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
Db 695 GAAGTGTGCTTAC 682

RESULT 6
AR089410/c AR089410 2007 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 169 from patent US 5994066.
DEFINITION AK089410
ACCESSION AK089410
VERSION AK089410.1 GI:10016167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2007)
AUTHORS Bergeron,M.C., Picard,F.J., Ouellette,M. and Roy,P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
FEATURES location/Qualifiers
source 1..2007 /organism='unknown'
BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 14; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
Db 1094 GAAGTGTGCTTAC 1081

RESULT 7
AR093610/c AR093610 2007 bp DNA linear PAT 08-SEP-2000
LOCUS Sequence 169 from patent US 6001564.
DEFINITION AK093610
ACCESSION AK093610
VERSION AK093610.1 GI:10020359
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2007)
AUTHORS Bergeron,M.C., Ouellette,M. and Roy,P.H.
TITLE Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
FEATURES location/Qualifiers
source 1..2007 /organism='unknown'
BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 14; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
Db 1094 GAAGTGTGCTTAC 1081

RESULT 8
SAPHP 2322 bp DNA linear ACT 12-SEP-1993
LOCUS Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
DEFINITION Y00688
ACCESSION Y00688.1 GI:46628
VERSION Y00688.1
KEYWORDS penicillin-binding protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
REFERENCE Bacteria: Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 2322)
AUTHORS Song,M.D., Machl,M., Dol,M., Ishino,F. and Matsushashi,M.
TITLE Evolution of an inducible penicillin-target protein in methicillin-resistant Staphylococcus aureus by gene fusion
JOURNAL PNAS Lett. 221 (1), 167-171 (1987)
MEDLINE 87304805
PUBMED 3305073
REFERENCE 2 (bases 1 to 2322)
AUTHORS Kyffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E., Barberis-Maino,U., Kayser,F.H. and Hegerl-Bachli,B.
TITLE Sequence comparison of mecA genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT Data kindly reviewed (13.1.88) by Matsushashi.
FEATURES location/Qualifiers
source 1..2322 /organism='Staphylococcus aureus'
/db_xref='taxon:1280'
1..2013
/note='penicillin-binding protein (AA 1-670)'
/transl_start=1
/transl_table=1
/protein_id='CA6684.1'
/db_xref='GI:46629'
/translation='MKKIKIVPLILVVVGFGIYFASKDK:INNIDAIDKKNFQVYKDSITKSDNGEVEEMTERPIKITYNSLSGYKDNIDDKIKKYSKKKRVADQYKKTINCGINDRNVQFNEFKEDGMMKLDWDHSVILPGKQDSIHLENLSERKILDRNNV ELANTGTHMRLGIVPKNVSKKDYKAIAKEISISDYINNWKIGYKMPSEHFTYKVKIMDEYLSDFPAKKFHLTNTFTSRNYPGKATSHLAGVGPINSEELKQKEYKQKDDAVKIGKGLLEKLYDKKLOHEDGVRVTVIVVDNSNTIAHTLIEKKKKDKDIOILTIDAKVOKSIVNMKNDYGSCTAIHPOTGELALVSPSDYVDFWYGMNSREYNKLTDPKKEPLNKFQTTSPGSRQKLTAMIGINNTLDDKTSYKTKIDGKGMKDSWGGYANTTRYEV VNGNIDIKQAISSDNIFFAVALELSKAFKFEKGMKLGVDIPSDYPTYNQISNK

BASE COUNT	940 a	324 c	389 g	669 t	
ORIGIN					NLDNEILLADSGYGGGELLINPVOLLSYSALENNGNINAPHLKDTQKNYKKNIIIS KENIINLNDGMOOVYKTKREDIYRSYANLKGSTALPKKOGSTGQIQWFIISYD DNPNNMAMINVKDVODKGMASYNAKISKVYDELLENKKYDIDE"
Query Match	100.0%	Score 14;	DB 1;	Length 2322;	
Best Local Similarity	100.0%	Pred. No. 5.1e+02;			
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1 GAAGGTGTCCTTAC 14				
DB	1100 GAAGGTGTCCTTAC 1087				
RESULT 9					
E03736/c					
LOCUS	E03736	2322 bp	DNA	linear	PAT 29-SEP-1992
DEFINITION	DNA sequence of PBP2' gene for determination of methicillin resistance.				
CESSION	E03736				
ERSTION	E03736.1	GI:2171951			
KEYWORDS	JP 1992169200-A/9.				
SOURCE	unidentified.				
ORGANISM	unidentified.				
REFERENCE	1 (bases 1 to 2322)				
AUTHORS	Matanabe,Y., Nakamura,E., Teraoka,H., Wada,K., Minamide,W. and Murakami,K.				
TITLE	DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE				
JOURNAL	Patent: JP 1992169200-A 9 17-JUN-1992;				
COMMENT	OS (methicillin resistant)staphylococcus aureus PN JP 1992169200-A/9 PD 17-JUN-1992 PF 31-OCT-1990 JP 1990296708 PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI, PI MINAMIDE MAKIO, MURAKAMI KAZUHISA PC C1201/68,C12N15/11; CC strandedness: Single; CC topology: linear; CC hypothetical: No; CC anti-sense: No; FH Key FH Locali in/Qualifiers FT misc-feature 1..2322 FT /note="PBP2' gene for determination of methicillin resistance" FT Location/Qualifiers 1..2322 /organism="unidentified" /db_xref="taxon:32644"				
BASE COUNT	939 a	324 c	390 g	669 t	
ORIGIN					
Query Match	100.0%	Score 14;	DB 6;	Length 2322;	
Best Local Similarity	100.0%	Pred. No. 5.1e+02;			
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1 GAAGGTGTCCTTAC 14				
DB	1100 GAAGGTGTCCTTAC 1087				
RESULT 10					
SEMECAP/c					
LOCUS	SEMECAPB	2454 bp	DNA	linear	BCT 12-SEP-1993
DEFINITION	S. epidermidis meca gene for PBP2' (penicillin binding protein 2').				
ACCESSION	X52592				
VERSION	X52592.1	GI:46993			
KEYWORDS	meca gene; methicillin resistance; penicillin-binding protein; penicillin-binding protein 2'.				

SOURCE	ORGANISM
REFERENCE	Staphylococcus epidermidis.
REFERENCE	Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE	1 (bases 1 to 2448)
REFERENCE	Ryffel, C.
REFERENCE	Direct Submission
REFERENCE	Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
REFERENCE	Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE	2 (bases 1 to 2454)
REFERENCE	Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
REFERENCE	Barberis-Maino, L., Kayser, F. H. and Berger-Baechi, B.
REFERENCE	Sequence comparison of meca genes from methicillin-resistant
REFERENCE	Staphylococcus aureus and staphylococcus epidermidis
REFERENCE	Gene (1990) In press
REFERENCE	3 (bases 1 to 2454)
REFERENCE	Ryffel, C.
REFERENCE	Direct Submission
REFERENCE	Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
REFERENCE	Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE	4 (bases 1 to 2454)
REFERENCE	Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
REFERENCE	Barberis-Maino, L., Kayser, F. H. and Berger-Baechi, B.
REFERENCE	Sequence comparison of meca genes isolated from
REFERENCE	methicillin-resistant Staphylococcus aureus and Staphylococcus
REFERENCE	epidermidis
REFERENCE	Gene 94 (1), 137-138 (1990)
REFERENCE	91033056
REFERENCE	2227446
REFERENCE	See also <X52593-4> and <Y00688>
REFERENCE	Data kindly reviewed (23-JUL-1990) by C. Ryffel.
REFERENCE	Location/Qualifiers
REFERENCE	1. 2454
REFERENCE	/organism="Staphylococcus epidermidis"
REFERENCE	/strain="WT55"
REFERENCE	/db_xref="taxon:1282"
REFERENCE	/clone="WT80/MT79"
REFERENCE	80. 85
REFERENCE	/note="-35 region"
REFERENCE	101. 105
REFERENCE	/note="-10 region"
REFERENCE	130. 134
REFERENCE	/note="ribosome binding site"
REFERENCE	141. 2159
REFERENCE	/note="primary transcript"
REFERENCE	141. 2147
REFERENCE	/note="PBP2' (AA 1 - 668)"
REFERENCE	/codon_start=1
REFERENCE	/transl_table=1
REFERENCE	/protein_id="CAA36828.1"
REFERENCE	/db_xref="GI:46994"
REFERENCE	/db_xref="SPTREMBL:O54113"
REFERENCE	/translation="MKIKIVPLILIVVVVPGCIYYPAASKDK:INNTIDAIEDKNFKQ
REFERENCE	VYDSSYTSKSDNGFVEMTERPIK IYNSLGKDI INODRKIKVSKNKKRVDAQYKIK
REFERENCE	TNGNDIDRNVQNFNEVEDGKMLDWDHSVILPGMKDQSHIENLSERKSIDRNV
REFERENCE	ELANTGTAIEIGIVPKNVSKDKYKAIKELSISEDIKQOMDNVQDDFVLKTVK
REFERENCE	KMEYIEGDFAKFHLLTNETPESRNPYLGKATSHLGVGPIINSEELKQEKYKQDA
REFERENCE	VICKKIGKELYDKRLOHEGCVATYIVDINSNTIAHLLIEKKKQGDIOLTIDAKYK
REFERENCE	SIYNNKKNDYGSTAIHPOTGRLLAIYSPSYVYPPYMGSMSEYNNKLEIDKKEHLL
REFERENCE	NKQOITTPGOSTOKILITAMGLNNKTLIDDTSTKIPKCKQKQKSGNGVNTREYVFN
REFERENCE	GNGLDQVALESNDISFFARVALLGSKRFEKPKKGLGVGEDIPSDYFVNAQISNNL
REFERENCE	DNGLILLADSGGGEILLINVOILTSIYSALENGGNINAPHLIDKTNKWKNNIISKE
REFERENCE	NIMMLDMQGVVNTKHKEDIYRSYANLICKSGTAEIKMKQGETGQIGWFIYSDKN
REFERENCE	PNMMATINVDYQDKMASYNAKISGVYDELVENCKKRYDIDE"
REFERENCE	441. 448
REFERENCE	/note="ataaac was ac in [1]"
REFERENCE	/citation-[1]
REFERENCE	641. 643
REFERENCE	/note="agc was ac in [1]"
REFERENCE	/citation-[1]
REFERENCE	652. 653
REFERENCE	/note="ta was tta in [1]"
REFERENCE	/citation-[1]
REFERENCE	731. 733

/note="caa was ca in [1]"
/citation=[1]
old_sequence 780..781
/note="ct was ctt in [1]"
/citation=[1]
BASE COUNT 997 a 345 c 398 g 714 t
ORIGIN

Query Match 100.0%; Score 14; DB 1; Length 2454;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGCTGTGCTTAC 14
|||||
Db 1234 GAAGCTGTGCTTAC 1221

RESULT 11
E09771/c 2455 bp RNA linear PAT 29-SEP-1997
LOCUS The base sequence of meca DNA.
DEFINITION E09771.1 GI:22026400
VERSION E09771.1 GI:22026400
KEYWORDS JP 1995209294-A/1.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 2455)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS Kono, M., Hiramatsu, K., Sasazu, M., Noguchi, M. and Suguro, K.
TITLE NOVEL "MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 1 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/1
PD 11-AUG-1995
PP 10-JAN-1994 JP 1994012226
PT KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC C12R1.19),
PC (C12P21/02,C12R1.19);
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FH source 1..2455
FT 134..2146 /organism="Staphylococcus aureus" FT CDS
FT 134..2146 /product="meca protein".
FEATURES
source 1..2455
Location/Qualifiers
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"
BASE COUNT 997 a 344 c 401 g 713 t
ORIGIN

Query Match 100.0%; Score 14; DB 6; Length 2455;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGCTGTGCTTAC 14
|||||
Db 1233 GAAGCTGTGCTTAC 1220

RESULT 12
SAMECAPB/c 2456 bp DNA linear BCT 12-SEP-1993
LOCUS SAMECAPB
DEFINITION S. aureus meca gene for PBP2' (penicillin binding protein 2').
ACCESSION X52593
VERSION X52593.1 GI:46610

KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; staphylococcus.
REFERENCE 1 (bases 1 to 2456)
AUTHORS Ryffel, C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
2 (bases 1 to 2456)
REFERENCE Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. F.,
Barberis-Maino, L., Kayser, F. H. and Berger-Bachi, B.
AUTHORS Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
TITLE Gene 94 (1), 137-138 (1990)
JOURNAL MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52592>, <X52594> and <Y00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.

FEATURES
source
Location/Qualifiers
1..2456
/organism="Staphylococcus aureus"
/strain="NCIC8325, isolate=BB270"
/db_xref="taxon:1280"
/clone_lib="EMBL-3"
80..85
/note="35 region"
101..105
/note="10 region"
130..134
/note="ribosome binding site"
141..2153
/note="primary transcript"
141..2147
/note="PBP2' (AA 1-668)"
/codon_start=1
/transl_table=11
/protein_id="CAA36829.1"
/db_xref="GI:46611"
/db_xref="SPTREMA1:053707"
/translation="MKKIKVPLILVVVVGSGIYFYAKDKEINNTDAIEDKNFKQ
VTKDSYISKSDNGEVEWTERPLIKIYNSLGVQDINIDRIKRSKNKRVDAQYIK
TYGNGIDRVQVFNFEKEDGMMKLDMDHSYIIPDMODOSIIRIENLSKSGKTLDRNV
ELANTGTHRLGIIVPKNVSKKDKAKAIKELISIEDYINNKWKIGYKMSFHEFTVK
KMEYLSDFAKKFFHLTTNETESRNYPLEKATSHLGVGPIINSEELKQEKYGYKDDA
VIGKGLKLYDKKLOHEDGYRVTIVDMSNTIAHLLEKKKKDKDLOLTDIAKVOK
SIYNNKNDYSGCTAIHPOTGELLAVSPSYDVPYPMCMNSPEYENKLTTPDKKEPLI,
NKFOITTSFGSTOKIITAMIGLNNKTLIDIKTSKIDGCKMOKIKSMGYNVTRYEVN
GNTDLQALLESSDNIFPARVALELGSKKEGKRGVGEDIPSDPYNAOISNVL
DNEILLADSGYGGGELLINPVOLISYLSALENNGNINAPHLIDKTNKVMKKNIIISKE
NINLLNDGQQVYVNTKTHEDIYRSYANLIGKSGTALMKKQSGSROIGMFTISYDKDN
PNMMAINVKDVODKCMASYNAKISGVYVDELYENCKKRYDIDE"

BASE COUNT 1001 a 344 c 396 g 715 t
ORIGIN

Query Match 100.0%; Score 14; DB 1; Length 2456;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGCTGTGCTTAC 14
|||||
Db 1234 GAAGCTGTGCTTAC 1221

RESULT 13
AX110445/c 2456 bp DNA linear PAT 30-APR-2001
LOCUS AX110445
DEFINITION Sequence 1178 from Patent WO0123604.
ACCESSION AX110445
VERSION AX110445.1 GI:13926737
KEYWORDS


```

/protein_id="CA73542.1"
/db_xref="GI:2791916"
/translation="MKKIKYPLLIYVVVGFYFYASKDKENINTDAIGDKNEKQ
VKDSSTISKSDNGEVDMEIERPIKITSLSGKIDINIDRKIKVSKNKKRVDQYTK
TNYGNIDRWQFNFKEDGMKLDMDHSVILPCMQKDSIHIEMLKSEKGIIDRNW
ELANTCTAAYEIGIYPKNVSKKDYKAIAKELISDYTKQMDQMWVDDTFVPLKTVK
KMEYLSDFPAKKFHLTTNETESRNYPLEKATSHLAGVCPINSEELKQEKYKGYKDDA
VIGKKGLEKLYDKLOHEDGYRVTIVDNSNTIAHTLIEKKKKDKDIOLEIDAKVOX
SIYNNMKNDQSGCTAIHPOTGELLALVSTPSYDYPPMGMSNEVVKLTEDKKEPL
NKFOITTSRSGSTILTAMIGLNKTIIDDKTSYKIDCKGQKDKSMGCVNTRREYVN
GRTIDKQATIESDNIFFPARYALEGSKFEGKMKLGVEDIPSDYPTNAQISNKL
DNETLLADSGYCGEILLINPVQILISYSALENNGNINAPHLKDTNKKVKNKIISKE
NINLLTGMQOVVAKTHKEDIYRSYANLIGKSGTAEI.KMKOGFTGRPIGMFTSYDKDN
PHLMAAINVKDVPDKGMASYNAKISGKYDELYENGKNKYDIDE"
complement(5537..6038)
/gene="ORF142"
complement(5537..5965)
/gene="ORF142"
/codon_start=1
/translation="CA73543.1"
/db_xref="GI:2791917"
/db_xref="SPTREMBL:O54520"
/translation="MKYDDPIVCETPKTKSLHITPEEIIOPATFPDPOYMHIDKKA
QSRKGIITASGMHTLISFKILWVECKYGEVAVAGTOMNNYKFIKPYPGNTLIYVIAE
ITNKSIRKENGELVTSLSYENEEIVFKEVTAIINNS"
complement(5972..5977)
/gene="ORF142"
complement(6010..6015)
/gene="ORF142"
complement(6033..6038)
/gene="ORF142"
complement(6062..6368)
/gene="NTOF101"
complement(6062..>6368)
/gene="NTOF101"
/codon_start=2
/translation="CA73544.1"
/protein_id="CA73544.1"
/db_xref="GI:2791918"
/db_xref="SPTREMBL:O54616"
/translation="SFNVVILVLAELIMPOYNRAVIFHTTSFREDMRTLDDYCNKIV
NTEDAKITLAKVKVKKFAGYFLNWTNKKPARANQLANMGVDGIFTDNADKMVHLSQ"
BASE COUNT 2230 a 998 c 884 g 2256 t
ORIGIN
Query Match 100.0%; Score 14; DB 1; Length 6368;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 1 GAAGGTGCTTAC 14
DB 4578 GAAGGTGCTTAC 4565

```

Search completed: December 10, 2002, 20:16:45
 Job time : 307.667 secs

us-09-865-579a-19.rni

Thu Dec 12 09:59:04 2002

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model
December 10, 2002, 17:12:39 : Search time 19.0838 Seconds
(without alignments)
224.980 Million cell updates/sec

Run on: US-09-865-579a-19
1 gaaggtgtgtctac 14

Title: US-09-865-579a-19
Perfect score: 14
Sequence: 1 gaaggtgtgtctac 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapect 1.0

Searched: 441362 seqs, 15338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	14	100.0	2007	2	US-08-743-637B-169	Sequence 169, App
2	14	100.0	2007	3	US-08-526-840B-169	Sequence 1710, App
3	14	100.0	2028	4	US-09-134-001C-1770	Sequence 336, App
4	13	92.9	1758	4	US-09-620-412C-336	Sequence 1, Appl
5	13	92.9	2068	1	US-08-309-341-1	Sequence 1, Appl
6	13	92.9	2068	1	US-08-608-267-1	Sequence 1, Appl
7	13	92.9	2068	1	US-08-608-452-1	Sequence 1, Appl
8	13	92.9	2068	1	US-08-608-224-1	Sequence 1, Appl
9	13	92.9	2068	2	US-08-967-149-1	Sequence 1, Appl
10	13	92.9	5265	4	US-09-556-877-174	Sequence 174, App
11	13	92.9	5265	4	US-09-620-412C-174	Sequence 104, App
12	13	92.9	6735	4	US-08-961-527-104	Sequence 357, App
13	12.4	88.6	807	4	US-08-961-527-357	Patent No. 5223425
14	12.4	88.6	863	6	5223425-1	Patent No. 5223425
15	12.4	88.6	1029	1	US-07-809-457A-15	Sequence 15, Appl
16	12.4	88.6	1029	1	US-08-553-943-15	Sequence 15, Appl
17	12.4	88.6	1029	5	PCT-US91-09437-15	Sequence 2, Appl
18	12.4	88.6	1393	1	US-08-052-205-2	Sequence 2, Appl
19	12.4	88.6	1393	1	US-08-595-974-2	Sequence 9, Appl
20	12.4	88.6	1416	4	US-09-330-611-9	Sequence 68, Appl
21	12.4	88.6	1451	4	US-08-031-143B-68	Sequence 3, Appl
22	12.4	88.6	1470	1	US-08-052-205-3	Sequence 3, Appl
23	12.4	88.6	1470	1	US-08-595-974-3	Sequence 1, Appl
24	12.4	88.6	2070	3	US-08-394-326-1	Sequence 1, Appl
25	12.4	88.6	2070	3	US-09-082-306-1	Sequence 1, Appl
26	12.4	88.6	3987	1	US-07-688-352C-19	Sequence 19, Appl
27	12.4	88.6	3987	1	US-07-688-352C-19	Sequence 19, Appl

28	12.4	88.6	3987	2	US-08-474-379C-19	Sequence 19, Appl
29	12.4	88.6	3987	3	US-09-146-249A-19	Sequence 19, Appl
30	12.4	88.6	3987	5	US-08-206-188B-19	Sequence 19, Appl
31	12.4	88.6	3987	5	PCT-US91-02714-19	Sequence 182, App
32	12.4	88.6	4550	4	US-09-338-907-182	Sequence 4, Appl
33	12.4	88.6	4550	4	US-09-218-207-182	Sequence 4, Appl
34	12.4	88.6	5816	4	US-09-220-641-4	Sequence 65, Appl
35	12.4	88.6	7898	4	US-08-984-709A-49	Sequence 65, Appl
36	12.4	88.6	11831	4	US-08-961-527-65	Sequence 66, App
37	12.4	88.6	50000	4	US-09-146-053-3	Sequence 769, App
38	12.4	85.7	330	4	US-09-134-001C-686	Sequence 1, Appl
39	12	85.7	877	4	US-09-605-785-769	Sequence 3, Appl
40	12	85.7	2026	2	US-08-559-492-1	Sequence 12, Appl
41	12	85.7	2368	4	US-09-343-011B-3	Sequence 11, Appl
42	12	85.7	3488	4	US-08-930-285-12	Sequence 1, Appl
43	12	85.7	3544	4	US-08-697-826A-11	Sequence 1, Appl
44	12	85.7	4315	2	US-08-781-802-1	Sequence 1, Appl
45	12	85.7	4315	4	US-08-694-078-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-743-637B-169/C
Sequence 169, Application US/08743637B

Patent No. 5994066

GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.

APPLICANT: PICARD, Francois J.

APPLICANT: QUELETTE, Marc

APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA PROBES AND APPLICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

Query Match 100.0% Score 14; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C/ 1 GAAGCTGCTTAC 14
Db 1094 GAAGCTGCTTAC 1081

RESULT 2

US-08-526-840B-169/C
Sequence 169, Application US/08526840B
Patent No. 6001564

GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: APPLICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
S-08-526-840B-169

Query Match 100.0%; Score 14; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAAGCTGCTTAC 14
1094 GAAGCTGCTTAC 1081

RESULT 3

S-09-134-001C-1710/C
Sequence 1710, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1996-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 14; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTTAC 14
Db 1115 GAAGCTGCTTAC 1102

RESULT 4

US-09-620-412C-336/C
Sequence 336, Application US/09620412C
Patent No. 6448234

GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121,469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 336
LENGTH: 1758
TYPE: DNA

ORGANISM: Chlamydia trachomatis
US-09-620-412C-336

Query Match 92.9%; Score 13; DB 4; Length 1758;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTTAC 13
Db 1451 GAAGCTGCTTAC 1439

RESULT 5

US-08-309-341-1/C
Sequence 1, Application US/08309341
Patent No. 5594119

GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5594119 No. 5594119disk of No. 5594119th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,341
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247,000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
FEATURE:
NAME/KEY: intron
LOCATION: 572..632
FEATURE:
NAME/KEY: CDS
LOCATION: join (571..633)
US-08-309-341-1

Query Match          92.9%; Score 13; DB 1; Length 2068;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 AAGCTGCTCTTAC 14
DB      583 AAGCTGCTCTTAC 571

RESULT 6
US-08-608-267-1/c
Sequence 1, Application US/08608267
Patent No. 5688663
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56886630 No. 5688663disk of No. 56886631h America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,267
FILING DATE: 28-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247,000-US
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
FEATURE:
NAME/KEY: intron
LOCATION: 572..632
FEATURE:
NAME/KEY: CDS
LOCATION: join (571..633)
US-08-608-267-1

Query Match          92.9%; Score 13; DB 1; Length 2068;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 AAGCTGCTCTTAC 14
DB      583 AAGCTGCTCTTAC 571

RESULT 7
US-08-608-452-1/c
Sequence 1, Application US/08608452
Patent No. 5693510
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56935100 No. 5693510disk of No. 56935101h America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,452
FILING DATE: 28-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247,000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
FEATURE:
```

NAME/KEY: inton
LOCATION: 572..632
FEATURE:
NAME/KEY: CDS
LOCATION: join (571..633)
US-08-608-452-1

Query Match 92.9%; Score 13; DB 1; Length 2068;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGCTGCTTAC 14
|||||
DB 583 AAGCTGCTTAC 571

RESULT 8
US-08-608-224-1/c

Sequence 1, Application US/08608224
Patent No. 5705376

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57053760 No. 5705376disk of No. 5705376th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,224
FILING DATE: 28-FEB-1996

CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247,000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger

FEATURE:

NAME/KEY: intron
LOCATION: 572..632

FEATURE:

NAME/KEY: CDS
LOCATION: join (571..633)
US-08-608-224-1

Query Match 92.9%; Score 13; DB 1; Length 2068;
Best Local Similarity 100.0%; Pred. No. 64;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGCTGCTTAC 14

|||||
DB 583 AAGCTGCTTAC 571

RESULT 9
US-08-967-149-1/c

Sequence 1, Application US/08967149
Patent No. 5939305

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59393050 No. 5939305disk of No. 5939305th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,149
FILING DATE:
CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/608,452
FILING DATE: 28-FEB-1996
APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247,000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger

FEATURE:

NAME/KEY: intron
LOCATION: 572..632

FEATURE:

NAME/KEY: CDS
LOCATION: join (571..633)
US-08-967-149-1

Query Match 92.9%; Score 13; DB 2; Length 2068;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGCTGCTTAC 14
|||||
DB 583 AAGCTGCTTAC 571

RESULT 10

US-09-556-877-174/c

Sequence 174, Application US/09556877
Patent No. 6432916

GENERAL INFORMATION:

APPLICANT: Probst, Peter
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yassir
APPLICANT: Fling, Steve
APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556.877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 174
LENGTH: 5265
TYPE: DNA
ORGANISM: Chlamydia
US-09-556-877-174

Query Match 92.9%; Score 13; DB 4; Length 5265;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTA 13
Db 2003 GAAGGTGCTTA 1991

RESULT 11
US-09-620-412C-174/C
Sequence 174, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620.412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 174
LENGTH: 5265
TYPE: DNA
ORGANISM: Chlamydia
US-09-620-412C-174

Query Match 92.9%; Score 13; DB 4; Length 5265;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTA 13
Db 2003 GAAGGTGCTTA 1991

RESULT 12
US-08-961-527-104/C
Sequence 104, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961.527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 6735 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-104

Query Match 92.9%; Score 13; DB 4; Length 6735;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGCTTAC 14
Db 5983 AAGGTGCTTAC 5971

RESULT 13
US-08-961-527-357
Sequence 357, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961.527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 357:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-961-527-357

Query Match 88.6%; Score 12.4; DB 4; Length 807;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGTGTGCTTAC 14
||||| |||||
DB 499 GAAGTGTGCTTAC 512

RESULT 14

5223425-1
; Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,
; BARRY M.; WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
; ID ACTIVITY
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/277,963
; FILING DATE: 30-NOV-1988
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 34,203
; FILING DATE: 02-APR-1987
; SEQ ID NO: 1:
; LENGTH: 863
5223425-1

Query Match 88.6%; Score 12.4; DB 6; Length 863;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGTGTGCTTAC 14
||||| |||||
DB 668 GAAGTGTGCTTAC 681

RESULT 15
5223425-9
; Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,
; BARRY M.; WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
; ID ACTIVITY
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/277,963
; FILING DATE: 30-NOV-1988
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 34,203
; FILING DATE: 02-APR-1987
; SEQ ID NO: 9:
; LENGTH: 863
5223425-9

Query Match 88.6%; Score 12.4; DB 6; Length 863;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGTGTGCTTAC 14
||||| |||||
DB 673 GAAGTGTGCTTAC 686

Search completed: December 10, 2002, 22:54:21
Job time : 21.2088 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 ; Search time 18.1453 Seconds

(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-19

Perfect score: 14

Sequence: 1 gaaggtgtgtctac 14

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_MA:*

- 1: /cgn2_6/ptodata/2/pubna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubna/PTCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubna/US07_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	14	10	US-09-865-579A-17
2	14	100.0	14	10	US-09-865-579A-19
3	14	100.0	2007	10	US-09-452-599-169
4	13	92.9	1758	10	US-09-841-132-336
5	13	92.9	5253	10	US-09-841-132-421
6	13	92.9	5253	10	US-09-841-132-556
7	13	92.9	5253	10	US-09-841-132-556
8	12.4	88.6	233	10	US-09-883-965-5426
9	12.4	88.6	399	10	US-09-815-242-9114
10	12.4	88.6	399	10	US-09-815-242-9472
11	12.4	88.6	408	10	US-09-783-590-3620
12	12.4	88.6	418	10	US-09-960-352-12566
13	12.4	88.6	459	10	US-09-864-761-1021
14	12.4	88.6	500	10	US-09-783-590-3621
15	12.4	88.6	759	10	US-09-974-300-2230
16	12.4	88.6	995	12	US-10-021-509-4
17	12.4	88.6	995	12	US-10-021-509-12
18	12.4	88.6	1173	9	US-09-938-842A-1515
19	12.4	88.6	1187	10	US-09-801-574-47

C 20	12.4	88.6	1323	10	US-09-815-242-9609	Sequence 9609, Ap
21	12.4	88.6	1416	9	US-09-891-641-70	Sequence 70, Appl
22	12.4	88.6	1416	9	US-09-847-010-9	Sequence 9, Appl1
C 23	12.4	88.6	1451	10	US-09-880-107-1595	Sequence 1595, Ap
C 24	12.4	88.6	1456	10	US-09-822-849A-159	Sequence 159, Ap
C 25	12.4	88.6	1836	10	US-09-864-761-16939	Sequence 16939, A
C 26	12.4	88.6	1836	9	US-09-938-842A-2286	Sequence 2286, Ap
C 27	12.4	88.6	4087	10	US-09-901-419-1	Sequence 1, Appl1
28	12.4	88.6	4550	9	US-09-853-526-182	Sequence 182, App
29	12.4	88.6	4550	10	US-09-901-484A-182	Sequence 182, App
C 30	12.4	88.6	4683	10	US-09-070-927A-193	Sequence 193, App
C 31	12.4	88.6	7642	9	US-09-938-842A-43	Sequence 43, Appl
C 32	12.4	88.6	10024	10	US-09-880-107-2430	Sequence 2430, Ap
C 33	12.4	88.6	32134	10	US-09-764-847-1057	Sequence 1057, Ap
C 34	12.4	88.6	32134	10	US-09-764-847-1057	Sequence 1057, Ap
C 35	12.4	88.6	32187	10	US-09-764-847-1535	Sequence 1535, Ap
C 36	12.4	88.6	32193	10	US-09-764-847-1535	Sequence 1549, Ap
C 37	12.4	88.6	167343	10	US-09-964-436-281	Sequence 281, App
C 38	12.4	88.6	167343	10	US-09-964-824A-273	Sequence 273, App
C 39	12.4	88.6	465237	10	US-09-933-267A-1	Sequence 1, Appl
C 40	12	85.7	103	10	US-09-783-590-9007	Sequence 9007, Ap
C 41	12	85.7	149	10	US-09-969-373-548	Sequence 548, App
C 42	12	85.7	160	10	US-09-864-761-32198	Sequence 32198, A
C 43	12	85.7	160	10	US-09-864-761-32240	Sequence 32240, A
C 44	12	85.7	165	10	US-09-815-242-2248	Sequence 2248, Ap
C 45	12	85.7	165	10	US-09-815-242-2261	Sequence 2261, Ap

ALIGNMENTS

RESULT 1
US-09-865-579A-17
; Sequence 17, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865, 579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to meca gene
; OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-17
Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGTGTCTTAC 14
DB 1 GAAGTGTCTTAC 14
RESULT 2
US-09-865-579A-19
; Sequence 19, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:

```

: APPLICANT: Taya, Toshiki
: APPLICANT: Ishiguro, Takahiko
: TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
: FILE REFERENCE: 9558-003-27
: CURRENT APPLICATION NUMBER: US/09/865,579A
: CURRENT FILING DATE: 2001-05-29
: PRIOR APPLICATION NUMBER: JP 2000-163149
: PRIOR FILING DATE: 2000-05-29
: PRIOR APPLICATION NUMBER: JP 2000-179394
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 19
: LENGTH: 14
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Primer
:
: S-09-865-579A-19
```

```

Query Match          100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 GAAGCTGCTTAC 14
DB 1 GAAGCTGCTTAC 14
```

```

RESULT 3
: US-09-452-599-169/c
: Sequence 169, Application US/09452599
: Patent No. US20020055101A1
: GENERAL INFORMATION:
: APPLICANT: Bergeron, Michel G.
: APPLICANT: Roy, Paul H.
: TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
: TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
: TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
: TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
: FILE REFERENCE: 1287.31
: CURRENT APPLICATION NUMBER: US/09/452,599
: CURRENT FILING DATE: 1999-12-01
: PRIOR APPLICATION NUMBER: 08/526,840
: PRIOR FILING DATE: 1995-09-11
: PRIOR APPLICATION NUMBER: 08/304,732
: PRIOR FILING DATE: 1994-09-12
: NUMBER OF SEQ ID NOS: 177
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 169
: LENGTH: 2007
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
:
: US-09-452-599-169
```

```

Query Match          100.0%; Score 14; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 GAAGCTGCTTAC 14
DB 1094 GAAGCTGCTTAC 1081
```

```

RESULT 4
: US-09-841-132-336/c
: Sequence 336, Application US/09841132
: Patent No. US20020061848A1
: GENERAL INFORMATION:
: APPLICANT: Bhatia, Ajay
```

```

: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Probst, Peter
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
: TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
: FILE REFERENCE: 210121.469C8
: CURRENT APPLICATION NUMBER: US/09/841,132
: CURRENT FILING DATE: 2001-04-23
: NUMBER OF SEQ ID NOS: 599
: SOFTWARE: FastSeq for Windows Version 3.0/4.0
: SEQ ID NO 336
: LENGTH: 1758
: TYPE: DNA
: ORGANISM: Chlamydia trachomatis
:
: US-09-841-132-336
```

```

Query Match          92.9%; Score 13; DB 10; Length 1758;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 GAAGCTGCTTAC 13
DB 1451 GAAGCTGCTTAC 1439
```

```

RESULT 5
: US-09-841-132-421/c
: Sequence 421, Application US/09841132
: Patent No. US20020061848A1
: GENERAL INFORMATION:
: APPLICANT: Bhatia, Ajay
: APPLICANT: Skeiky, Yasir A.W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
: TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
: FILE REFERENCE: 210121.469C8
: CURRENT APPLICATION NUMBER: US/09/841,132
: CURRENT FILING DATE: 2001-04-23
: NUMBER OF SEQ ID NOS: 599
: SOFTWARE: FastSeq for Windows Version 3.0/4.0
: SEQ ID NO 421
: LENGTH: 5253
: TYPE: DNA
: ORGANISM: Chlamydia trachomatis serovar D
:
: US-09-841-132-421
```

```

Query Match          92.9%; Score 13; DB 10; Length 5253;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 GAAGCTGCTTAC 13
DB 1994 GAAGCTGCTTAC 1982
```

```

RESULT 6
: US-09-841-132-556/c
: Sequence 556, Application US/09841132
: Patent No. US20020061848A1
: GENERAL INFORMATION:
: APPLICANT: Bhatia, Ajay
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Probst, Peter
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
: TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
: FILE REFERENCE: 210121.469C8
: CURRENT APPLICATION NUMBER: US/09/841,132
: CURRENT FILING DATE: 2001-04-23
: NUMBER OF SEQ ID NOS: 599
: SOFTWARE: FastSeq for Windows Version 3.0/4.0
: SEQ ID NO 556
: LENGTH: 5253
: TYPE: DNA
: ORGANISM: C. Trachomatis D serovar
```

US-09-841-132-556

Query Match
Best Local Similarity 92.9%; Score 13; DB 10; Length 5253;
Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 13
|||||
Db 1994 GAAGGTGCTTAC 1982

RESULT 7

US-09-841-132-174/C
; Sequence 174, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 174
; LENGTH: 5265
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-174

Query Match
Best Local Similarity 92.9%; Score 13; DB 10; Length 5265;
Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 13
|||||
Db 2003 GAAGGTGCTTAC 1991

RESULT 8

US-09-983-965-5426
; Sequence 5426, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengding
; APPLICANT: Byatt, John C.
; APPLICANT: Malhalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 5426
; LENGTH: 233
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 44-LIB34-067-01-E1-C8
US-09-983-965-5426

Query Match
Best Local Similarity 88.6%; Score 12.4; DB 10; Length 233;
Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 14

Db 118 GAAGGTGCTTAC 131

RESULT 9
US-09-815-242-9114
; Sequence 9114, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9114
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(399)
US-09-815-242-9114

Query Match
Best Local Similarity 88.6%; Score 12.4; DB 10; Length 399;
Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 14
|||||
Db 328 GAAGGTGCTTAC 341

RESULT 10
US-09-815-242-9472
; Sequence 9472, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242

```

: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9472
: LENGTH: 399
: TYPE: DNA
: ORGANISM: Streptococcus pneumoniae
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(399)
US-09-815-242-9472

```

```

Query Match      88.6%: Score 12.4; DB 10; Length 399;
Best Local Similarity 92.9%: Pred. No. 2.1e+02;
Matches 13: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
Oy      1 GAAGCTGTCCTTAC 14
        |||||
Db      328 GAAGTTGCTTAC 341

```

```

RESULT 11
US-09-783-590-3620
: Sequence 3620, Application US/09783590
: Patent No. US20020110850A1
: GENERAL INFORMATION:
: APPLICANT: Dillon, Patrick J.
: APPLICANT: Haseltine, William A.
: APPLICANT: Li, Haodong
: APPLICANT: Rosen, Craig A.
: APPLICANT: Ruben, Steven M.
: TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
: FILE REFERENCE: PO-16,2C1
: CURRENT FILING DATE: 2000-02-15
: PRIOR APPLICATION NUMBER: 08/420,856
: PRIOR FILING DATE: 1995-04-12
: PRIOR APPLICATION NUMBER: 08/346,731
: PRIOR FILING DATE: 1994-11-21
: NUMBER OF SEQ ID NOS: 12485
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3620
: LENGTH: 408
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (73)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (320)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (340)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (352)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature

```

```

: LOCATION: (356)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (399)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (402)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (406)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-3620

```

```

Query Match      88.6%: Score 12.4; DB 10; Length 408;
Best Local Similarity 92.9%: Pred. No. 2.1e+02;
Matches 13: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
Oy      1 GAAGCTGTCCTTAC 14
        |||||
Db      299 GAAGCTGCTTAC 312

```

```

RESULT 12
US-09-960-352-12566/C
: Sequence 12566, Application US/09960352
: Patent No. US20020137139A1
: GENERAL INFORMATION:
: APPLICANT: Warren, Wesley C.
: APPLICANT: Tao, Ningbing
: APPLICANT: Byatt, John C.
: APPLICANT: Mathalagan, Nagappan
: TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION ANI
: FILE REFERENCE: 16511.006/37-21(10298)C
: CURRENT FILING DATE: 2001-09-24
: NUMBER OF SEQ ID NOS: 15112
: SEQ ID NO 12566
: LENGTH: 418
: TYPE: DNA
: ORGANISM: Bos laurus
: OTHER INFORMATION: Clone ID: 54-LIB188-016-Q1-E1-F10
US-09-960-352-12566

```

```

Query Match      88.6%: Score 12.4; DB 10; Length 418;
Best Local Similarity 92.9%: Pred. No. 2.1e+02;
Matches 13: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
Oy      1 GAAGCTGTCCTTAC 14
        |||||
Db      66 GAAGGTGCTGAC 53

```

```

RESULT 13
US-09-864-761-102
: Sequence 102, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
: FILE REFERENCE: Aeomica-X-1
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03

```

```
? PRIOR APPLICATION NUMBER: GB 24263.6
? PRIOR FILING DATE: 2000-10-04
? PRIOR APPLICATION NUMBER: US 60/236,359
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: PCT/US01/00666
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00667
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00664
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00669
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00665
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00663
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00662
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00661
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 09/608,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
? SEQ ID NO 102
? LENGTH: 459
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AC007281.3
? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
? OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.1
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
? OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
? US-09-864-761-102

Query Match      88.6%; Score 12.4; DB 10; length 459;
Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GAAGGTGCTTAC 14
DB 143 GAAGCTTCTTAC 156
```

RESULT 14

```
US-09-783-590-3621
? Sequence 3621, Application US/09783590
? Patent No. US2002010850A1
? GENERAL INFORMATION:
? APPLICANT: Dillon, Patrick J.
? APPLICANT: Haseltine, William A.
? APPLICANT: Li, Haodong
? APPLICANT: Rosen, Craig A.
? APPLICANT: Ruben, Steven M.
? TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
? FILE REFERENCE: PO-16.2c1
? CURRENT APPLICATION NUMBER: US/09/783,590
? PRIOR FILING DATE: 2000-02-15
? PRIOR APPLICATION NUMBER: 08/420,856
? PRIOR FILING DATE: 1995-04-12
? PRIOR APPLICATION NUMBER: 08/346,731
```

```
? PRIOR FILING DATE: 1994-11-21
? NUMBER OF SEQ ID NOS: 12485
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 3621
? LENGTH: 500
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (73)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (146)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (240)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (246)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (275)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (336)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (377)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (380)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (388)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (390)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (413)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (436)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (450)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (455)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (459)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (477)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (487)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (499)
? OTHER INFORMATION: n equals a,t,g, or c
? US-09-783-590-3621

Query Match      88.6%; Score 12.4; DB 10; length 500;
Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

OY 1 GAAGGTGTCTTAC 14
|||||
DB 301 GAAGGTGTCTTAC 314

RESULT 15

US-09-974-300-2230
; Sequence 2230, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2230
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2230

Query Match 88.6%; Score 12.4; DB 10; Length 759;
Best Local Similarity 92.9%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAAGGTGTCTTAC 14
|||||
DB 550 GAAGGTGTCTTAC 563

Search completed: December 11, 2002, 06:03:08
Job time : 20.1453 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OH nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 : Search time 36.2905 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-18

Perfect score: 28
Sequence: 1 aaattgggtacagatgatacttcgtt 28

Scoring table:
IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_MA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PC1_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PC1US_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	US-09-865-579A-18	Sequence 18, Appl
2	28	100.0	2007	US-09-452-599-169	Sequence 169, App
3	18	64.3	232	US-09-880-107-262	Sequence 262, App
4	18	64.3	277	US-09-920-300A-1187	Sequence 1187, App
5	18	64.3	277	US-10-033-528-1187	Sequence 1187, App
6	18	64.3	1079	US-09-834-975-802	Sequence 802, App
7	17.8	63.6	2000	US-09-938-842A-2769	Sequence 2769, App
8	17.6	62.9	4356	US-09-815-242-3949	Sequence 3949, App
9	17.6	62.9	21252	US-09-815-242-6637	Sequence 6637, App
10	17.6	62.9	1233	US-09-070-927A-94	Sequence 94, Appl
11	17.4	62.1	1233	US-09-974-300-2472	Sequence 2472, Appl
12	17.4	62.1	1318	US-09-826-508-27	Sequence 27, Appl
13	17.4	62.1	1987	US-09-917-800A-1338	Sequence 1338, App
14	17.4	62.1	12445	US-09-070-927A-242	Sequence 242, App
15	17.4	62.1	15745	US-09-764-877-3236	Sequence 3236, App
16	17.2	61.4	339	US-09-867-701-6331	Sequence 6331, App
17	17.2	61.4	421	US-09-867-701-6415	Sequence 6415, App
18	17	60.7	213	US-09-878-574-14790	Sequence 14790, A
19	17	60.7	293	US-09-738-973-534	Sequence 534, App

20	17	60.7	3612	10	US-09-880-107-2353	Sequence 2353, App
21	17	60.7	6147	9	US-09-938-842A-2441	Sequence 2441, App
22	17	60.7	7923	10	US-09-864-864-297	Sequence 297, App
23	16.8	60.0	164	10	US-09-878-574-11991	Sequence 11991, A
24	16.8	60.0	264	10	US-09-815-343-89	Sequence 89, Appl
25	16.8	60.0	376	10	US-09-783-590-11404	Sequence 11404, A
26	16.8	60.0	393	9	US-10-046-935-2142	Sequence 2142, App
27	16.8	60.0	393	9	US-09-878-178-2142	Sequence 2142, App
28	16.8	60.0	476	10	US-09-864-761-10674	Sequence 10674, A
29	16.8	60.0	1116	9	US-09-931-457A-12	Sequence 12, Appl
30	16.8	60.0	8395	10	US-09-070-927A-217	Sequence 217, App
31	16.8	60.0	15613	10	US-09-874-877-3525	Sequence 3525, App
32	16.8	60.0	31208	10	US-09-852-067-3	Sequence 3, Appl
33	16.8	60.0	198285	10	US-09-880-107-3814	Sequence 3814, App
34	16.6	59.3	394	10	US-09-878-574-2552	Sequence 2552, App
35	16.6	59.3	580	10	US-09-864-761-12786	Sequence 12786, A
36	16.4	58.6	180	10	US-09-923-876-1440	Sequence 1440, A
37	16.4	58.6	296	10	US-09-960-352-11565	Sequence 11565, A
38	16.4	58.6	339	10	US-09-960-352-11565	Sequence 5204, App
39	16.4	58.6	422	10	US-09-864-761-3746	Sequence 3746, App
40	16.4	58.6	430	10	US-09-864-761-1508	Sequence 1508, App
41	16.4	58.6	462	10	US-09-867-701-4231	Sequence 4231, App
42	16.4	58.6	552	10	US-09-974-300-3381	Sequence 3381, App
43	16.4	58.6	3700	10	US-09-917-800A-1539	Sequence 1539, App
44	16.2	57.9	93	10	US-09-864-761-26662	Sequence 26662, A
45	16.2	57.9	360	10	US-09-974-300-8286	Sequence 8286, App

ALIGNMENTS

RESULT 1
US-09-865-579A-18
Sequence 18, Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865,579A
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-09-865-579A-18
Query Match 100.0%; Score 28; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAATTGGTACAGATGATGATCTTGGT 28
DB 1 AAATTGGTACAGATGATGATCTTGGT 28
RESULT 2
US-09-452-599-169
Sequence 169, Application US/09452599
Patent No. US20020055101A1
GENERAL INFORMATION:
APPLICANT: Bergeron, Michel G.

```
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; US-09-452-599-169
```

```
Query Match          100.0%; Score 28; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 AATTGGCTACAGATGATGATCTTGGTT 28
Db 608 AATTGGCTACAGATGATGATCTTGGTT 635
```

```
RESULT 3
US-09-880-107-262
; Sequence 262, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 262
; LENGTH: 232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AAI29390
; US-09-880-107-262
```

```
Query Match          64.3%; Score 18; DB 10; Length 232;
Best Local Similarity 80.8%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY 3 ATTGGTACAGATGATGATCTTGGTT 28
Db 172 ATTGGTACAGATGATGATCTTGGTT 197
```

```
RESULT 4
US-09-920-300A-1187
; Sequence 1187, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
```

```
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1187
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-920-300A-1187
```

```
Query Match          64.3%; Score 18; DB 10; Length 277;
Best Local Similarity 80.8%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY 3 ATTGGTACAGATGATGATCTTGGTT 28
Db 89 ATTGGTACAGATGATGATCTTGGTT 114
```

```
RESULT 5
US-10-033-528-1187
; Sequence 1187, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastaSeq for Windows Version 4.0
; SEQ ID NO 1187
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-033-528-1187
```

```
Query Match          64.3%; Score 18; DB 12; Length 277;
Best Local Similarity 80.8%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY 3 ATTGGTACAGATGATGATCTTGGTT 28
Db 89 ATTGGTACAGATGATGATCTTGGTT 114
```

```
RESULT 6
US-09-834-975-802/C
; Sequence 802, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Hufel, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
```



```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 802
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1079)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-802

Query Match          64.3%; Score 18; DB 10; Length 1079;
Best Local Similarity 80.8%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3  ATTGGGTACAAGATGATACCTTCGTT 28
      ||| ||||| ||||| ||| |||
Db      781  ATTGCTACATGATCATCTTCGTTT 756

; RESULT 7
; Sequence 2769, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2769
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2769

Query Match          63.6%; Score 17.8; DB 9; Length 2000;
Best Local Similarity 90.5%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8  GTACAGATGATACCTTCGTT 28
      || ||||| ||||| |||||
Db      1603  GTCCAGATGATACCATTCGTT 1583

; RESULT 8
; Sequence 3949, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
```

```
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3949
; LENGTH: 4329
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-3949

Query Match          62.9%; Score 17.6; DB 10; Length 4329;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4  TTGGTACAAGATGATACCTTCGT 27
      ||| ||||| ||||| ||| |||
Db      894  TAGTGTACAAGATGATACCTTCAT 917

; RESULT 9
; Sequence 6637, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6637
; LENGTH: 4356
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4356)
```



```

; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1338
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 D38381
; US-09-917-800A-1338

Query Match      62.1%; Score 17.4; DB 10; Length 1987;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AATTGGGTACAGATGATACCTTCGTT 28
      |||||||  |||  |||  |||  |||  |||
DB      1166 AATTGGTACATCTTAGACTTCATT 1140

RESULT 14
US-09-070-927A-242
; Sequence 242, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
;              Patrick J. Dillon
;              Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
;
```

```

; REFERENCE/DOCKET NUMBER: P8369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12445 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-070-927A-242

Query Match      62.1%; Score 17.4; DB 10; Length 12445;
Best Local Similarity 77.8%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AATTGGGTACAGATGATACCTTCGTT 28
      |||||||  |||  |||  |||  |||  |||
DB      11938 AATGGGACACGACAGATATTTTCGTT 11964

RESULT 15
US-09-764-877-3236
; Sequence 3236, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3236
; LENGTH: 15745
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-877-3236

Query Match      62.1%; Score 17.4; DB 10; Length 15745;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AATTGGGTACAGATGATACCTTCGTT 28
      |||||||  |||  |||  |||  |||  |||
DB      4132 AATTGGACACATGCAAAATTAATTCGTT 4158
```

Search completed: December 11, 2002, 06:03:06
Job time : 45.2905 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 ; Search time 38.1676 Seconds
(Without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579A-18

Perfect score: 28
Sequence: 1 aaatggglaacaaatgataccttgcgt 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 44362 seqs, 15338381 residues

Jcal number of hits satisfying chosen parameters: 682724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	2007	2 US-08-743-637B-169	Sequence 169, App
2	28	100.0	2007	3 US-08-526-840B-169	Sequence 169, App
3	28	100.0	2028	4 US-09-134-001C-1710	Sequence 1710, App
4	17.4	62.1	1318	3 US-09-183-253-3	Sequence 3, App1
5	17.4	62.1	4249	4 US-09-071-035-403	Sequence 403, App
6	17.4	62.1	4359	4 US-09-071-035-401	Sequence 401, App
7	17.4	62.1	84495	4 US-09-797-906-3	Sequence 3, App1
8	16.8	60.0	1379	4 US-09-499-505-6	Sequence 6, App1
9	16.8	60.0	1379	4 US-09-626-410-6	Sequence 6, App1
10	16.8	60.0	1379	4 US-09-116-188-6	Sequence 6, App1
11	16.8	60.0	1379	4 US-09-626-047-6	Sequence 6, App1
12	16.8	60.0	1379	4 US-09-626-343-6	Sequence 6, App1
13	16.8	60.0	1379	4 US-09-354-922-7	Sequence 7, App1
14	16.8	60.0	2539	1 US-07-885-970A-28	Sequence 28, App1
15	16.8	60.0	2539	1 US-08-298-827A-28	Sequence 28, App1
16	16.8	60.0	2539	1 US-08-298-827A-28	Sequence 28, App1
17	16.8	60.0	28171	4 US-08-961-527-22	Sequence 22, App1
18	16.8	58.6	585	3 US-08-882-501-28	Sequence 28, App1
19	16.4	58.6	51259	3 US-08-781-891-209	Sequence 209, App
20	16.2	57.9	2268	4 US-09-351-414-1	Sequence 1, App1
21	16.2	57.9	4854	4 US-08-961-527-178	Sequence 178, App
22	16.2	57.9	112132	4 US-09-741-150-3	Sequence 3, App1
23	16	57.1	3054	4 US-08-961-527-183	Sequence 183, App
24	16	57.1	14654	4 US-08-961-527-106	Sequence 106, App
25	16	57.1	4411529	4 US-09-103-840A-1	Sequence 1, App1
26	15.8	56.4	542	4 US-09-173-300-27	Sequence 27, App1
27	15.8	56.4	731	4 US-09-328-111-438	Sequence 438, App

C 28	15.8	56.4	1343	4 US-09-499-505-5	Sequence 5, App1
C 29	15.8	56.4	1343	4 US-09-626-410-5	Sequence 5, App1
C 30	15.8	56.4	1343	4 US-09-116-188-5	Sequence 5, App1
C 31	15.8	56.4	1343	4 US-09-626-047-5	Sequence 5, App1
C 32	15.8	56.4	1343	4 US-09-626-343-5	Sequence 5, App1
C 33	15.8	56.4	1343	4 US-09-354-922-6	Sequence 6, App1
C 34	15.8	56.4	1380	4 US-09-499-505-4	Sequence 4, App1
C 35	15.8	56.4	1380	4 US-09-626-410-4	Sequence 4, App1
C 36	15.8	56.4	1380	4 US-09-116-188-4	Sequence 4, App1
C 37	15.8	56.4	1380	4 US-09-626-047-4	Sequence 4, App1
C 38	15.8	56.4	1380	4 US-09-626-343-4	Sequence 4, App1
C 39	15.8	56.4	1380	4 US-09-354-922-5	Sequence 5, App1
C 40	15.8	56.4	1382	4 US-09-499-505-2	Sequence 2, App1
C 41	15.8	56.4	1382	4 US-09-626-410-2	Sequence 2, App1
C 42	15.8	56.4	1382	4 US-09-116-188-2	Sequence 2, App1
C 43	15.8	56.4	1382	4 US-09-626-047-2	Sequence 2, App1
C 44	15.8	56.4	1382	4 US-09-626-343-2	Sequence 2, App1
C 45	15.8	56.4	1382	4 US-09-354-922-3	Sequence 3, App1

ALIGNMENTS

RESULT 1
US-08-743-637B-169
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: OUELLETTE & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0%; Score 28; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGGGTACAGATGATACCTTGCTT 28
|||||
Db 608 AATGGGTACAGATGATACCTTGCTT 635

RESULT 2

US-08-526-840B-169
Sequence 169, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: OVARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGGGTACAGATGATACCTTGCTT 28
|||||
Db 608 AATGGGTACAGATGATACCTTGCTT 635

RESULT 3

US-09-134-001C-1710
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelte-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 28; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGGGTACAGATGATACCTTGCTT 28
|||||
Db 630 AATGGGTACAGATGATACCTTGCTT 657

RESULT 4

US-09-183-253-3/C
Sequence 3, Application US/09183253
Patent No. 6043054
GENERAL INFORMATION:
APPLICANT: VAMTER, LISA
APPLICANT: STAMERS, MELANIE
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,253
FILING DATE: 30-OCT-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9817907.0
FILING DATE: 17-AUG-1998
APPLICATION NUMBER: 60/075,306
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70395
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-183-253-3


```

US-09-499-505-6/c
: Sequence 6, Application US/09499505
: Patent No. 6251674
: GENERAL INFORMATION:
: APPLICANT: DEL CARDAYRE, STEPHEN
: APPLICANT: TOBIN, MATTHEW
: APPLICANT: STEMMER, WILLEM P.C.
: APPLICANT: NESS, JON E.
: APPLICANT: MINSHULL, JEREMY
: APPLICANT: PATTEN, PHILLIP
: APPLICANT: SUBRAMANIA, VENKITSWARAN
: APPLICANT: CASTLE, LINDA
: APPLICANT: KREBBER, CLAUD M.
: APPLICANT: BASS, STEVE
: TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
: TITLE OF INVENTION: SEQUENCE RECOMBINATION
: FILE REFERENCE: 02-020720US
: CURRENT APPLICATION NUMBER: US/09/499,505
: CURRENT FILING DATE: 2000-02-07
: PRIOR APPLICATION NUMBER: 09/116,188
: PRIOR FILING DATE: 1998-07-15
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: Patentia Ver. 2.0
: SEQ ID NO 6
: LENGTH: 1379
: TYPE: DNA
: ORGANISM: Escherichia coli
US-09-499-505-6

```

Query Match	60.0%	Score 16.8	DB 4	Length 1379
Best Local Similarity	90.0%	Pred. No. 62		
Matches 18	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	8	GTACACAGATGATACCTTCGT	27	
DB	1061	GTACAGATTGATACCTTCGT	1042	

```

RESULT 9
US-09-626-410-6/c
: Sequence 6, Application US/09626410
: Patent No. 6287862
: GENERAL INFORMATION:
: APPLICANT: DEL, CARDAYRE, STEPHEN
: APPLICANT: TOBIN, MATTHEW
: APPLICANT: STEMMER, WILLEM P.C.
: APPLICANT: NESS, JON E.
: APPLICANT: MINSHOLL, JEREMY
: APPLICANT: PATTEN, PHILLIP
: APPLICANT: SUBRAMANIA, VENKTESWARAN
: APPLICANT: CASTLE, LINDA
: APPLICANT: KREBBER, CLAUDS M.
: APPLICANT: BASS, STEVE
: TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
: FILE REFERENCE: 02-020720US
: CURRENT APPLICATION NUMBER: US/09/626,410
: CURRENT FILING DATE: 2000-07-26
: PRIOR FILING DATE: 07-15-1998
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 1379
: TYPE: DNA
: ORGANISM: Escherichia coli
: US-09-626-410-6

```

Query Match	60.0%	Score 16.8:	DB 4:	Length 1379:
Best Local Similarity	90.0%:	Pred. No. 62:		
Matches 18:	Conservative 0:	Mismatches 2:	Indels 0:	Gaps 0
8 GTACAGATGATACCTTCGT	27			

```

DB          1061 GTAGAACTTCATACCTTGGT 1042
              ||| ||| ||||| ||||| |||
RESULT 10
US-09-116-188-6/c
? Sequence 6, Application US/09116188
? Patent No. 6326204
? GENERAL INFORMATION:
APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: KINSHULL, JEREMY
APPLICANT: FATTEN, PHILLIP
APPLICANT: SUBRAMANJA, VENKITSAMARAN
APPLICANT: CASTLE, LINDA
APPLICANT: KREIBER, CLAUD M.
APPLICANT: BASS, STEVE
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
FILE REFERENCE: 02-020720US
CURRENT APPLICATION NUMBER: US/09/116,188
CURRENT FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1379
TYPE: DNA
ORGANISM: Escherichia coli
US-09-116-188-6
```

Query Match	60.0%	Score 16.8	DB 4	length 1379
Best Local Similarity	90.0%	Pred. No. 62		
Matches 18	Conservative	0	Mismatches 2	Indels 0
Gaps				0
Q7	8	GTACACATGATCACTTCCT	27	
Db	1061	GTAGAAATTGATACCTTCCT	1042	

```

RESULT 11
US-09-626-047-6/c
: Sequence 6, Application US/09626047
: Patent No. 6335198
: GENERAL INFORMATION:
: APPLICANT: DEL CARDAYRE, STEPHEN
: APPLICANT: TOBIN, MATTHEW
: APPLICANT: STEMMER, WILHEM P.C.
: APPLICANT: NESS, JON E.
: APPLICANT: MINSHULL, JEREMY
: APPLICANT: PATTEN, PHILLIP
: APPLICANT: SUBRAMANIA, VENKITSWARAN
: APPLICANT: CASTLE, LINDA
: APPLICANT: KREBER, CLAUD M.
: APPLICANT: BASS, STEVE
: TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
: FILE REFERENCE: 02-020720US
: CURRENT APPLICATION NUMBER: US/09/626,047
: CURRENT FILING DATE: 2000-07-26
: PRIOR APPLICATION NUMBER: 09/116,188
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 1379
: TYPE: DNA
: ORGANISM: Escherichia coli
: US-09-626-047-6

```

Query Match	60.08;	Score 16.8;	DB 4;	Length 1379;
Best Local Similarity	90.08;	Pred. NO. 62;		

rb 910 AAGTAGTAAATATGCTACTTAGTT 883

RESULT 15

US-08-298-687A-28/C
 ; Sequence 28: Application US/08298687A
 ; Patent No. 5521078
 ; GENERAL INFORMATION:
 ; APPLICANT: John, Malyakal E.
 ; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
 ; TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
 ; STREET: P.O. Box 2113, First Wisconsin Plaza
 ; CITY: Madison
 ; STATE: Wisconsin
 ; COUNTRY: USA
 ; ZIP: 53701
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Microsoft Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/298,687A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/617,239
 ; FILING DATE: 21-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/253,243
 ; FILING DATE: 04-OCT-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seay, Nicholas J.
 ; REGISTRATION NUMBER: 27,386
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (608) 283-2478
 ; TELEFAX: (608) 251-5139
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2539 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Gossypium barbadense
 ; STRAIN: Sea Island
 ; IMMEDIATE SOURCE:
 ; LIBRARY: EMBL-SI
 ; CLONE: SIB8
 ; US-08-298-687A-28

Query Match 60.0%; Score 16.8; DB 1; Length 2539;

Best Local Similarity 75.0%; Pred. No. 68;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 AAATTGGTACAGATGATACCTTCGTT 28

Db 910 AAGTAGTAAATATGCTACTTAGTT 883

Search completed: December 10, 2002, 22:54:19
 Job time : 58.2926 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 : Search time 38.1676 Seconds
(without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579a-22

Sequence: 1 aaagaaaaagatgcgaagatattcaa 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued_Patents_NA:*
2: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
3: /cgn2_6/ptodata/1/lna/5B_COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/lna/6B_COMB.seq:*
6: /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	2007	2	US-08-743-637B-169
2	28	100.0	2007	3	US-08-526-840B-169
3	28	100.0	2028	4	US-09-134-001C-1710
4	20	71.4	29	3	US-09-109-957-4
5	20	71.4	29	3	US-09-109-957-5
6	20	71.4	2775	1	US-08-149-096A-1
7	20	71.4	2830	4	US-09-221-017B-730
8	19.8	70.7	1847	1	US-07-808-455A-2
9	18.8	67.1	1863	2	US-08-455-073A-3
10	18.6	66.4	2415	4	US-09-134-001C-2381
11	18.6	66.4	6156	4	US-08-891-640-1
12	18.6	65.7	273	2	US-09-723-535-3
13	18.4	65.7	345	4	US-08-737-298-1
14	18.4	65.7	1240	1	US-09-328-111-506
15	18.4	65.7	1430	4	US-08-248-466B-6
16	18.4	65.7	1510	4	US-09-357-251-17
17	18.4	65.7	1532	1	US-08-248-466B-3
18	18.4	65.7	1972	1	US-08-248-466B-11
19	18.4	65.7	1972	1	US-08-463-048-1
20	18.4	65.7	1972	1	US-08-463-229-1
21	18.4	65.7	1972	2	US-08-302-891-1
22	18.4	65.7	2040	1	US-08-599-252-103
23	18.4	65.7	2040	5	PCT-US96-06352-103
24	18.4	65.7	2558	4	PCT-US96-06583-103
25	18.4	65.7	2892	2	US-08-936-165A-214
26	18.4	65.7	4157	2	US-08-874-186-44
27	18.4	65.7	4157	2	US-08-871-266B-1

C 28	18.4	65.7	4157	2	US-08-819-458A-1	Sequence 1, Appl
C 29	18.4	65.7	4157	3	US-09-018-864A-1	Sequence 1, Appl
C 30	18.4	65.7	4157	3	US-08-871-267B-1	Sequence 1, Appl
C 31	18.4	65.7	4157	2	US-09-618-419-1	Sequence 1, Appl
C 32	18.4	65.7	14855	2	US-08-687-080-59	Sequence 59, Appl
C 33	18.4	64.3	39	3	US-08-975-902-47	Sequence 47, Appl
C 34	18.4	64.3	39	3	US-09-251-565-47	Sequence 47, Appl
C 35	18.4	64.3	1879	4	US-09-601-091-1	Sequence 1, Appl
C 36	18.4	64.3	2024	4	US-09-601-091-3	Sequence 3, Appl
C 37	18.4	64.3	2024	4	US-09-398-392A-51	Sequence 51, Appl
C 38	17.8	63.6	24	1	US-07-808-455A-6	Sequence 6, Appl
C 39	17.8	63.6	1907	4	US-09-443-184-40	Sequence 40, Appl
C 40	17.6	62.9	774	4	US-09-134-001C-2190	Sequence 2190, Ap
C 41	17.6	62.9	2626	4	US-09-632-538C-35	Sequence 35, Appl
C 42	17.6	62.9	22481	4	US-08-367-841A-43	Sequence 43, Appl
C 43	17.6	62.9	22481	5	PCT-US95-07201-43	Sequence 43, Appl
C 44	17.6	62.9	22484	4	US-09-875-223-2	Sequence 2, Appl
C 45	17.4	62.1	57	1	US-08-044-506B-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-743-637B-169
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586, 90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0% Score 28 DB 2 Length 2007:

Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCAAGATATTCA 28
Db 948 AAAGAAAAAGATGCAAGATATTCA 975

RESULT 2

US-08-526-840B-169
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OUELLETTE & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526, 840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994

; ATTORNEY/AGENT INFORMATION:
; NAME: HAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850,86,90012
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-526-840B-169

Query Match 100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCAAGATATTCA 28
Db 948 AAAGAAAAAGATGCAAGATATTCA 975

RESULT 3

US-09-134-001C-1710
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucellette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710

; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.

US-09-134-001C-1710

Query Match 100.0%; Score 28; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCAAGATATTCA 28
Db 969 AAAGAAAAAGATGCAAGATATTCA 996

RESULT 4

US-09-109-957-4
; Sequence 4, Application US/09109957
; Patent No. 6136533
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Modrusan, Zora D.
; APPLICANT: Pische, Isabelle A.
; APPLICANT: Duck, Peter D.
; APPLICANT: Cloney, Lynn P.
; APPLICANT: Wong, Alfred C.K.
; TITLE OF INVENTION: ADDITIVES FOR USE IN CYCLING PROBE REACTIONS
; FILE REFERENCE: 480094,419
; CURRENT APPLICATION NUMBER: US/09/109,957
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of

US-09-109-957-4

Query Match 71.4%; Score 20; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 23;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCAAG 20
Db 10 AAAGAAAAAGATGCAAG 29

RESULT 5

US-09-109-957-5/C
; Sequence 5, Application US/09109957
; Patent No. 6136533
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Modrusan, Zora D.
; APPLICANT: Pische, Isabelle A.
; APPLICANT: Duck, Peter D.
; APPLICANT: Cloney, Lynn P.
; APPLICANT: Wong, Alfred C.K.


```
; Sequence 2, Application US/07808455A
; Patent No. 5405745
; GENERAL INFORMATION:
; APPLICANT: Gorman, Jessica A.
; TITLE OF INVENTION: METHOD FOR DETECTING CANDIDA ALBICANS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burton Rodney
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/808,455A
; FILING DATE: 19911217
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Booden, James M.
; REGISTRATION NUMBER: 32,962
; REFERENCE/DOCKET NUMBER: GP65
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 921-4163
; TELEFAX: (609) 921-4526
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1747 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-808-455A-2

Query Match          70.7%; Score 19.8; DB 1; Length 1747;
Best Local Similarity 91.3%; Pred. No. 43;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAAAAGATGCGCAAGATATT 25
   1 ||||| ||||| ||||| ||||| ||
   DB 704 AAAAAAAGATGCGCAAGATTTT 726

-RESULT 9
-08-455-073A-3
Sequence 3, Application US/08455073A
; Patent No. 5876949
; GENERAL INFORMATION:
; APPLICANT: Gideon Dreyfuss
; APPLICANT: MIKIKO C. Stomi
; APPLICANT: Yan Zhang
; TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods
; TITLE OF INVENTION: Of Making And Using The Same
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5876949rls
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,073A
```

```
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-2201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1863 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-455-073A-3

Query Match          67.1%; Score 18.8; DB 2; Length 1863;
Best Local Similarity 90.9%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AAAAGATGCGCAAGATATTCAA 28
   ||| ||||| ||||| ||||| ||
   DB 894 AAAAAATGCGCAAGATTTCAA 915

-RESULT 10
-09-134-001C-2381
Sequence 2381, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCC
; FILE REFERENCE: CTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2381
; LENGTH: 2415
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-2381

Query Match          66.4%; Score 18.6; DB 4; Length 2415;
Best Local Similarity 84.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATT 25
   ||| ||||| ||||| ||||| ||
   DB 1203 AAATAAAAAGATGCTAAGATAAT 1227

-RESULT 11
-08-891-640-1/C
Sequence 1, Application US/08891640
; Patent No. 6268173
; GENERAL INFORMATION:
; APPLICANT: Chambon, Pierre
; APPLICANT: Gronemeyer, Hinrich
; APPLICANT: Voegel, Johannes
; APPLICANT: Lutz, Yves
; TITLE OF INVENTION: Transcriptional Intermediary Factor-2
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
```

```

; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,640
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,247
; FILING DATE: 12-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1383.0130001/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6156 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 163..4554
; US-08-891-640-1

Query Match          66.4%; Score 18.6; DB 4; Length 6156;
Best Local Similarity 84.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAGAGAAAAAGATGCGCAAGATATT 25
    |||||  |||||  |||||  |||||  |||||
Db 5264 AAGAGAAAAACACGAAAAAATATT 5240

RESULT 12
US-09-723-535-3/C
; Sequence 3, Application US/09723535
; Patent No. 6355483
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-2 EXPRESSION
; FILE REFERENCE: RTS-0225
; CURRENT APPLICATION NUMBER: US/09/723,535
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 6156
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (163)..(4557)
; US-09-723-535-3

Query Match          66.4%; Score 18.6; DB 4; Length 6156;
Best Local Similarity 84.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAGAGAAAAAGATGCGCAAGATATT 25
    |||||  |||||  |||||  |||||  |||||
Db 5264 AAGAGAAAAACACGAAAAAATATT 5240

RESULT 13

; US-08-737-298-1
; Sequence 1, Application US/08737298
; Patent No. 5910629
; GENERAL INFORMATION:
; APPLICANT: STRITTMAYER, Gunter
; TITLE OF INVENTION: CHIMERIC GENES COMPRISING A
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,298
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-121P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..273
; OTHER INFORMATION: /note="273 bp prp1-1 fragment,
; OTHER INFORMATION: corresponding to position 402 to -130 of the prp1-1
; US-08-737-298-1

Query Match          65.7%; Score 18.4; DB 2; Length 273;
Best Local Similarity 78.6%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAGAGAAAAAGATGCGCAAGATATTCAA 28
    |||  |||||  |||||  |||||  |||||  ||
Db 51 AAATTAAATAATGTCAATAATATTAA 78

RESULT 14
US-09-328-111-506
; Sequence 506, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endegame, Willson O.
; APPLICANT: Stohmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Carino, Theodore J.
; APPLICANT: Dertl, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
```

```

; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 506
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(545)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-506

Query Match          65.7%; Score 18.4; DB 4; length 545;
Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 AAAGAAAAAAGATGCCAAGATTATTCAA 28
    ||||| ||||| ||||| ||||| |||||
DB 153 AAGCAAAAAAGACGCGCAAAATATACCA 180

RESULT 15
US-08-248-466B-6
; Sequence 6, Application US/08248466B
; Patent No. 5629182
; GENERAL INFORMATION:
; APPLICANT: CHOPIN, MARIE-CRISTINE
; APPLICANT: CUZEL, PIERRE-JEAN
; TITLE OF INVENTION: CLONING OF DNA FRAGMENTS ENCODING A
; TITLE OF INVENTION: MECHANISM FOR RESISTANCE TO BACTERIOPHAGES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,466B
; FILING DATE: 24-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,959
; FILING DATE: 15-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90/11381
; FILING DATE: 14-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NO. 5629182man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 384-033-0 PCT FWC CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1240 base pairs
; TYPE: nucleic acid
```

```

; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -35_signal
; LOCATION: 33..38
; FEATURE:
; NAME/KEY: -10_signal
; LOCATION: 57..62
; FEATURE:
; NAME/KEY: RBS
; LOCATION: 133..137
US-08-248-466B-6

Query Match          65.7%; Score 18.4; DB 1; length 1240;
Best Local Similarity 78.6%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 AAAGAAAAAAGATGCCAAGATTATTCAA 28
    ||||| ||||| ||||| ||||| |||||
DB 238 AAGAGATAAGATTCCAAAGATTAACCA 265
```

Search completed: December 10, 2002, 22:54:35
Job time : 40.2926 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 ; Search time 1025.47 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-21
Perfect score: 20
Sequence: 1 gtaagtgatgataatcttgcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
otal number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	18	90.0	543	14	BQ299830 QV1-KT002
C 2	17.4	87.0	197	9	AU036282 AU036282
C 3	17.4	87.0	622	10	BH761716 BMBAC34G
C 4	17.4	87.0	537	13	AV821890 AV821890
C 5	17	85.0	722	17	BM303591 SNEST461
C 6	17	85.0	722	17	BH468476 BOHRM34TF

Result No.	Score	Query Match	Length DB	ID	Description
C 7	17	85.0	812	17	BH588212 BOHR103TF
C 8	16.8	84.0	329	14	T75914
C 9	16.8	84.0	417	10	T45901
C 10	16.8	84.0	431	14	AV807336
C 11	16.8	84.0	618	13	BM077153 TREST-A02
C 12	16.4	82.0	171	17	A2050909 RPCT-23-4
C 13	16.4	82.0	393	14	A0492427 HS-5143_B
C 14	16.4	82.0	418	10	AW760469
C 15	16.4	82.0	425	17	BH320276
C 16	16.4	82.0	433	17	AO818960
C 17	16.4	82.0	467	10	AM634994
C 18	16.4	82.0	509	13	B1941756
C 19	16.4	82.0	567	17	BH767554
C 20	16.4	82.0	592	9	A1257715
C 21	16.4	82.0	592	17	AO250543
C 22	16.4	82.0	618	17	A2722668
C 23	16.4	82.0	693	9	A1975290
C 24	16.4	82.0	706	12	BF974745
C 25	16.4	82.0	720	9	AU234559
C 26	16.4	82.0	729	17	BH013591
C 27	16.4	82.0	858	12	BG742644
C 28	16	80.0	391	17	AO012704
C 29	16	80.0	478	17	AO338636
C 30	16	80.0	772	12	BG784784
C 31	16	80.0	801	17	BH488655
C 32	15.8	79.0	182	14	BQ513203
C 33	15.8	79.0	184	13	BJ518549
C 34	15.8	79.0	240	10	BM073140
C 35	15.8	79.0	275	17	A2696726
C 36	15.8	79.0	282	17	A2979689
C 37	15.8	79.0	293	9	AA531485
C 38	15.8	79.0	291	14	BQ370240
C 39	15.8	79.0	299	17	AO145901
C 40	15.8	79.0	318	17	AO067016
C 41	15.8	79.0	331	17	BH65762
C 42	15.8	79.0	365	9	AA163000
C 43	15.8	79.0	400	17	CNS00NG8
C 44	15.8	79.0	420	17	AL760169
C 45	15.8	79.0	423	17	AO434889

ALIGNMENTS

RESULT 1
LOCUS BQ299830/c
DEFINITION OVI-KT0023-131100-475-c07 KT0023 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ299830
VERSION BQ299830.1 GI:20815352
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 543)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baita,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l-QV1&t2-QV1-KT0023-131100-475-c07&t3=2000-11-13&t4=1)

Seq primer: puc 18 forward
 High quality sequence start: 53
 High quality sequence stop: 95.
 Location/Qualifiers

FEATURES

source

1..543
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="KT0023"
 /dev_stage="Adult"
 /note="Organ: bladder tumor; Vector: puc18; Site: 1: Sma1; Site: 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 ASE COUNT 164 a 114 c 101 g 164 t
 ORIGIN

Query Match 90.0%; Score 18; DB 14; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTACTGATATCTTGGC 19
 |||||||
 Db 45 TTACTGATATCTTGGC 28

RESULT 2 197 bp mRNA linear EST 29-SEP-1999
 AU036282/c LOCUS
 AU036282 Polyandrocampa misakiensis white spot budding stage
 DEFINITION
 AU036282 Polyandrocampa misakiensis cDNA, mRNA sequence.
 ACCESSION
 AU036282.1 GI:4527243
 VERSION
 AU036282.1
 KEYWORDS
 EST.
 SOURCE
 Polyandrocampa misakiensis.
 ORGANISM
 Polyandrocampa misakiensis.
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Stolidobranchia; Styelidae; Polyandrocampa.

REFERENCE
 1 (bases 1 to 197)
 Kawamura, K., Hayata, D., Fujiwara, S. and Yubisui, T.
 Serine protease inhibitors expressed in the process of budding of
 L. bufoles as revealed by EST analysis
 J. Biochem. 124 (5), 1004-1012 (1998)
 JOURNAL
 MEDLINE
 COMMENT
 Contact: Kawamura K
 Faculty of Science
 Kochi University
 2-5-1, Akebono-cho, Kochi 780, Japan
 Tel: +81-888-44-8313
 Fax: +81-888-44-8313
 Email: kazuk@cc.kochi-u.ac.jp.

FEATURES

source

1..197
 /organism="Polyandrocampa misakiensis"
 /strain="white spot"
 /db_xref="taxon:7723"
 /clone_lib="Polyandrocampa misakiensis white spot budding stage"
 /dev_stage="budding stage"
 BASE COUNT 55 a 31 c 36 g 75 t
 ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 197;
 Best Local Similarity 94.7%; Pred. No. 4.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTACTGATATCTTGGC 19
 |||||||
 Db 43 GTTACTGATATCTTGGC 25

RESULT 3 622 bp DNA linear GSS 20-MAR-2002
 BH761716/c LOCUS
 BH761716 BMBAC324G04T7_P5U Brugia malayi Genomic Bac Library 3 Brugia malayi
 DEFINITION
 BH761716 genomic DNA sequence.
 ACCESSION
 BH761716
 VERSION
 BH761716.1 GI:19555979
 KEYWORDS
 GSS.
 SOURCE
 Brugia malayi.
 ORGANISM
 Brugia malayi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.

REFERENCE
 1 (bases 1 to 622)
 Whitton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster, J., Gulliano, D., Slatko, B. and Blaxter, M.
 Genome survey sequences from the human parasitic nematode Brugia malayi
 TITLE
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Blaxter M.
 Institute of Cell, Animal and Population Biology
 University of Edinburgh
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JT, UK
 Tel: +44 131 650 6760
 Fax: +44 131 670 5450
 Email: mark.blaxter@ed.ac.uk
 Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by the Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK.
 Seq primer: T7 (TTATACGACTCACTATAGG)
 Class: BAC ends.

FEATURES

source

1..622
 /organism="Brugia malayi"
 /strain="T7RS"
 /db_xref="taxon:6279"
 /clone_lib="Brugia malayi Genomic Bac Library 3"
 /sex="Mixed (male and female)"
 /tissue_type="whole parasite"
 /dev_stage="microfilaria (iii)"
 /note="Vector: pBAC3.6; Site: 1: BamH I; Brugia malayi genomic DNA was partially cleaved with Sau3A I and size fractionated. 7,392 clones were generated with mean insert size ~48 kbp. The library was constructed by Claire Whitton, Blaxter Nematode Genetics Lab, University of Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing Unit, The Sanger Centre, Cambridge, UK."
 BASE COUNT 200 a 83 c 106 g 233 t
 ORIGIN

Query Match 87.0%; Score 17.4; DB 17; Length 622;
 Best Local Similarity 94.7%; Pred. No. 5e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTACTGATATCTTGGC 20
 |||||||
 Db 391 TTACTGATATCTTGGC 373

RESULT 4 672 bp mRNA linear EST 01-APR-2002
 AV821890/c LOCUS
 AV821890 RAE14 Arabidopsis thaliana cDNA clone RAE104-17-K09 5',
 DEFINITION
 mRNA sequence.
 ACCESSION
 AV821890
 VERSION
 AV821890.1 GI:19863921

KEYWORDS EST.
SOURCE Unale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 672)
AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamaya, A., Satou, M., Nakajima, M.,
Omori, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, T.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,
and Shinozaki, K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified Bluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/Plant/index_e.html) for
further details.

FEATURES
source
1..672
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF104-17-K09"
/clone_lib="RAF14"
/dev_stage="roselte plants"
/lab_host="SOLR"
/note="Site_1: SstI; Site_2: XhoI; subjected to
cold-treated(1,2,5,10,24 hr)"

BASE COUNT 209 a 124 c 165 g 174 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 672;
Best Local Similarity 94.7%; Pred. No. 5,1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTAGTTGATATCTTGGC 20
1 |||||||||||||||
Db 383 TGAGTTGAATATCTTGGC 365

RESULT 5
3M303591/c 537 bp mRNA linear EST 02-JAN-2002
DEFINITION SNEST461h11.y1 csn 1 S neurona invitro merizoite cDNA Sarcocystis
neurona cDNA 5', mRNA sequence.
ACCESSION BM303591
VERSION BM303591.1 GI:18035295
KEYWORDS EST.
SOURCE Sarcocystis neurona.
ORGANISM Sarcocystis neurona.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Sarcocystis.
REFERENCE 1 (bases 1 to 537)
AUTHORS Howe, D.K., Stamper, S., Tang, K., Sibley, L.D., Clifton, S., Marra, M.,
Hillier, L., Pape, D., Martin, J., Wylie, T., Thelais, B., Bowers, Y.,
Gibbons, M., Ritter, E., McCann, R., Blistain, A., Bennett, J., Schmitt,
A., Ronko, I., Tsagareishvili, R., Fedele, M., Belaygorod, U.,
Franklin, C., Carr, L.M., Grow, A., Maguire, L., Madkins, J., Ritchey, J.,
Waterston, R. and Wilson, R.
TITLE Sarcocystis neurona EST project
JOURNAL Unpublished (2000)
COMMENT Contact: Daniel K. Howe
Sarcocystis neurona EST project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

FEATURES
source
1..537
/organism="Sarcocystis neurona"
/strain="Sn3"
/db_xref="taxon:42890"
/clone_lib="csn 1 S neurona invitro merizoite cDNA"
/dev_stage="merozoite"
/lab_host="DH10B"
/note="Vector: phuescript SK-; Site_1: KccOI; Site_2:
XhoI; The library was constructed by Dan Howe, University
of Kentucky. cDNAs were synthesized from poly(A)+ RNA
by oligo d(T) priming and directionally cloned into the
Uni-ZAP XR lambda vector. The library was mass excised
as phagemids and rescued in SOLR cells. The plasmid
library was recovered from the SOLR cells and transformed
in mass into DH10B cells for sequencing. WARNING: the
library contains a small percentage of cDNAs derived from
the bovine host cells."

BASE COUNT 129 a 129 c 139 g 140 t
ORIGIN

Query Match 85.0%; Score 17; DB 13; Length 537;
Best Local Similarity 100.0%; Pred. No. 7,6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTTGAATATCTTGGC 20
|||||||||||||
Db 149 AGTTGAATATCTTGGC 133

RESULT 6
BH468476 722 bp DNA linear GSS 13-DEC-2001
LOCUS BOHRM34TF BOHR Brassica oleracea genomic clone BOHRM34, DNA
DEFINITION Sequence.
ACCESSION BH468476
VERSION BH468476.1 GI:17673478
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 722)
AUTHORS Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOHRM34TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: ctown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
source
1..722
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHRM34"
/clone_lib="BOHR"
/note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT 285 a 109 c 103 g 225 t

ORIGIN

Query Match 85.0%; Score 17; DB 17; Length 722;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTACGTTGATATCTTT 17
 |||||||
 Db 533 GTTAGTTGAATATCTTT 549

RESULT 7
 BH588212/c 812 bp DNA linear GSS 15-DEC-2001
 LOCUS BOHB037F BOHB Brassica oleracea genomic clone BOHB103, DNA
 DEFINITION sequence.
 ACCESSION BH588212
 VERSION BH588212.1 GI:17840670
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 812)
 Town, C.D., Van Aken, S., Utterback, T., and Fraser, C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished (2001)
 COMMENT Other GSSs: BOHB103TR
 Contact: Chris Town
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: RP
 Class: Sheared ends.
 Location/Qualifiers
 1. 812
 /organism="Brassica oleracea"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone="BOHB103"
 /clone_1lb="BOHB"
 /note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
 genomic DNA inserted into PHOS1 using BstXI linkers"
 BASE COUNT 263 a 205 c 136 g 208 t

ORIGIN

Query Match 85.0%; Score 17; DB 17; Length 812;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTAGTTGATATCTTTC 18
 |||||||
 Db 37 TTAGTTGAATATCTTTC 21

RESULT 8
 T75914/c 329 bp mRNA linear EST 09-JAN-1998
 LOCUS 10692 Lambda-PRL2 Arabidopsis thaliana cDNA clone 148D147, mRNA
 DEFINITION sequence.
 ACCESSION T75914
 VERSION T75914.1 GI:934966
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 329)

AUTHORS Newman, T., debruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh
 , L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel
 , E. and Somerville, C.
 TITLE Genes galore: a summary of methods for accessing results from
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 JOURNAL Plant Physiol. 106, 1241-1255 (1994)
 MEDLINE 95148729
 COMMENT On Apr 14, 1993 this sequence version replaced gi:692676.
 Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
 Lansing, MI
 Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313c@edlm.cl.msu.edu
 Seq primer: T7 dye primer.
 Location/Qualifiers
 1. 329
 /organism="Arabidopsis thaliana"
 /strain="var columbia"
 /db_xref="taxon:3702"
 /clone="148D147"
 /clone_1lb="Lambda-PRL2"
 /note="Vector: lambda Z1p-10x; Site_1: Sal; Site_2: Not;
 lambda PRL2 is a cDNA library derived from equal
 quantiles of 4 pools of mRNA. The mRNA sources were 1) 7
 day germinated etiolated seedlings; 2) tissue culture
 grown roots; 3) staged plants half with 24 hour light
 cycle, half on 16 hr light, 8 hour dark - rosettes; 4)
 same plants as 3 but aerial tissue (stems, flowers and
 siliques. The vector is BRL's lambda Z1p-10x. The cDNA
 inserts were directionally cloned with Sal-I Not arms using
 oligo dt primed cDNA. "

BASE COUNT 104 a 45 c 73 g 97 t 10 others

ORIGIN

Query Match 84.0%; Score 16.8; DB 14; Length 329;
 Best Local Similarity 90.0%; Pred. No. 8.9e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTACGTTGATATCTTCCC 20
 |||||||
 Db 59 GTTAGTTGAACATCTTGCC 40

RESULT 9
 T45901/c 417 bp mRNA linear EST 04-AUG-1998
 LOCUS 9164 Lambda-PRL2 Arabidopsis thaliana cDNA clone 133J247, mRNA
 DEFINITION sequence.
 ACCESSION T45901
 VERSION T45901.1 GI:2762614
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 417)
 Newman, T., debruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh
 , L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel
 , E. and Somerville, C.
 TITLE Genes galore: a summary of methods for accessing results from
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 JOURNAL Plant Physiol. 106, 1241-1255 (1994)
 MEDLINE 95148729
 COMMENT On Jan 9, 1998 this sequence version replaced gi:934153.
 Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
 Lansing, MI

Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313tcn@ibm.cj.msu.edu
 Seq primer: T7 dye primer.

FEATURES
 source
 Location/Qualifiers

1. 417
 /organism="Arabidopsis thaliana"
 /strain="var columbiana"
 /db_xref="taxon:3702"

Query Match 84.0% Score 16.8; DB 14; Length 417;
 Best Local Similarity 90.0% Pred. No. 9.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 135 a 62 c 112 g 92 t 16 others
 ORIGIN
 1 GTTACTGCAATATCTTGCC 20
 ||| ||||| ||||| |||||
 Db 307 GTTGTTGACATCTTGCC 288

RESULT 10 431 bp mRNA linear EST 29-MAR-2002
 AV807336
 LOCUS AV807336 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-49-P22 3',
 DEFINITION mRNA sequence.
 ACCESSION AV807336
 VERSION AV807336.1 GI:19841321
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

REFERENCE
 AUTHORS Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
 Rosidae, eurosids 11; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 431)
 Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
 and Shinozaki, K.

TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki

Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: masek@rcc.riken.go.jp

Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified lambda PUC-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified plasmid vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
 details.

FEATURES
 source
 Location/Qualifiers
 1. 431
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /clone="RAFL09-49-P22"
 /clone_lib="RAFL9"

/dev_stage="plants at various developmental stages from
 germination to mature seeds"
 /lab_host="DH108"
 /note="Site_1: BamHI; Site_2: SalI; subjected to
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
 hr) treatments"

BASE COUNT 132 a 99 c 68 g 132 t
 ORIGIN

Query Match 84.0% Score 16.8; DB 10; Length 431;
 Best Local Similarity 90.0% Pred. No. 9.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTACTGCAATATCTTGCC 20
 ||| ||||| ||||| |||||
 Db 303 GTTGTTGACATCTTGCC 322

RESULT 11 618 bp mRNA linear EST 05-FEB-2002
 BM077153
 LOCUS BM077153
 DEFINITION TREST-A0283 Hypocrea jecorina cDNA clone TREST-A0283 5', mRNA
 sequence.
 ACCESSION BM077153
 VERSION BM077153.1 GI:18498335
 KEYWORDS EST.
 SOURCE Hypocrea jecorina.
 ORGANISM Hypocrea jecorina
 Eukaryota: Fungi: Ascomycota: Pezizomycotina: Sordariomycetes:
 Hypocreales: Hypocreaceae: Hypocrea.

REFERENCE
 AUTHORS Chamberg, F.S., Bonaccorsi, E.D., Ferreira, A.J.S., Ramos, A.S.P.,
 Ferreira, J.R.Jr., Abraham-Neto, J., Parah, J.P.S. and El-Dorri, H.
 Elucidation of the metabolic fate of glucose in the filamentous
 fungus Trichoderma reesei using expressed sequence tag (EST)
 analysis and cDNA microarrays
 J Biol Chem. 277 (16), 13983-13988 (2002)
 21950703

JOURNAL MEDLINE
 COMMENT Contact: El Dorri, Hamza
 Department of Biochemistry
 Institute of Chemistry, University of Sao Paulo
 Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,
 BRASIL

Tel: (55) 11-38183848
 Fax: (55) 11-38183848
 Email: dorri@iq.usp.br

PCR Primers
 FORWARD: Universal M13 forward primer
 BACKWARD: Universal M13 reverse primer
 Plate: 3 row: H column: 7
 Seq primer: M13 reverse primer
 High quality sequence stop: 618
 POLYA-No.

FEATURES
 source
 Location/Qualifiers

1. 618
 /organism="Hypocrea jecorina"
 /strain="QM9414 (ATCC26921)"
 /db_xref="taxon:51453"

/clone="TREST-A"
 /clone_lib="TREST-A"
 /sex="Asexual"
 /tissue_type="Mycelia"
 /dev_stage="18 hr glycerol-grown culture"
 /lab_host="E. coli SOLR cells (kanamycin resistant)"
 /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; end of the cDNA cloned into EcoRI site of
 pBluescript. Primer: Oligo (dT). Average insert size: 1,2
 kb; Uni-ZAP XR Vector system -5' adaptor sequence:
 5'-GAATTCGACGACGAG3' -3' adaptor sequence:
 5'-CTCAGCTTTTCTTTTCTTTTCTTTT3''

BASE COUNT 108 a 176 c 162 g 172 t
 ORIGIN

Query Match 84.0%: Score 16.8; DB 13; Length 618;
 Best Local Similarity 90.0%: Pred. No. 9, 6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTACTGGAATATCTTTG 20
 ||||||| ||| |||||
 DB 75 GTTACTGGAATCTTGCC 94

RESULT 12
 AZ059099 171 bp DNA linear GSS 30-MAR-2000
 LOCUS RPCI-23-426115.TV RPCI-23 Mus musculus genomic clone RPCI-23-426115
 DEFINITION DNA sequence.
 ACCESSION AZ059099
 VERSION AZ059099.1 GI:7350336
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 171)
 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Aktinet,
 B., Levin, M., McGann, S., Tsegaye, G., Geer, K., Kroll, M., de Jong, P.,
 and Fraser, C. M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other GSS: RPCI-23-426115.TV
 CONTACT: Shaving Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buitalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buitalo.edu/orderingframe.htm)
 or from Resear ch Genetics (info@resgen.com). BAC end page:
 http://www.tigr.org/tldb/Bac_ends/mouse/bac_end_intro.html
 plate: 426 row: 1 column: 15
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source location/Qualifiers

1..171
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-426115"
 /clone.lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBACe3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 40 a 31 c 29 g 71 t
 ORIGIN

Query Match 82.0%: Score 16.4; DB 17; Length 171;
 Best Local Similarity 94.4%: Pred. No. 1, 3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTACTGGAATATCTTTG 18
 ||||||| ||| |||||
 DB 24 GTTACTGGAATTTCTTTG 41

RESULT 13
 AQ492427 393 bp DNA linear GSS 28-APR-1999
 LOCUS HS.5143.B2.D11-SP6E RPCI-11 Human Male BAC library Homo sapiens
 DEFINITION genomic clone Plate-719 Col-22 Row-H, DNA sequence.
 ACCESSION AQ492427
 VERSION AQ492427.1 GI:4691915
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 393)
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and
 Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 99380589

TITLE
 JOURNAL
 MEDLINE
 COMMENT
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buitalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buitalo.edu/ordering_bac.htm)
 or from Resear ch Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 plate: 719 row: H column: 22
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 393.

FEATURES

source location/Qualifiers

1..393
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate-719 Col-22 Row-H"
 /clone.lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACe3.6 vector at EcoRI sites"
 BASE COUNT 109 a 59 c 69 g 152 t 4 others
 ORIGIN

Query Match 82.0%: Score 16.4; DB 17; Length 393;
 Best Local Similarity 94.4%: Pred. No. 1, 4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTACTGGAATATCTTTG 18
 ||||||| ||| |||||
 DB 37 GTTACTGGAATACCTTTG 54

RESULT 14
 AW760469 418 bp mRNA linear EST 03-DEC-2001
 LOCUS s150g04.y1 Gm-cl027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-cl027-4783 5', similar to SW: H32_MEDSA P11105 HISTONE H3.2,
 MINOR. [3] SW: H32_MEDSA TR: Q43202 ; mRNA sequence.
 ACCESSION AW760469
 VERSION AW760469.1 GI:7692361
 KEYWORDS EST.
 SOURCE soybean.

ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 607.084 Seconds

(without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579a-22

Perfect score: 28

Sequence: 1 aagaagaaagatgcaagatattcaaa 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

otal number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rod:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_higo_hum:*
40: em_higo_mus:*
41: em_higo_other:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	DB ID	Description
1	28	100.0	28	AX306863	AX306863 Sequence
2	28	100.0	39	AX306869	AX306869 Sequence
3	28	100.0	1789	E09772	E09772 The base se
4	28	100.0	2007	AR089410	AR089410 Sequence
5	28	100.0	2007	AR093610	AR093610 Sequence
6	28	100.0	2332	SABBP	Y00688 Staphylococ
7	28	100.0	2332	E03736	E03736 DNA sequenc
8	28	100.0	2454	SEMECAPB	X52592 S. epidermi
9	28	100.0	2455	E09771	E09771 The base se
10	28	100.0	2456	SAMECAPB	X52593 S. aureus m
11	28	100.0	2456	AX110445	AX110445 Sequence
12	28	100.0	5596	SSK8MECA	Y13096 S.scluri me
13	28	100.0	6368	SSK3MECA2	Y14051 Staphylococ
14	28	100.0	9047	SAMECAPB	AB063173 Staphyloc
15	28	100.0	21777	AB063173	AB063172 Staphyloc
16	28	100.0	26030	AB063172	AB063172 Staphyloc
17	28	100.0	39332	AB033763	AB033763 Staphyloc
18	28	100.0	58237	D86934	D86934 Staphylococ
19	28	100.0	68256	AB037671	AB037671 Staphyloc
20	28	100.0	290250	AP004822	AP004822 Staphyloc
21	28	100.0	298050	AP003129	AP003129 Staphyloc
22	28	100.0	349999	AP003358	AP003358 Staphyloc
23	26.4	94.3	5806	SSK3MECA1	Y13052 S.scluri me
24	23.2	82.9	5068	SSK1MECA	Y09223 S.scluri me
25	23.2	82.9	6684	SSK1MECA	Y13094 S.scluri me
26	23.2	82.9	109792	AL158820	AL158820 Homo sapi
27	23.2	82.9	131238	HSAA05021	AL121673 Human DNA
28	23.2	82.9	151163	HSAA05021	AL121673 Human DNA
29	23.2	82.9	243457	AC0099414	AC0099414 Mus muscu
30	22.4	80.0	153468	AC022730	AC022730 Homo sapi
31	22.2	79.3	20786	AP004516	AP004516 Lotus jap
32	22.2	79.3	150728	AL158034	AL158034 Homo sapi
33	22.2	79.3	155340	AC079856	AC079856 Homo sapi
34	22.2	79.3	164598	AC093212	AC093212 Homo sapi
35	22.2	79.3	165434	AC022448	AC022448 Homo sapi
36	22.2	79.3	196117	AC110078	AC110078 Homo sapi
37	22.2	79.3	201340	AC018872	AC018872 Homo sapi
38	21.8	77.9	624	PD088230	U88230 Puccinia dr
39	21.8	77.9	151389	AC097513	AC097513 Homo sapi
40	21.8	77.9	170931	AC129656	AC129656 Rattus no
41	21.6	77.1	33446	AC090352	AC090352 Homo sapi
42	21.6	77.1	64102	AC102773	AC102773 Mus muscu
43	21.6	77.1	71235	AC005009	AC005009 Homo sapi
44	21.6	77.1	71591	AL772369	AL772369 Human DNA
45	21.6	77.1	83809	AL136145	AL136145 Human DNA

ALIGNMENTS

RESULT 1
AX306863
LOCUS
DEFINITION Sequence 22 from Patent EP1160333.
ACCESSION AX306863
VERSION AX306863.1 GI:117894685
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 Taya, T., Ishiguro, T. and Saito, J.
AUTHORS
TITLE Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
JOURNAL Patent: EP 1160333-A 22 05-DEC-2001

FEATURES Tosoh Corporation (JP)
source Location/Qualifiers
1..28
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 17 a 2 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Py 1 AAGAGAAAAAGATGGCAAGATATTCAA 28
Db 1 AAGAGAAAAAGATGGCAAGATATTCAA 28

RESULT 2
AX306869/c AX306869 39 bp DNA linear PAT 14-DEC-2001
LOCUS Sequence 28 from Patent EPI1160333.
ACCESSION AX306869
VERSION AX306869.1 GI:17894691
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Taya,T., Ishiguro,T. and Saito,J.
TITLE Oligonucleotides and method for detection of meca gene of methicillin-resistant *Staphylococcus aureus*
JOURNAL Patent: EP 1160333-A 28 05-DEC-2001;
Tosoh Corporation (JP)
FEATURES Location/Qualifiers
source 1..39
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Probe"

BASE COUNT 5 a 7 c 4 g 23 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Py 1 AAGAGAAAAAGATGGCAAGATATTCAA 28
Db 33 AAGAGAAAAAGATGGCAAGATATTCAA 6

RESULT 3
E09772 1789 bp RNA linear PAT 29-SEP-1997
LOCUS The base sequence of modified meca DNA.
DEFINITION E09772
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS JP 1995209294-A/2.
Staphylococcus aureus.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 1789)
AUTHORS Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
TITLE NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 2 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PI 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA.

PI SUGURO KAZUYA
PC G01N33/53, C07K14/31, C12N1/21, C12N15/09, C12P21/02, (C12N1/21, PC
C12R1:19),
PC (C12P21/02, C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH FT source 1..1789
FT 1..1608 /organism="Staphylococcus aureus" FT CDS
FT /product="Modified meca".
FEATURES Location/Qualifiers
source 1..1789
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

BASE COUNT 735 a 263 c 302 g 489 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 1789;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Py 1 AAGAGAAAAAGATGGCAAGATATTCAA 28
Db 549 AAGAGAAAAAGATGGCAAGATATTCAA 576

RESULT 4
AR089410 AR089410 2007 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 169 from patent US 5994066.
DEFINITION AR089410
ACCESSION AR089410
VERSION AR089410.1 GI:10016167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..2007
/organism="unknown"

BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Py 1 AAGAGAAAAAGATGGCAAGATATTCAA 28
Db 948 AAGAGAAAAAGATGGCAAGATATTCAA 975

RESULT 5
AR093610 AR093610 2007 bp DNA linear PAT 08-SEP-2000
LOCUS Unknown.
DEFINITION AR093610
ACCESSION AR093610
VERSION AR093610.1 GI:10020359
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron,M.G., Ouellette,M. and Roy,P.H.
TITLE Species specific and universal DNA probes and amplification primers

to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
Patent: US 6001564-A 169 14-DEC-1999;

JOURNAL
FEATURES

Location/Qualifiers
1..2007

BASE COUNT 855 a 270 c 341 g 541 t

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAAAAAAGATGCCAAGATATTCAA 28
|||||

DB 948 AAGAAAAAAGATGCCAAGATATTCAA 975

RESULT 6

APBP

DEFINITION 2322 bp DNA linear BCT 12-SEP-1993
Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.

ACCESSION

VERSION Y00688.1 GI:46628
KEYWORDS penicillin-binding protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus

REFERENCE

AUTHORS

1 (bases 1 to 2322)
Song,M.D., Machi,M., Doi,M., Ishino,F. and Matsushashi,M.
Evolution of an inducible penicillin-target protein in
methicillin-resistant Staphylococcus aureus by gene fusion

JOURNAL

PUBMED 87304805
FEBS Lett. 221 (1), 167-171 (1987)

REFERENCE

AUTHORS

2 (bases 1 to 2322)
Kyffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.F.,
Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus

JOURNAL

PUBMED 91033056
epidermidis
Gene 94 (1), 137-138 (1990)

COMMENT

FEATURES

source

CDS

Location/Qualifiers
1..2322
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"
1..2013
/note="penicillin-binding protein (AA 1-670)"
/codon_start=1
/transl_table=11
/protein_id="CAA68684.1"
/db_xref="GI:46629"
/db_xref="SWISS-PROT:P07944"
/translation="MKIKIIVLILIVVPGIYFVASKDEINNTIDAEKPKFKO
VTKDSYISKDNGEVEKTERPIKITYNSLGYKDIOTDRKIKKSKNKKRPADQYKIK
TNYGIDNRVQFNFVEKEDGMKLDHSHVILPGMKDOSHIEHLKSRGKILDRNNV
ELANTGIDNRVQFNFVEKEDGMKLDHSHVILPGMKDOSHIEHLKSRGKILDRNNV
KMDVILSDPAKFKPHLTNMTESRNPPLKATSHLIGYVGPINSEELKQEKYKDDA
VIGKKGLFKIYDKKLOHEDGYRTIVRVDNNSNTAHTLIEKKKDGODIOLTDKAV
OKSIYNMKNDYSGCTAIHPOTGELLAVTSPYVYPPMYGMSMEYENKLTEDKKEP
LLNKFOITTSRGTOKITAMGLNKKTLDTKSTKIGCKGKQKSKGYNVTFEY
VNGNDLQVLESNDIFPARVALELGSKEKKGKGLGVGDIPSDTPTNAQISNK
NLDEILADSGYGGGELLINVOILSTYSALENNGNINAPHLIDTNNKWKNNIIS
KENINILNDGMOVYNNKTHKEDIYRSVANNLIGKSGTALKKMKOGCTGQIGFISYDK
DNPMMMAIINKVDODKCMASYNAKISGVYDELYENCKRYDIDE"

BASE COUNT

940 a 324 c 389 g 669 t

ORIGIN

Query Match 100.0%; Score 28; DB 1; Length 2322;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

1 AAGAAAAAAGATGCCAAGATATTCAA 28
|||||

DB 954 AAGAAAAAAGATGCCAAGATATTCAA 981

RESULT 7

LOCUS

DEFINITION 2322 bp DNA linear PAT 29-SEP-1997
DNA sequence of PBP2' gene for determination of methicillin resistance.

ACCESSION

VERSION E03736.1 GI:2171951
KEYWORDS JP 1992169200-A/9.

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 2322)
Murakami,K., Nakamura,E., Teraoka,H., Wada,K., Minamide,W. and
Murakami,K.
DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
Patent: JP 1992169200-A 9 17-JUN-1992;

JOURNAL

COMMENT

OS

(methicillin resistant)staphylococcus aureus
PN JP 1992169200-A/9
PD 17-JUN-1992
PF 31-OCT-1990 JP 1990296708
PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI,
PI MINAMIDE MAKIYO, MURAKAMI KAZUHIISA
PC C1201/68,C12N15/11;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;

FH

FT

misc.feature 1..2322
/note="PBP2' gene for determination of FT
methicillin resistance".

FT

FT

FT

FT

FT

Location/Qualifiers
1..2322
/organism="unidentified"
/db_xref="taxon:32644"

FEATURES

source

BASE COUNT 939 a 324 c 390 g 669 t

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2322;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

1 AAGAAAAAAGATGCCAAGATATTCAA 28
|||||

DB

DB

954 AAGAAAAAAGATGCCAAGATATTCAA 981

RESULT 8

SEMECAPB

LOCUS

DEFINITION 2454 bp DNA linear BCT 12-SEP-1993
S. epidermidis meca gene for PBP2' (penicillin binding protein 2').

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Direct Submission

JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE 2 (bases 1 to 2454)
AUTHORS Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E., Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
TITLE Sequence comparison of meca genes from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
JOURNAL 3 (bases 1 to 2454)
REFERENCE Ryffel,C.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE 4 (bases 1 to 2454)
AUTHORS Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E., Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
TITLE Sequence comparison of meca genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
COMMENT See also <X52593-4> and <Y00688>.
PUBMED 2227446
FEATURES Data kindly reviewed (23-JUL-1990) by C. Ryffel.
SOURCE location/Qualifiers
1..2454
/organism="Staphylococcus epidermidis"
/strain="WT55"
/db_xref="taxon:1282"
/clone="WT80/MT79"
80..85
/note="35 region"
101..105
/note="10 region"
130..134
/note="ribosome binding site"
141..2159
/note="primary transcript"
141..2147
/note="PBP2' (AA 1 - 668)"
/codon_start=1
/transl_table=1
/protein_id="CAA36828.1"
/db_xref="GI:46994"
/db_xref="SPTREMBL:O54113"
/translation="MKRIKIVPLILIVVVGCIYVYASKKEINNTIDAIEDKNFKQ
VYKSSYISKSDNGEVEEMTERPIKINSLGVKDINTQDRKIKVSKNKRKRVDOYKIK
TNGNIDRWQFNFVKEGDMKLDMDHSLIIPGMQDOSIHIENLSEKGLIDRNWV
ELANTGTAEVIGIVPNVSKKDYKAIKELISIDYIKOOMDNMVAQDDTFVLKTVK
KMEVYLSDFAKKPHLTTNETSRNYPILGAKTSHLGLYVGPINSEELKOKEYKAKDA
VICKGKLEKLYDKKLOHEDGYRVTYVDNSNTAHLTLIEKKKDKGKDIOUDDAKYKA
STYNNKNDGSGTAIHPOTGELLALVSTPSYVYPPMGKSNEEYINKLLEDEKPEL
NKEQITTSRSTOKILTAMIGLNKKTLDDTSYKIDGKGQKDSKSGVNTVTEYVN
GNDLKOALIESDNIPFARVALELGSKEKKEKKGKLCVGEDIPSDYFVNAOISNNL
DNEIILADSGYCGGELLINPVQILSTYSALENNGNINAPHLKDTNKNVKKNIISK
NINLITDGMQOYVKTHKEDIYRSYANLICKSGTALFKMKOGFTGHOIGPISYDKON
PNMMAINVKDQVDDKGMASYNNAKISGVYDELTENGNKKRYDIDE"
old_sequence 441..448
/note="altaaac was ac in [1]"
old_sequence 641..643
/citation-[1]
old_sequence 652..653
/citation-[1]
old_sequence 731..733
/note="ta was tta in [1]"
old_sequence 780..781
/note="caa was ca in [1]"
old_sequence 780..781
/note="ct was ctt in [1]"
/citation-[1]
BASE COUNT 997 a 345 c 398 g 714 t

ORIGIN
Query Match 100.0%; Score 28; DB 1; Length 2454;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGAAAAAAGATGCGCAAGATATTCAA 28
Db 1088 AAGAAAAAAGATGCGCAAGATATTCAA 1115
RESULT 9
E09771 2455 bp RNA linear PAT 29-SEP-1997
LOCUS The base sequence of meca DNA.
DEFINITION E09771
ACCESSION E09771
VERSION E09771.1 GI:22026400
KEYWORDS JP 1995209294-A/1.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2455)
AUTHORS Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
TITLE NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
PATENT: JP 1995209294-A 1 11-AUG-1995;
JOURNAL KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
COMMENT PN JP 1995209294-A/1
PD 11-AUG-1995
PP 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KENICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53.C07K14/31.C12N1/21.C12N15/09.C12P21/02.C12N1/21. PC
C12R1:19).
PC (C12P21/02.C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key location/Qualifiers
FT source 1..2455
FT 134..2146 /organism="Staphylococcus aureus" FT CDS
FEATURES FT
source location/product="meca protein".
1..2455 /organism="Staphylococcus aureus"
/db_xref="taxon:1280"
BASE COUNT 997 a 344 c 401 g 713 t
OY 1 AAGAAAAAAGATGCGCAAGATATTCAA 28
Db 1087 AAGAAAAAAGATGCGCAAGATATTCAA 1114
Query Match 100.0%; Score 28; DB 6; Length 2455;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGAAAAAAGATGCGCAAGATATTCAA 28
Db 1087 AAGAAAAAAGATGCGCAAGATATTCAA 1114
RESULT 10
SAMECAPB 2456 bp DNA linear BCT 12-SEP-1993
LOCUS S. aureus meca gene for PBP2' (penicillin binding protein 2').
DEFINITION A052593
ACCESSION A052593
VERSION A052593.1 GI:46610
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2456)

AUTHORS Ryffel, C.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of Medical Microbiology, Gioriasstr 32, CH-8028 Zuerich, Switzerland
 REFERENCE 2 (bases 1 to 2456)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machlin, I., Reynolds, P.E., Barberis-Maino, L., Kayser, F.H. and Berger-Bach, B.
 TITLE Sequence comparison of meca genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT See also <X52592> and <X00688>.
 DATA kindly reviewed (23-JUL-1990) by C. Ryffel.
 FEATURES
 Source
 Location/Qualifiers
 1..2456
 /organism="Staphylococcus aureus"
 /strain="NCTC8325, isolate-BB270"
 /db_xref="taxon:1280"
 /clone_1lb="EMBL-3"
 80..85
 /note="35 region"
 101..105
 /note="10 region"
 130..134
 /note="ribosome binding site"
 141..2153
 /note="Primary transcript"
 141..2147
 /note="PBP2' (AA 1-668)"
 /codon_start=1
 /protein_id="CAA36829.1"
 /db_xref="GI:46611"
 /translation="MKKIKIVPLILIVVVGFGIYFVASKDEINNTIDAIEDKKNFKO
 VYKDSYISKDNCEVENTERPIKLYNSLGYKDIIDORIKIKVSKNKKRVDAYKIK
 TNGNIDNVOENFCEKEDGMMKLDMDHSVILIPGMOKDSIIHENTKSRGKILDBNN
 ELANTGTHMRGLGIPIKYNYSKKDYAKINELSTSDYINNKIKIGYKNIIPSEFTYK
 KMDYLSDFAKPHLITTTETESRNPLEKATSHLGIYGPINSEELKQEKYKIDDA
 VIKRKGLEKLYDKLQHEHDYRVITVDNSNTIAHTLLEKKKDKDKDIOITIDAVOK
 SYNNKMDVSGSIAIPQTEGLALAVSTPSYDVYPPWYGMSNEYNKLTEDKKEPL
 NKPOITTPSGSTOKILTPAMIGLNNKTLDKSYKIDGCMOKDKMGCVNTRYEVN
 GNIDLKQIESSDNIFEFARVALLESGKKEFGKKGAGVEDIPSDYPYNAQISNKE
 DNELLADSGYGOEELINPVOLISYALSALNNNGINAPHLIKOTKKNVWKNKISKE
 NINILNDSMOQVYNTKIKEDYRSTANIGSGTRLELKMKGESGRQIGWFLISYDKDN
 PNMMKATINVKVDYDKGMASYNKAKISCKVYDELVENGNNKKYDIDE"
 NAME COUNT 1001 a 344 c 396 g 715 t
 ORIGIN
 Query Match 100.0%; Score 28; DB 1; Length 2456;
 Best Local Similarity 100.0%; Pred. No. 4.1;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGAGAAAAAGATGCCAAGATATTCAA 28
 |||||||||||||||||||||||||||||||
 Db 1088 AAGAGAAAAAGATGCCAAGATATTCAA 1115
 RESULT 11
 AX110445 2456 bp DNA linear PAT 30-APR-2001
 LOCUS Sequence 1178 from Patent WO0123604.
 DEFINITION AX110445
 ACCESSION AX110445
 VERSION AX110445.1 GI:13926737
 KEYWORDS
 SOURCE Staphylococcus aureus subsp. aureus NCTC 8325.
 ORGANISM Staphylococcus aureus subsp. aureus NCTC 8325
 Bacteria: Firmicutes: Bacillales: Staphylococcus.
 REFERENCE 1 (bases 1 to 2456)
 AUTHORS Bergeon, M.C., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
 Picard, F.J. and Roy, P.H.

TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms
 REFERENCE Patent: WO 0123604-A 1178 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES
 Source
 Location/Qualifiers
 1..2456
 /organism="Staphylococcus aureus subsp. aureus NCTC 8325"
 /db_xref="taxon:93061"
 BASE COUNT 1001 a 344 c 396 g 715 t
 ORIGIN
 Query Match 100.0%; Score 28; DB 6; Length 2456;
 Best Local Similarity 100.0%; Pred. No. 4.1;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGAGAAAAAGATGCCAAGATATTCAA 28
 |||||||||||||||||||||||||||||||
 Db 1088 AAGAGAAAAAGATGCCAAGATATTCAA 1115
 RESULT 12
 SSK8MECA 5596 bp DNA linear BCT 16-JAN-1998
 LOCUS S.scituri meca gene, strain K8 (ATCC700063).
 DEFINITION Y13096
 ACCESSION Y13096
 KEYWORDS Y13096.1 GI:2791919
 VERSION meca gene; meci gene; mecR1 gene; NTOREF101; NTOREF78; ORF142.
 SOURCE Staphylococcus scituri.
 ORGANISM Staphylococcus scituri
 Bacteria: Firmicutes: Bacillales: Staphylococcus.
 REFERENCE Wu, S., de Lencastre, H. and Tomasz, A.
 AUTHORS 1 (bases 1 to 5596)
 TITLE Genetic organization of the meca region in methicillin-susceptible
 JOURNAL and methicillin-resistant strains of Staphylococcus scituri
 MEDLINE J. Bacteriol. 180 (2), 236-242 (1998)
 PUBMED 9440511
 COMMENT 2 (bases 1 to 5596)
 FEATURES
 Source
 Location/Qualifiers
 1..5596
 /organism="Staphylococcus scituri"
 /strain="K8 (ATCC700063)"
 /sub_species="rodentius"
 /db_xref="taxon:1296"
 1..236
 /gene="NTOREF78"
 <1..236
 /gene="NTOREF78"
 /codon_start=3
 /transl_table=11
 /protein_id="CAA73550.1"
 /db_xref="GI:2791920"
 /db_xref="SPTREMBL:O54284"
 /translation="AFKLPDCHGTSKUNLIEODHRHIVKRTYOSINTAKTTLK
 GIECIYALVKKNRSI.OIYGFSPCHEISIMLAS"
 complement(485..856)
 /gene="mecI"
 complement(485..856)
 /gene="mecI"
 /codon_start=1
 /transl_table=11
 /product="MecI protein"
 /protein_id="CAA73545.1"
 /db_xref="GI:2791921"
 /db_xref="SPTREMBL:O54285"
 /translation="MDNKTYEISSAEMVPMNIIMKKKASANYHIEIYONOKDSKPT
 IRTLITRLYKGFIDRRKDNKIFQYYSILVESDIDIKYTSKNFINKVGCFNSLVINP
 VKEDLSDDEIEELRNILNKK"

gene complement(join(856. .2613,2620. .2626,2638. .2643))
/gene="mecR1"
CDS complement(856. .2613)
/gene="mecR1"
/codon_start=1
/transl_table=11
/product="MecR1 protein"
/protein_id="CA73546.1"
/db_xref="GI:2791922"
/translation="MISSFLMSTSIISLTITCVFLVRLMYIKYTONIMSKIMLVLV
VSTILPILPYKISNFTFSKDMNRNVSDDTSSVSHMLDGOSSVTOKDAIINQOFER
SNITVMILLWVFGSLCLEFMIAFRQIDVKKSSLESSTYLNELRVQSKMOPFK
HITISSNIDNPVFGVLVKSQIVLPVVEVTMDKEIEYIILHELSHVSHDIIFNO
LYVFKMIFFMFPALYISKTMDCCEVCDRNVKLILNREHIRGESILKCSILKS
OHINNVAOYLIGNSNIKERVKYIALYDSMPKPNRNKRIYAVIVGCSISLLOAPLS
AHVQODYETVVSQKLNOLAPYFKGDSFVLVNERBOAIVSYNPESSORSPTNT
KYIYALMAFDONLISLNHTEQCDKHQYPPKEMNOONLNSMKYSVNNYELNLKH
LRQDEKSYLDLIEYGNBEISGENITNNESSLKISALEOVNLLNKKOHNFPNKAI
EKVENSMTLKQDKYKYVGKTGTIVNHKEANGWVGVEYTKDNTYYFATHLKGEDNA
NGEKAQOISERILKEMELI"
gene complement(865. .869)
/gene="mecI"
RBS complement(865. .869)
/gene="mecI"
RBS complement(2620. .2626)
/gene="mecR1"
-10_signal complement(2638. .2643)
/gene="mecR1"
gene 2652. .2657
/gene="mecR1"
-35_signal 2652. .2657
/gene="mecR1"
gene complement(2663. .2668)
/gene="mecR1"
-35_signal complement(2663. .2668)
/gene="mecR1"
gene 2676. .4719
/gene="mecR1"
-10_signal 2676. .2681
/gene="mecR1"
RBS 2702. .2707
/gene="mecR1"
CDS 2713. .4719
/gene="mecR1"
/codon_start=1
/transl_table=11
/product="MecA protein"
/protein_id="CA73547.1"
/db_xref="GI:2791923"
/db_xref="SPTREMBL:054286"
/translation="MKKIKIYPLILIVVVGFGIYFYASKDKEINNTLDATEDKNFKO
VYKDSYISKSDNCEVEETRPPIKITIYNSLGYKODINODRKIKKSKKKRDAOYKIK
TNGNIDRNOVFNVEKDGMMKLMDHSHV11PGMKQDOSIHENLKSBRGLIDRNMY
ELANTGTAYEIGVIPKNVSKDYKAIAKEISIDSY1KQOMDQWVDDTFVPLKYK
KMEYLSDFAKFHLITTNESERNYPLEKATSHLGYVGPINSELSKQKEYKGKYDA
VIGKGLKLEKIDKLOHEDGYRATIVDONSNTIAHTLEKKKDKGKDIQTLIDAKVOK
SIYNNKNDGCGTA1HPOTGELLALVSTPSDYVPEYMGSGNEENKILTEDKKEPLL
NKQITTSPGSTOKILITAMIGLNKKTLDKTSYKIDCKGMOKDSMGCVNTRYEVVN
GNIDLKOAISSDNIFFARVALEIGSKKFFEKGMKLCYGEDIPSDYPPYNAQISKNL
DNETLLADSGYGEELINPVQILSISALENNGNINAPHILKDTKKNVKKNTISSE
NINLITDGMQOVNKTKEIDYRSYANLIGKSGAELKMKOGETGRQIGWPIISYDKDN
PNMMMAIINVKDQKGMASYNKISGRVYDELYENGKNKYDIDE"
gene complement(4765. .5266)
/gene="ORF142"
CDS complement(4765. .5193)
/gene="ORF142"
/codon_start=1
/transl_table=11
/protein_id="CA73548.1"
/db_xref="GI:2791924"
/db_xref="SPTREMBL:054520"
/translation="MKYDDPIVGETFKTKSLHTEDEELIOPATTEFDPOYMIIDKEKAE
QSRFGI1ASGMHTLSISFKLWEEGKTEEGEVVAGTOMNNVKTIKPYPGNTLVIAE

RBS ITNKS1KKEGTYVSLSTYNEHEIVFKEGTALINNS"
complement(5200. .5205)
/gene="ORF142"
-10_signal complement(5238. .5243)
/gene="ORF142"
-35_signal complement(5261. .5266)
/gene="ORF142"
gene complement(5290. .5596)
/gene="NTORF101"
CDS complement(5290. .>5596)
/gene="NTORF101"
/codon_start=2
/transl_table=11
/protein_id="CA73549.1"
/db_xref="GI:2791925"
/db_xref="SPTREMBL:054616"
/translation="SFNVVLKLAEBEIMPOTYNAVIFHTTSPFEDMFTLLDYCNAKIV
NTEDAKLTAKVKKVKEAGYELNVTNVTNPARANQLANMGVDGIFTDNADKNVHLSQ"
BASE COUNT 1991 a 856 c 821 g 1928 t
ORIGIN
Query Match 100.0%; Score 28; DB 1; Length 5596;
Best Local Similarity 100.0%; Pred. No. 3.7; Mismatches 0; Gaps 0;
Matches 28; Conservative 0; Indels 0;
OY 1 AAGGAAAAAGATGGCAAGATATTCAA 28
DB 3660 AAGCAAAAAAGATGCCAAGATATTCAA 3687
RESULT 13
SSK3MECA2
LOCUS SSK3MECA2 6368 bp DNA linear BCT 16-JAN-1998
DEFINITION S.scituri meca2 gene, strain K3 (MM2).
ACCESSION Y13095
VERSION Y13095.1 GI:2791912
KEYWORDS CTR0F261 gene; meca2 gene; mecI gene; mecr1 gene; NTORF101; ORF142.
SOURCE Staphylococcus scituri.
ORGANISM Staphylococcus scituri.
REFERENCE Wu,S., de Lencastre,H. and Tomasz,A.
AUTHORS Genetic organization of the meca region in methicillin-susceptible
TITLE and methicillin-resistant strains of Staphylococcus scituri
J. Bacteriol. 180 (2), 236-242 (1998)
JOURNAL 98101461
MEDLINE 9440511
PUBMED 2 (bases 1 to 6368)
REFERENCE Wu,S.
AUTHORS Direct Submission
TITLE Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
JOURNAL University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences L14020, X52593, Y09223.
FEATURES
source Location/Qualifiers
1. .6368
/organism="Staphylococcus scituri"
/strain="K3 (MM2)"
/sub_species="rodentius"
/db_xref="taxon:1296"
complement(1. .883)
/gene="CTR0F261"
complement(<1. .784)
/gene="CTR0F261"
/codon_start=1
/transl_table=11
/protein_id="CA73539.1"
/db_xref="GI:2791913"
/db_xref="SPTREMBL:054280"
/translation="MENIININDMKRLREIYNHNNISPTQISKNLEINKATISSII,
NKLKYSILVNEVGCDSTKSGCRKPIILKYNHLVGYFISIDLYSSVEVWYNYFDCNV
IKHRSYDLPDEKVSIIISIIKKHIDIOEKIDTYNGLIGVSYIIGHVVDNROHVTYI,PP
HETGCSIAKRIKETTNPVYVEDEANISALIEYENFNHNSYNNLALSLSHKIGAGL
IINQILIRGANGEGEIGKTLVSVSDNVEIFHKIEDIFSOEA"

[illegible]

	gene	ELANTGAAVETIGIVPKNVKSKDDKAIAKEUITSIPDYIKOOMDNWQODDFVLAKTV KMDEYLSDPFAKKRHLLTNTNEPESRNPYLEKATSLHGLGVCPINSEELOKRYKGIKDA VIGKRGLEKLKYDKLLOHEDESVRTIYDNSNTLAHTIEKRKKDGKDLOLTIDAKVK SITNNMKNDSGSCTAIHPOTGELLALVTSTSYDVYPPIYMKSNEYNKLVTEDEKPL NKOYITTSPTSGSTOKILTPMGELGNKKTLTDISTYKIDGQMQRSGWGYVTVYEVN ENIDLAKOIESSDIFPARVALLEGSKPFKKMKLGVDGIDPSDVPFYAOJISNKL DNIELLDADSGGGGEILLINVOILISITSALENNGINAPHLIDTKRWKKNIISK NILNLDTMOOVYVKKTHKEEDITYRSYALIGKSGTAELKMKOGCTGRIGMFISYADKN PHLMMAINVADYDPKGMASYNAKTISGKVYDELVEYNGKKKIDIDE"					
CDS		/gene="ORF142" complement(5537, .5965) /gene="ORF142" /codon_start=1 /transl_table=11 /protein_id="CAA33543.1" /db_xref="GI:2791917" /db_xref="SPTREMBL:O54520" /translation="MKYDDIIVGTFEFTKSLHITTEEIIOFATTFPDPOVMIDKEKAE OSRRKGIIASGMHTLISFKLWEEGVCGEVAGQOMNWNIKIPVYPCNTLYVIAE ITNKKSIKKENGMLVTVSLTYNNEEIIVFGVETALLINS"					
RBS		complement(5972, .5977) /gene="ORF142" complement(6010, .6015) /gene="ORF142" complement(6033, .6038) /gene="ORF142" complement(6062, .6368) /gene="NTORF101" complement(6062, .>6368) /gene="NTORF101" complement(6062, .6368) /gene="NTORF101"					
gene		/codon_start=2 /transl_table=11 /protein_id="CAA33544.1" /db_xref="GI:2791918" /db_xref="SPTREMBL:O54616" /translation="SFNVVIVLAFELIMPOYINRAVIFHTTSPREDKRTLIDYCNAKIV NTEBAKYLTKKVMKVVKGAGYELAVWTVYVKKARANOIANMGVDSIGFTDNMRMYLSO"					
CDS							
BASE COUNT	2230 a 998 c 884 g 2256 t						
ORIGIN							
Query Match	100.0%; Score 28; DB 1; Length 6368;						
Best Local Similarity	100.0%; Prd. NO. 3.7; 0; Indels 0; Gaps 0;						
Matches 28; Conservative 0; Mismatches							
QY 1 AAAGAAAAAAGATGGCAAGAATTATTCGA 28 							
Dbb 4432 AAAGAAAAAAGATGGCAAGAATTATTCGA 4439							
RESULT 14 SAMEACARI1							
LOCUS	SAMEACARI1						
DEFINITION	Staphylococcus aureus mecA, mecRI gene, BCT 16-JAN-1998						
ACCESSION	Y14051						
VERSION	Y14051.1 GI:2791983						
KEYWORDS	mecA gene; mecI gene; mecRI gene; ORF142; ORF145; ORF224; ORF44; PRB2A; repressor protein; transposase.						
SOURCE	Staphylococcus aureus						
ORGANISM	Bacteria; Firmicutes; Bacillales; Staphylococcus. 1 (bases 1 to 9047)						
REFERENCE	Wu,S. Direct Submission						
AUTHORS	Submitted (27-JUN-1997) S. Wu, Laboratory of Microbiology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA						
JOURNAL	2 (bases 1 to 9047) Wu,S., de lencastre,H. and Tomasz,A. Genetic organization of the mecA region in methicillin-susceptible and methicillin-resistant strains of Staphylococcus sciuri						
TITLE	J. Bacteriol. 180 (2), 236-242 (1998)						
JOURNAL	98101461						
MEDLINE							

PUBMED FEATURES source	9440511	location/Qualifiers 1. 9047 /organism="Staphylococcus aureus" /strain="BMS-1" /db_xref="taxon:1280" complement(<1. .505) /note="ORF168" /codon_start=1 /transl_table=11 /product="putative repressor" /protein_id="CAA74373.1" /db_xref="GI:2791984" /db_xref="SPTREMBL:053708" /translation="MYNYFDGNYLKHESYDLDPKEVSSILSIKKHIDIOEKIDTYNG LLGVSVAIHGVNNEOHVTLPEHTEGISIACKIKETVNPVVEANLMSALERN FNHLSSYNNLIALSIHKIGAGLIINNQLVRANGANGEGIKTLVSKVSDNVEIFHKI EDIFSOEA"
CDS		complement(1244. .1615) /gene="mecI" complement(1244. .1615) /gene="mecI" /codon_start=1 /transl_table=11 /product="MecI protein" /protein_id="CAA74374.1" /db_xref="GI:2791985" /translation="MDNKKYELISSAEWEVNNIIMKKYASANNIIEEIOQKQMSPKT IRLIRLRYKKGFIIDRKKDKFIQYYSLSVESDIIKYTSKNFINKYKGGFNSLVNF VEKEDLSODEIEELRNILKK" complement(1615. .3372) /gene="mecR1" complement(1615. .3372) /gene="mecR1" /codon_start=1 /transl_table=11 /product="MecR1 protein" /protein_id="CAA74375.1" /db_xref="GI:2791986" /translation="MLSSFLMLSLISSLLTICVFLVRLMRYKTTONIMSHKIMLVLY VSTLPIPIFYKISNFTFSKDMNRRNSDITSSVHMLDGOSSVTKDLAINVQNET SNITVILLIIVFGSLCLFMYIKAFQIDIVIKSSLSLESSYLRKLVCOQKQFYK HITISSNIDNPFGVLGKYSQIVLPVVVETIMDKKEIYILHETLSHVSHLIEFQ LYVFKMIFWNPALYISKTMNDCEKVDNRNKLINRHEHTRCESLILCSILKS OHINNAOYLLGFNSNIKERVYIAYDMPKRNKRRIIVAYIVCSISLLIQAPLLS AHVOQKRYETNVSKKINOLAPYFKGDSFVLNREQAYSIYNPESKORYSPNST YKTYLADAFDONLSLNTEDQDKHQTFPEKNODONLNSMKSVNNTYELNKH LRQDEKSYLDLIEYGNELISGENENESSLKISALEOVNLKMKQNNMHFDNKA EKVENSITLKQKDTYKYVGTGIVNHEANGMFGVETKDTYFATHLKGEDNA NGEKAQOISERIILEMELI"
gene		3472. .5478 /gene="meca" 3472. .5478 /gene="meca" /codon_start=1 /transl_table=11 /product="PBP2A" /protein_id="CAA74376.1" /db_xref="GI:2791987" /db_xref="SPTREMBL:053707" /translation="MKKITYPLLLIYVYVFGIYFASKDEINNTIDAIEDKRFQ VVKDSYISKSDNGEVEWTEPIKITYNSLVDKINIDQRKIKKYSKKKRVADQYKIK TNYGNIIDRNVQFNPKEDGMKLDMDHSHVILPGQKQSIHIEMLKSERGLIDRRNV ELANGTIDHMLGIVPKNVSKDYKALAEKISIEDYINNWKIKGYMKIPSPFKETVYK KDEYLSDFAKKFTLTNETESRNYPLEKATSHLLGVGINSLELKOKEXYKQKDA VIGKGLIEKLYDKKLOHEDGYRTIYDNNSTIAHLIEKKKKDKRQIOLITDAKQV SIYNNKNDGSGTAIHPOGELLALVSTSYDYPPMYGMSNEVYKLTEDKKEPIL NKFOITTSPOSTOKITLAMIGLNNKTLDDKTSKIDGKQKQKDSQWGVATRVREYV GNIDLOQALIESSDNIFFARVALIEGSKKPFKMKKIDGVDIDSDYPPYVAQISNNKL DNEIILLADSCYGOCEILINPVOILISYSALENNGNINAPLIDTKKRVKKNITISE NINLNDGMOOVNKTIEKEDIYSYANLIGKSGTAELKMGESGROIGFISYDKDN PNMMAIINVKDVODKMAVNAKISGKYVDELXNGKKYDIDE"
CDS		complement(5524. .5952) /note="ORF142" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="CAA74377.1" /db_xref="GI:2791988" /db_xref="SPTREMBL:054520" /translation="MKYDQFIJGTEFTKSLHITPEEPIIOFATTPPOYVHIDKEKAE QSRPKGIASGMHTLISISPKLWBEQYGEVAGQOMNVKIKKYYIPGNTLYVIAE ITNKSIIKENGCIYVTSLSYWNENEELVFGEVYALINNS" complement(6049. .6183) /note="ORF44" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="CAA74378.1" /db_xref="GI:2791989" /db_xref="SPTREMBL:054083" /translation="MYKAGYELNVTWVTKPARANOLANKVDGIFTDNADKVVHLISQ " complement(6354. .6791) /note="ORF145" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="CAA74379.1" /db_xref="GI:2791990" /db_xref="SPTREMBL:099387" /translation="MLTVYGRGLPSKAPENTIASFKASEVEGINMLELDAVITKDE OLIIHDYLERTTNNSGEITELNVDIKRASGSMGEKFEDEHPTFPDYVKIANE YNNINLVETLKIGTGNGLATSKSMKVQVEQJLNLNQNOBELI" 8096. .8770 /note="ORF224" /codon_start=1 /transl_table=11 /product="putative transposase" /protein_id="CAA74380.1" /db_xref="GI:2791991" /translation="MNYFRKQKQKNDVITVAVGYLYRYTISYRDISFIIIRRGVNVNH STYRWQDETAPLIIQIWKKKHKKAYKMDIETVTKIKKWSYLVRAIDAECHTLIJ WLKQRDNHSAVAFIEKRLIKQFSKPOKVTIDQAPSTVAAKVIKAFKLPDCHTSK YLNMLQEDRHHKVRKTRQSIINTAKNTLKGIECIYALYKKRNRSLQYGFSPCHEI SIMLAS"
gene		
CDS		
BASE COUNT	3099 a 1469 c 1257 g 3222 t	
ORIGIN		
Query Match	100.0%:	Score 28; DB 1; Length 9047;
Best Local Similarity	100.0%:	Pred. No. 3.6;
Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
0Y	1 AAAGAAAAAGATGCAAGATATTCA 28	
Db	4419 AAAGAAAAAGATGCAAGATATTCA 4446	
RESULT 15		
AB063173	21777 bp	DNA linear BCT 09-Apr-2002
LOCUS	Staphylococcus aureus DNA, type-IV staphylococcal cassette	
DEFINITION	chromosome mec, strain:JCSCL978(8/6-3P).	
ACCESSION	AB063173	
VERSION	AB063173.1	GI:17025993
KEYWORDS		
SOURCE		
ORGANISM	Staphylococcus aureus (strain:JCSCL978(8/6-3P)) DNA.	
REFERENCE	1 Bacteria; Firmicutes; Bacillales; Staphylococcus.	
AUTHORS	Hiramatsu, K., Cui, L., Kuroda, M. and Ito, T.	
TITLE	The emergence and evolution of methicillin-resistant Staphylococcus	
JOURNAL	aureus	
MEDLINE	Trends Microbiol. 9 (10), 486-493 (2001)	
	21482917	

REFERENCE 2
AUTHORS Ma,X.X., Ito,T., Tienasaitorn,C., Jamklang,M., Chongtrakool,P.,
TITLE Boyle-Vavria,S., Baum,R.S. and Hiramatsu,K.
Novel type of Staphylococcal Cassette Chromosome mec identified in
Community-Acquired Methicillin-Resistant Staphylococcus aureus
Strains
JOURNAL Antimicrob. Agents Chemother. 46 (4), 1147-1152 (2002)
MEDLINE 21895198
REFERENCE 3 (bases 1 to 21777)
AUTHORS Xue,M.X., Ito,T., Hiramatsu,K. and Tienasaitorn,C.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2001) Teryuo Ito, Juntendo University, Department
of Bacteriology, Hongo 2-1-1, Bunkyo-ku, Tokyo 113-8421, Japan
(E-mail:teruyacmed.juntendo.ac.jp, Tel:81-3-5802-1041,
Fax:81-3-5684-7830)
FEATURES
source Location/Qualifiers
1. 21777
/organism="Staphylococcus aureus"
/strain="JCS1978(8/6-3p)"
/db_xref="taxon:1280"
/note="community-acquired MRSA strain isolated at the
University of Chicago children's hospital"
301. 21221
/note="302. 21222 or 303. 21223 or 304. 21224
type-IV SCCmec of JCS1978(8/6-3p)"
301. 326
/note="inverted complementary repeat(IR-L) of SCCmec of
JCS1978"
CDS
/rpl_type=inverted
complement(325. 1446)
/note="ORF No. CM001"
/codon_start=-1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72122.1"
/db_xref="GI:17025994"
/translation="MKMSYQIKIVMGPKSYLINEFLHOPYITLEDYIIKIDSLTRNLVE
KFTDNVEILDKIILAKTESYSGITSAALSNFIOIYNKSIEFGNGIILLOPPSVI
NOIKNSFENQYAFCEYEYPRKDLAVLNINKESTRELEGOYNALIKRIILASLYLTKKE
SRKSTVLMLYGSPGSGKTEMSKTISECGKLFKROMSNKNTMYEDVITFGNNHPS
LARDLERESNVLDERFDKYNELNSAFYTDGIGEDISOYKATMRSGITITGSE
KGEAOIRRELDPIYRFDPIEFALNDEAKNLIITRISEFPKTLSDNEKSLIPRE
EILKQYMIKI KQFTNYRHKMLVENDINLRILISAMLP"
complement(1424. 2194)
/note="ORF No. CM002"
/codon_start=-1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72123.1"
/db_xref="GI:17025995"
/translation="MKLIYFDESTADYLTAKTIIONGRESKOTIETKKNOKOTSLGKFG
IGPMSKYFESLFSIEGMMGNINRTSEKYVEKTLTNILSDFKLANEDELGITKPS
EYKLSYVENSIAHFOTISPIYLSMDGNVLVDEDSININKMHEITKLKAGYEIILAKK
NENECIVRHNKAFVNNYNLIDLSOMOLTLGVKYGIIIDIQNLPNOMAINSIGFONKY
VTSISEFTVNSFNNEOSIILEMYDII LAGVEVENLSN"
2311. 3741
/note="ORF No. M001"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72124.1"
/db_xref="GI:17025996"
/translation="MNFENYFTGKDKMLKCONLSSEKMKNSMDKLEFVYKLDITKKY
SNPSATNGYSFNLFELEFLKILLNTIEDFPYPSAKKEDDIDLEELAKKNSHFIR
ITITNTSIDINKDALKAQIYASENYSFTLEWLSAOSKSDALSFTNYNLSLDR
SSKLYRKLARIIDELMFTLMEQNTYDNEFNKQLYRVHOYDKENNAETPVYVNHDE
PDDKNSNENHGVTKYISNKPSTIKYSERTNKKLLDPEIIDLANKLYPSLAKRIINH
ITAYDIONGDESKIREKIKKMEIYKVPNNGYFLDIEDDLFTNYORLIINTIDVYKSS
TEFONFESRIDNIINSKPLISNDKFNFIKDFLSIKFSFNFIHINROSYIHGGIN
SNQYDSFLNDLYRIHLIDKYSNKDIEPLSKINTELTNAFQLFKEIKESQIKDEIY
SKKYNDLSSMSIAKALSETLNDLNE"
3861. 5651
/note="ORF No. M002"
CDS

/codon_start=-1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72125.1"
/db_xref="GI:17025997"
/translation="MNNNIEKQYPPYFLNSNGEYVTPKSNNDVEKITLSSPIIEN
KFLDSTGYEKLITDKNTEREASDITLTKRLPOLIKYGNINRRTIKSLVALOS
MKOSLPLSLYTGVGVLQSDDEGMVLSLQPYFSKEIEQSOANEIICETHYDLQPKGT
FQSMWEMYLKQVKGNNLLELAVIFGISALVTSFLRKHAFEGIIFFSTGQSGTS
TAASLAVSAGNPTKGNETLFRSMNATRNALDEGLSNNGIPIVEDELSATFROTG
LYLSITEGQRORSNNGEYKTPKNGTGVISTSEYFSDNSKONGDLVRTIENR
FTKDATNSDNIKTVALNGCHVILPYAKYLIINBEDYVIOQMEKEDHMFESIKDEFNN
TGTMRKRAVITTSKTIIGRLSTDIIDIANIRDTVIDYTHHTVSRSLADRAIDVIT
QFVAQNRGKFSDEGALKMFEENGILSIKDDHIEVMILANVRKOMLNNOHPODVNVV
NALRDKGFLADRGRTTRSVKNSNGKQSLVFYHLKLDVEFASITGLTKDKSLON
WTPSDNKAKEIFKSNANGIGPSGVHEDF"
5732. 5797
/note="ORF No. M003"
/codon_start=-1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72126.1"
/db_xref="GI:17025998"
/translation="MDLEIELADLVIFELNGTND"
5885. 7234
/gene="ccrA"
5885. 7234
/gene="ccrA"
5885. 7234
/note="ORF No. M004"
/codon_start=-1
/transl_table=11
/product="cassette chromosome recombinase A"
/protein_id="BAB72127.1"
/db_xref="GI:17025999"
/translation="MKQYIGYRQSTMKQOOSLAQOALEATAEKHHIOHINFYSDKO
SGRKDNRSYRQMTOLIOGOCDDILCCYRLNRLHRMKNALIKLICQYHVALISVH
DGYPMDOAFRLKLNIFLSLAELESNDNGEYVKNGLQAKQOGOLITTHAPFGYDGH
NCTPIINONESPTVRAENVYIKGGYKKIADLEEDNYINROBYAVNITIMNNGC
GNVINOYGFEDMFPSTIVSANYEQADRRLDKOTQTSDDQLOKIKCPCCNATLT
NNTIRKKNHTLTYVCPKMNASRVEYCDKRIINAOTLEKVLVEGRDFYONORTIKI
KKAIDKRIKRNIRKHNHILTEOLIEKLAQSIDAETFEREOTQSLROOPQDTISNG
HOIQHTIONIDIKRFTLINILYPIETIHTKDKNLIGIYFKNFPIINIVQAOSSIA"
7256. 8884
/gene="ccrB"
7256. 8884
/gene="ccrB"
/note="ORF No. M005"
/codon_start=-1
/transl_table=11
/product="cassette chromosome recombinase B"
/protein_id="BAB72128.1"
/db_xref="GI:17026000"
/translation="MOQLKTRVGIVYRVSTEMOSTEGYSIDGQINQIKEXCDFHHFE
VMDIYADROI SCKSMNRPELOMLKIDAKGNDICVMIYKTNHIAHNTSDLLKIVEDIH
KONVEFSLSEMEVENTSSGKLMLOIILASFSEERNILVENYPMQOTRBAQGYOON
LPLGDKIIPDSKHEMLINOHENANIVKYIPESYAKGGYKRIANALNHGCVYRKGRPF
SISSTIYLANPEYIGKIQFAKYKMSERBGGLNDKPYLAGSKSPITINDIMKQV
MKKQVSKQPOYHGAKTNLGTGIIHCPOCGAAMASNTTNTLKDTKTRITRYSCSNF
RNKGSKVCANSVRADVIEDVYMKOILETVKSDKYIQRVAVANVENKVGGAALHHD
AYKQOYDEVQPKLNNLIKTIEDNDLTSVIPRSIOKYEKQNLITNDINOAKNOONH
DKSLFDAKOISKLIOIHFDIKHIEKSRILKALYIISVIDRIDIKKGNHKKQYVYIKLI
NNEILIKLFNNKQDLDEVHISFSSSLPLPQTLVLT!"
9406. 9756
/note="ORF No. M006"
/codon_start=-1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72129.1"
/db_xref="GI:17026001"
/translation="MKTIOELKQYITTHFOJSSNNEMECALFEAAENILPERIND
SPLVHLIETIYTYNDELNELSTIFPELMTANNOLISVGLIUIFDMDFLITDTONII
DERHLKQGGQDHE"
9843. 10154

CDS

```

/note="ORF No. M007"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="BAB72130.1"
/db_xref="GI:17026002"
/translation="MKINRYITRGINESIPLDIQLIMHMYEKKDNQPHTDYLIHFKL
QEDENILSTHEOEOPTYKLEYHYNYEKNQNALPKKYVIREDVDVAFYVMLPEE
Y"
CDS
10166..10675
/note="ORF No. M008"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="BAB72131.1"
/db_xref="GI:17026003"
/translation="MMNTIKSTHTEAIFSDDEQHRYLKKTMDKKACTVITMYPH
LDGYLSIDLTFTVLIINOLANSERYGAYLVNLFENIPTPENLKHINKNPYDERTDIHLM
KAISSDTVILATGATAKRPVYIDVPEQMBMLPKKKVKRLINPYTNETIMHPLNPK
AKQKWLKKS"
10676..12334
/note="ORF No. M009"
/pseudo
/codon_start=1
/transl_table=1
/complement(12557..13543)
/gene="mecR1"
/pseudo
/complement(12557..13543)
/gene="mecR1"
/note="ORF No. CM003"
/pseudo
/codon_start=1
/transl_table=1
/product="signal transducer protein MecR1"
13643..15649
/gene="mecA"
13643..15649
/gene="mecA"

```

Query Match: 100.0%; Score 28; DB 1; Length 21777;
 Best local Similarity 100.0%; Pred. No. 3.3;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAGATGGCAAGATATTCAA 28
 ||||||||||||||||||||||||||||
 DB 14590 AAAGAAAAGATGGCAAGATATTCAA 14617

arch completed: December 10, 2002, 20:16:59
 job time : 614.209 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 ; Search time 182.547 Seconds

(without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579A-22

Perfect score: 28

Sequence: 1 aagaagaaagatgacaaagattatca 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N.Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*

12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*

16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*

18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*

19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*

20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28	100.0	28	24	ABR85922	Methicillin resist
2	28	100.0	39	24	ABR85928	Methicillin resist
3	28	100.0	59	20	AAK05905	Oligonucleotide pro
4	28	100.0	59	20	AAK15477	Oligonucleotide pro
5	28	100.0	89	20	AAK05906	Oligonucleotide pro
6	28	100.0	89	20	AAK15478	Probe mecA945-89
7	28	100.0	108	20	AAK15487	Probe mecA913-1020
8	28	100.0	1789	16	AAK04536	Staphylococcus aur
9	28	100.0	2007	13	AAQ28599	Encodes penicillin

10	28	100.0	2007	17	AAT28568	Bacterial antibiotic
11	28	100.0	2007	19	AAV68337	Penicillin binding
12	28	100.0	2007	22	ABA76993	Antibiotic resist
13	28	100.0	2028	24	ABN92247	Staphylococcus epi
14	28	100.0	2110	14	AAK05213	Sequence of the me
15	28	100.0	2322	13	AAK025905	pBP2'. Synthetic.
16	28	100.0	2455	16	AAT04538	Staphylococcus aur
17	28	100.0	2456	22	AAH01187	Staphylococcus aur
18	22.8	81.4	618	22	AAH88033	Peppermint plant o
19	21.6	77.1	47	20	AAK05908	Oligonucleotide pro
20	21.6	77.1	47	20	AAK120935	Probe mecA945-9A1
21	20.8	74.3	427	22	AAI120935	Human breast cance
22	20.8	74.3	428	22	AAI12050	Human breast cance
23	20.6	73.6	2429	22	AAK25890	Human cDNA cncod
24	20.6	73.6	35832	23	ABL18726	Drosophila melanog
25	20.6	73.6	368004	24	ABL57909	Human transposite
26	20	71.4	29	20	AAK05907	Oligonucleotide pro
27	20	71.4	29	20	AAK05907	Oligonucleotide pro
28	20	71.4	29	20	AAK05909	Oligonucleotide pro
29	20	71.4	29	20	AAK05910	Oligonucleotide pro
30	20	71.4	29	20	AAK05904	Oligonucleotide pr
31	20	71.4	29	20	AAK15481	Probe mecA945-29f2
32	20	71.4	29	20	AAK15482	Probe mecA945-29f2
33	20	71.4	29	20	AAK15475	Probe mecA945-29f
34	20	71.4	29	20	AAK15476	Probe mecA945-29f
35	20	71.4	29	20	AAK05680	Probe mecA945-29f
36	20	71.4	29	20	AAK05681	Chimeric mecA945-2
37	20	71.4	36	20	AAK15488	meCA945-T target s
38	20	71.4	36	20	AAK15489	Probe mecA938-36 f
39	20	71.4	144	21	AAK13722	Human secreted pro
40	20	71.4	456	23	ABV07140	Human prostate exp
41	20	71.4	562	22	AAK92373	Human cDNA 3'-end
42	20	71.4	1611	24	ABL52343	Mouse FLIP-C encod
43	20	71.4	2037	22	AAK94091	Human full-length
44	20	71.4	2326	24	ABQ70674	Listeria monocytrog
45	20	71.4	2775	17	AAK47511	kat androgen recep

ALIGNMENTS

RESULT 1
ABR85922
ID ABR85922 standard, DNA: 28 BP.
AC ABR85922;
XX
XX
DT 16-AUG-2002 (first entry)
XX
XX
DE Methicillin resistant Staphylococcus aureus detection primer #22.
XX
XX
KW Methicillin resistant Staphylococcus Aureus; MRSA; primer; ss;
KW meca: probe.
XX
XX
OS Staphylococcus aureus.
PN EPI160333-A2.
XX
XX
PD 05-DEC-2001.
XX
XX
PF 29-MAY-2001; 2001EP-0112100.
XX
XX
PR 29-MAY-2000; 2000JP-0163149.
XX
XX
PR 09-JUN-2000; 2000JP-0179394.
XX
XX
PA (TOYJ) TOSOH CORP.
XX
XX
PI Taya T, Ishiguro T, Saito J;
XX
XX
DR WPI: 2002-395832/43.
XX
XX
PT New oligonucleotide specific for the meca methicillin-resistance gene,
useful for cleavage, detection and amplification of the gene or related

```

PT mRNA -
XX
XX Claim 5; Page 20; 28pp; English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
XX and amplifying the meca gene (associated with methicillin resistance in
XX Staphylococcus aureus) or its derived RNA. The invention also comprises
XX a detection method employing an RNA amplification process, using RNA
XX derived from the meca gene as template. Also disclosed is a detection
XX method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
XX amplification process in the presence of a complementary oligonucleotide
XX probe labelled with an intercalated fluorescent dye, where complementary
XX binding of the probe to the RNA transcription product results in a
XX change in the fluorescent property relative to that of a situation where
XX a complex formation is absent, and then measuring the fluorescence
XX intensity of the reaction solution. The oligonucleotides may be used as
XX primers or probes, for detecting methicillin-resistant S. aureus in
XX clinical samples. They may also be used therapeutically to inhibit RNA
XX reverse transcription or translation. These oligonucleotides permit
XX rapid and very sensitive detection/identification of the meca gene, at a
XX relatively low temperature without the need for heat denaturation of
XX target RNA. The present sequence represents a methicillin resistant
XX Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
XX
SQ Sequence 28 BP; 17 A; 2 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 28; DB 24; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCGCAAAATATTCAA 28
Db 1 AAAGAAAAAGATGCGCAAAATATTCAA 28

RESULT 2
ABK85928/C
ID ABK85928 standard; DNA; 39 BP.
XX
XX ABK85928:
XX
XX 16-AUG-2002 (first entry)
XX
XX Methicillin resistant Staphylococcus aureus cleavage probe #3.
XX
XX Methicillin resistant Staphylococcus Aureus; MRSA; primer; ss;
XX meca; probe.
XX
XX Staphylococcus aureus.
XX
J Key Location/Qualifiers
FT modified_base 39
FT /*tag= a
FT /note= "Amidated"
XX
XX EP1160333-A2.
XX
XX 05-DEC-2001.
XX
XX 29-MAY-2001; 2001EP-0112100.
XX
XX 29-MAY-2000; 2000JP-0163149.
XX
XX 09-JUN-2000; 2000JP-0179394.
XX
XX (TOYJ ) TOSOH CORP.
XX
XX Taya T, Ishiguro T, Saito J;
XX
XX WPI; 2002-395832/43.
XX
XX New oligonucleotide specific for the meca methicillin-resistance gene,
XX useful for cleavage, detection and amplification of the gene or related
XX mRNA
XX

```

```

XX
XX Example 2; Page 22; 28pp; English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
XX and amplifying the meca gene (associated with methicillin resistance in
XX Staphylococcus aureus) or its derived RNA. The invention also comprises
XX a detection method employing an RNA amplification process, using RNA
XX derived from the meca gene as template. Also disclosed is a detection
XX method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
XX amplification process in the presence of a complementary oligonucleotide
XX probe labelled with an intercalated fluorescent dye, where complementary
XX binding of the probe to the RNA transcription product results in a
XX change in the fluorescent property relative to that of a situation where
XX a complex formation is absent, and then measuring the fluorescence
XX intensity of the reaction solution. The oligonucleotides may be used as
XX primers or probes, for detecting methicillin-resistant S. aureus in
XX clinical samples. They may also be used therapeutically to inhibit RNA
XX reverse transcription or translation. These oligonucleotides permit
XX rapid and very sensitive detection/identification of the meca gene, at a
XX relatively low temperature without the need for heat denaturation of
XX target RNA. The present sequence represents a methicillin resistant
XX Staphylococcus aureus (MRSA) cleaving probe used in the detection
XX method of the invention.
XX
SQ Sequence 39 BP; 5 A; 7 C; 4 G; 23 T; 0 other;

Query Match 100.0%; Score 28; DB 24; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCGCAAAATATTCAA 28
Db 33 AAAGAAAAAGATGCGCAAAATATTCAA 6

RESULT 3
AAK05905
ID AAK05905 standard; RNA; 59 BP.
XX
XX AAK05905:
XX
XX 07-MAY-1999 (first entry)
XX
XX Oligonucleotide probe meca932-59R.
XX
XX Hybridization; RNase H; scissile linkage; nucleic acid detection;
XX gene detection; polyamine; probe; ss.
XX
XX Synthetic.
XX
XX WO9501570-A2.
XX
XX 14-JAN-1999.
XX
XX 03-JUL-1998; 98WO-CA00631.
XX
XX 22-JUN-1998; 98US-0090273.
XX
XX 03-JUL-1997; 97US-0051827.
XX
XX 18-MAY-1998; 98US-0086021.
XX
XX (IDBI-) ID BIOMEDICAL CORP.
XX
XX Bryan RN, Cloney LP, Farnworth BA, Marostemaki AJ;
XX
XX WPI; 1999-106070/09.
XX
XX Increasing the hybridization rate between two nucleic acids - using
XX ribonuclease H (RNase H) and/or a polyamine, useful for detecting
XX nucleic acids of interest in a sample
XX
XX Example 1; Page 15; 45pp; English.
XX
XX The invention relates to methods of increasing the hybridization rate
XX

```

CC between two nucleic acids. One method comprises construction of two
CC nucleic acids and a polyamine, and hybridizing both nucleic acids
CC together, under suitable conditions. Also provided is a similar method
CC involving two nucleic acids with RNase H, where both nucleic acids do
CC not contain a scissile linkage, and if one nucleic acid is DNA, then the
CC other is RNA. The methods are useful for (in)directly detecting nucleic
CC acids of interest in a sample. They may be applied to short and long
CC nucleic acids. The acceleration of rate reactions in gene detection
CC assays, using RNase H and/or polyamines (under conditions of low salt
CC concentration), produces a lower background and, therefore, a greater
CC signal to noise ratio. Sequences AAX05903-914 represent oligonucleotide
CC probes used in the course of the invention.

XX
SQ Sequence 59 BP; 30 A; 8 C; 9 G; 12 U; 0 other;

Query Match 100.0%; Score 28; DB 20; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.23;
Matches 24; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Y 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
JB 22 AAAGAAAAAGATGCGCAAGATATTCAA 49

RESULT 4
AAX15477
ID AAX15477 standard; RNA; 59 BP.

AC AAX15477;

DT 07-MAY-1999 (first entry)

DE Probe mecA932-59R for detecting an antibiotic resistant mecA gene.

XX
KM Antibiotic resistant mecA gene; transmission; treatment;
KM methicillin resistant; Staphylococcus; probe; ss.

OS Synthetic.
XX Staphylococcus sp.

PN WO9901572-A2.

PD 14-JAN-1999.

XX
PV 03-JUL-1998; 98WO-CA00633.

XX
PR 22-JUN-1998; 98US-0090276.

PR 03-JUL-1997; 97US-0051643.

XX
R 18-MAY-1998; 98US-0086020.

XX
PA (IDBI-) ID BIOMEDICAL CORP.

XX
PI Bekkaoui F, Cloney LP;

XX
DR WPI; 1999-106072/09.

XX
PT Method for determining the presence of an antibiotic resistant mecA
PT gene in a sample - using a scissile link containing nucleic acid
PT probe for antibiotic resistant mecA gene

XX
PS Example 1; Page 16; 59pp; English.

XX
CC The present sequence represents a probe used for determining the
CC presence of an antibiotic resistant mecA gene in a biological sample.

CC The method provides a means for the rapid detection, for both
CC the prevention of transmission and treatment of, methicillin resistant
CC Staphylococcus species.

XX
SQ Sequence 59 BP; 30 A; 8 C; 9 G; 12 U; 0 other;

Query Match 100.0%; Score 28; DB 20; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.23;
Matches 24; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
DB 22 AAAGAAAAAGATGCGCAAGATATTCAA 49

RESULT 5
AAX05906/C
ID AAX05906 standard; DNA; 89 BP.

AC AAX05906;

XX
DT 07-MAY-1999 (first entry)

XX
DE Oligonucleotide probe ccmecA915-89.

XX
KM Hybridization: RNase H; scissile linkage; nucleic acid detection;
KM gene detection; polyamine; probe; ss.

XX
OS Synthetic.

PN WO9901570-A2.

PD 14-JAN-1999.

XX
PV 03-JUL-1998; 98WO-CA00633.

XX
PR 22-JUN-1998; 98US-0090273.

PR 03-JUL-1997; 97US-0051827.

XX
R 18-MAY-1998; 98US-0086021.

XX
PA (IDBI-) ID BIOMEDICAL CORP.

XX
PI Bryan RN, Cloney LP, Farnworth BA, Marostemaki AJ;

XX
DR WPI; 1999-106070/09.

XX
PT Increasing the hybridization rate between two nucleic acids - using
PT ribonuclease H (RNase H) and/or a polyamine, useful for detecting
PT nucleic acids of interest in a sample

XX
PS Example 1; Page 15; 45pp; English.

XX
CC The invention relates to methods of increasing the hybridization rate
CC between two nucleic acids. One method comprises construction of two
CC nucleic acids and a polyamine, and hybridizing both nucleic acids
CC together, under suitable conditions. Also provided is a similar method
CC involving two nucleic acids with RNase H, where both nucleic acids do
CC not contain a scissile linkage, and if one nucleic acid is DNA, then the
CC other is RNA. The methods are useful for (in)directly detecting nucleic
CC acids of interest in a sample. They may be applied to short and long
CC nucleic acids. The acceleration of rate reactions in gene detection
CC assays, using RNase H and/or polyamines (under conditions of low salt
CC concentration), produces a lower background and, therefore, a greater
CC signal to noise ratio. Sequences AAX05903-914 represent oligonucleotide
CC probes used in the course of the invention.

XX
SQ Sequence 89 BP; 20 A; 13 C; 13 G; 43 T; 0 other;

Query Match 100.0%; Score 28; DB 20; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
DB 50 AAAGAAAAAGATGCGCAAGATATTCAA 23

RESULT 6
AAX15478/C
ID AAX15478 standard; DNA; 89 BP.

XX
AC AAX15478;

XX

```

XX 07-MAY-1999 (first entry)
DT Probe cmeCA945-89 for detecting an antibiotic resistant mecA gene.
XX
DE Antibiotic resistant mecA gene; transmission; treatment:
XX methicillin resistant; Staphylococcus; probe; ss.
KM
XX Synthetic.
OS
XX Staphylococcus sp.
OS
XX WO9901572-A2.
PN
XX
XX 14-JAN-1999.
PD
XX
XX 03-JUL-1998; 98WO-CA00633.
PF
XX
XX 22-JUN-1998; 98US-0090276.
PR
XX 03-JUL-1997; 97US-0051643.
PR
XX 18-MAY-1998; 98US-0086020.
PR
XX
XX (IDBI-) ID BIOMEDICAL CORP.
XX
XX Bekkaoui F, Cloney LP;
PI
XX
XX WPI; 1999-106072/09.
DR
XX
XX Method for determining the presence of an antibiotic resistant mecA
PT gene in a sample - using a scissile link containing nucleic acid
PT
XX
XX Claim 5; Page 16; 59pp; English.
PS
XX
XX The present sequence represents a probe used for determining the
CC presence of an antibiotic resistant mecA gene in a biological sample.
CC The method provides a means for the rapid detection, for both
CC the prevention of transmission and treatment of, methicillin resistant
CC Staphylococcus species.
CC
XX
XX Sequence 89 BP; 20 A; 13 C; 13 G; 43 T; 0 other;
SQ
Query Match 100.0%; Score 28; DB 20; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGAAAAAGATGCCAAGATATTCAA 28
DB 50 AAAGAAAAAGATGCCAAGATATTCAA 23
AA15487
AA15487 standard; DNA; 108 BP.
XX
XX AAX15487;
AC
XX
XX 07-MAY-1999 (first entry)
DT
XX
XX Probe mecA913-1020 for detecting an antibiotic resistant mecA gene.
DE
XX
XX Antibiotic resistant mecA gene; transmission; treatment;
KM methicillin resistant; Staphylococcus; probe; ss.
KM
XX Synthetic.
OS
XX Staphylococcus sp.
OS
XX WO9901572-A2.
PN
XX
XX 14-JAN-1999.
PD
XX
XX 03-JUL-1998; 98WO-CA00633.
PF
XX
XX 22-JUN-1998; 98US-0090276.
PR

```

```

PR 03-JUL-1997; 97US-0051643.
PR 18-MAY-1998; 98US-0086020.
XX
XX (IDBI-) ID BIOMEDICAL CORP.
XX
XX Bekkaoui F, Cloney LP;
PI
XX
XX WPI; 1999-106072/09.
DR
XX
XX Method for determining the presence of an antibiotic resistant mecA
PT gene in a sample - using a scissile link containing nucleic acid
PT
XX
XX Claim 4; Page 17; 59pp; English.
PS
XX
XX The present sequence represents a probe used for determining the
CC presence of an antibiotic resistant mecA gene in a biological sample.
CC The method provides a means for the rapid detection, for both
CC the prevention of transmission and treatment of, methicillin resistant
CC Staphylococcus species.
CC
XX
XX Sequence 108 BP; 53 A; 14 C; 16 G; 25 T; 0 other;
SQ
Query Match 100.0%; Score 28; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGAAAAAGATGCCAAGATATTCAA 28
DB 42 AAAGAAAAAGATGCCAAGATATTCAA 69
RESULT 8
AAT04536
ID AAT04536 standard; cDNA to mRNA; 1789 BP.
XX
XX AAT04536;
AC
XX
XX 11-APR-1996 (first entry)
DT
XX
XX Staphylococcus aureus 'mecA' protein coding sequence.
DE
XX
XX methicillin-resistant Staphylococcus aureus; MRSA; 'mecA' protein;
KM antibiotic resistance; ds.
KM
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH 1..1608
FT /product= 'mecA' protein
FT CDS
XX
XX JP07209294-A.
XX
XX 11-AUG-1995.
PD
XX
XX 10-JAN-1994; 94JP-0012226.
PF
XX
XX 10-JAN-1994; 94JP-0012226.
PR
XX
XX (DENK-) DENKA SEIKEN KK.
PA (KANAWA) KANAWA M.
PA (MITU) MITSUBISHI CHEM CORP.
XX
XX WPI; 1995-313917/41.
DR
XX
XX P-PSDB; AAR80035.
DR
XX
XX New 'mecA' protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
PT
XX
XX Claim 5; Page 11-13; 15pp; Japanese.
PS
XX
XX The present sequence codes for the 'mecA' protein which controls

```

CC methicillin resistance in methicillin-resistant Staph. aureus. The
 CC 'mec A' protein (mol. wt. 40000) is useful for preparation of
 CC antisera specific for MRSA, thereby allowing methicillin-resistant
 CC and methicillin-sensitive strains to be distinguished. The coding
 CC sequence was obtained by PCR amplification of the mec A sequence
 CC (see AAT04538) using primers AAT04537 and AAT04539.
 CC N.B. In the sequence listing of the patent specification, the
 CC sequence length is stated to be 1785 bp.
 CC
 CC Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;
 SO
 Query Match 100.0%; Score 28; DB 16; Length 1789;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGCAAAAAGATGCCAAGATATTCAA 28
 DB 549 AAGCAAAAAGATGCCAAGATATTCAA 576
 fSUI/T 9
 ID AAG28599 standard; DNA; 2007 BP.
 AC AAG28599;
 XX
 XX 19-FEB-1993 (first entry)
 DF Encodes penicillin binding protein PBP2A-27R.
 XX
 XX Penicillin; antibiotic; bacteria; methicillin; staphylococci;
 KW soluble; chelating peptide; MRS infection; methicillin resistant;
 KW strain.
 XX
 XX Staphylococcus aureus strain 27R.
 OS
 XX
 FU Key Location/Qualifiers
 FT CDS 1..2007
 FT /tag= a
 XX
 XX EP505151-A.
 PN
 XX
 PD 23-SEP-1992.
 XX
 PF 18-MAR-1992; 92EP-0302298.
 XX
 PR 19-MAR-1991; 91US-0672704.
 XX
 XX (ELIL) LILLY & CO ELI.
 XX
 PI Blaszcak IC, Skatrud PL, Smith MC, Wu CYE;
 XX
 DR WPI; 1992-318034/39.
 XX
 XX Polynucleotide cpd. encoding PBP 2A-27R protein or its deriv. -
 PT contains PBP isolated from staphylococcus aureus and is used to
 PT treat methicillin resistant staphylococci
 XX
 XX Disclosure; Page 14; 101pp; English.
 PS
 XX This sequence encodes a PBP2A penicillin binding protein isolated
 CC from S. aureus strain 27R. A cDNA library was constructed from
 CC S. aureus DNA in lambda phage EMBL3. Packaging extracts from this
 CC then used to infect E. coli CJ236. Plaques were screened for the
 CC presence of the mecA-27R gene by a probe produced by PCR amplification
 CC of the mecA gene using primers Q28600.1. Positive plaques were purified
 CC and digested with HindIII, and this fragment digested with XbaI and
 CC cloned into M13amp18 and M13amp19 for sequencing.
 CC
 CC Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
 SO
 Query Match 100.0%; Score 28; DB 13; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 0.34;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGCAAAAAGATGCCAAGATATTCAA 28
 DB 948 AAGCAAAAAGATGCCAAGATATTCAA 975
 RESULT 10
 AAT28568
 ID AAT28568 standard; DNA; 2007 BP.
 AC AAT28568;
 XX
 XX 01-APR-1997 (first entry)
 DT
 XX
 DE Bacterial antibiotic resistance gene, mecA, probe.
 KW
 KW Detection; probe; amplification primer; bacterial pathogen; pneumonia;
 KW Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
 KW Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
 KW Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
 KW Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
 KW Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis;
 KW infection; intra-abdominal infection; skin infection;
 KW bacterial resistance; beta-lactam antibiotic; ds.
 XX
 OS Synthetic.
 XX
 PN W0960858t-A2.
 XX
 PD 21-MAR-1996.
 XX
 PF 12-SEP-1995; 95WO-CA00528.
 XX
 PR 12-SEP-1995. 94US-0304732.
 XX
 XX (BERG) BERGERON M G.
 PA (OUEL) OUELLETTE M.
 PA (ROY P H.) ROY P H.
 XX
 PI Bergeron MC, Ouellette M, Roy PH;
 XX
 DR WPI; 1996-179953/18.
 XX
 XX Method for the detection of bacterial species using probes and
 PT primers - allows detection and quantification of antibiotic
 PT resistant bacteria in patients, the environment and food
 XX
 PS Claim 91: Page 144-145; 216pp; English.
 XX
 CC The sequences given in AAT28560-76 represent fragments derived from
 CC bacterial antibiotic resistance genes which were used as probes in the
 CC method of the invention for the detection of bacterial species in a
 CC sample. The method of the invention comprises using probes and/or
 CC amplification primers which are specific, ubiquitous and sensitive for
 CC determining the presence and/or amount of nucleic acids from selected
 CC bacterial species in any sample, where the bacterial nucleic acid
 CC comprises a selected target region hybridisable with the probes or
 CC primers. The method comprises contacting the sample with the probes
 CC or primers and detecting the presence and/or amount of hybridised
 CC primers or amplification products as and indication of the presence
 CC and/or amount of the bacterial species. This method may be used to
 CC detect commonly encountered bacterial pathogens, e.g. Escherichia coli,
 CC Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis,
 CC Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus
 CC epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus,
 CC Streptococcus pyogenes, Haemophilus influenzae and Moraxella
 CC catarrhalis. These bacterial species are associated with approx. 90% of
 CC urinary tract infections and with a high percentage of other severe
 CC infections, skin infections and other severe respiratory tract
 CC infections. The method may also be used to evaluate a bacterial
 CC resistance to beta-lactam antibiotics.

XX Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
SQ
Query Match 100.0%; Score 28; DB 17; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGCAAAAAGATGCCAAGATATTCAA 28
AAAAAAAAAAAAAAAAAAAAAAAAAAAA
DB 948 AAGCAAAAAGATGCCAAGATATTCAA 975
RESULT 11
AAV68337
ID AAV68337 standard; DNA; 2007 BP.
XX
XX AAV68337;
XX
XX 21-JUN-1999 (first entry)
XX
XX Penicillin binding protein PBP2A meca-27R gene of *S. aureus* 27R.
X Penicillin binding protein; PBP2A-27A; meca-27R gene;
KW methicillin resistance; antibiotic; assay; purification; ss.
XX
XX Staphylococcus aureus.
XX
XX EP875578-A2.
XX
XX 04-NOV-1998.
XX
XX 18-MAR-1992; 92EP-0302298.
XX
XX 19-MAR-1991; 91US-0672704.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Blaszcak LC, Skatrud PL, Smith MC, Wu CE;
PI
XX WPI: 1998-559443/48.
DR P-PSDB: AAM81149.
XX
XX New Staphylococcus aureus soluble penicillin-binding proteins and
PT their derivatives - useful for screening for compounds effective
PT against methicillin resistant organisms
XX
XX
PS Disclosure; Page 14-16; 97pp; English.
XX
XX This meca-27R gene encodes penicillin binding protein 2A (PBP2A-27R)
CC responsible for the methicillin resistance of Staphylococcus aureus
CC strain 27R. The invention provides new PBPs of formula SP-L-PBP2As,
CC where: SP is 0 or a signal peptide (preferably from the ampC, ompA or
CC beta-lactamase gene product); L is Met-Val or a compound of formula
CC Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see
CC AAM81151-58) of formula (His)_x-(Ala)_y-(His)_z and A-an amino acid,
CC x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above
CC polypeptide where each monomer unit is the same or different; Pro
CC is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see
CC AAM81159-62). Also claimed are polynucleotides encoding specific
CC soluble PBP2A compounds. The new PBP2A-27R proteins are useful for
CC assaying for agents useful as antibiotics against methicillin
CC resistant Staphylococcus strains by creating a kinetically inert
CC complex between a support-immobilised transition ion and a modified
CC soluble PBP2A protein comprising a chelating agent, which screens
CC for agents which bind to PBP2A proteins (disclosed). Soluble forms
CC of PBP2A-27R protein facilitate crystallisation as they lack their
CC transmembrane association region, and so are useful for x-ray
CC crystallography studies of the protein, assisting in the design of
CC antibiotic compounds against methicillin resistant Staphylococcus
CC strains (disclosed). The chelating peptide operably linked to the
CC BPA-27R proteins is useful for purifying PBPs.
XX
XX Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
SQ

Query Match 100.0%; Score 28; DB 19; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGCAAAAAGATGCCAAGATATTCAA 28
AAAAAAAAAAAAAAAAAAAAAAAAAAAA
DB 948 AAGCAAAAAGATGCCAAGATATTCAA 975
RESULT 12
ABA76993
ID ABA76993 standard; DNA; 2007 BP.
XX
XX ABA76993;
XX
XX 28-JAN-2002 (first entry)
XX
XX Antibiotic resistance detection polynucleotide SEQ ID NO 169.
XX
XX Detection; bacterial species; animal; food; environment;
KW antibiotic resistance; ds.
XX
XX Unidentified.
XX
XX NZ501596-A.
XX
XX 29-JUN-2001.
XX
XX 12-SEP-1995; 95N2-0501596.
XX
XX 12-SEP-1995; 95N2-0501596.
XX
XX (IDI1-) IDI INFECTIO DIAGNOSTIC INC.
XX
XX Bergeron MC, Ouellette M, Roy PH;
PI
XX WPI: 2001-613034/71.
DR
XX Method for detecting target bacterial species in a sample, comprises
PT detecting the presence or amount of bacterial nucleic acid amplified by
PT a primer derived from bacterial DNA, specific for the target bacterial
PT species -
XX
XX Claim 16; Page 159-160; 168pp; English.
XX
XX The invention relates to detecting target bacterial species suspected to
CC be present in a sample, comprising contacting nucleic acids of target
CC bacterial species with an amplification primer pair derived from a
CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target
CC bacterial species but ubiquitous for different strains, amplifying the
CC nucleic acid and detecting the presence or amount of an amplified
CC sequence as an indication of the presence or amount of the target
CC bacterial species. The invention includes primers and probes
CC (ABA76862-ABA76984) against the target bacterial species, especially
CC *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *P. mirabilis*, *S. pneumoniae*,
CC *S. aureus*, *S. epidermidis*, *E. faecalis*, *S. saprophyticus*, *S. pyogenes*,
CC *H. influenzae*, *M. catarrhalis* and/or group A Streptococci producing
CC exotoxin A gene spe A, suspected to be present in a sample which is
CC obtained from human patients, animals, environment or food, and which
CC consists of one or more bacterial colonies. Oligonucleotide
CC probes and primers complementary to the bacterial genes encoding
CC resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadB,
CC aacC1, aacC2, aacC3, aacA, meca, vanA, vanH, vanX, salA, aacA-apd, vat,
CC vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify
CC commonly encountered and clinically important resistance genes. The
CC invention provides a rapid method of bacterial identification that can be
CC achieved, which reduces the time currently required for the
CC identification of pathogens in the clinical laboratory.
XX
XX Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
SQ
Query Match 100.0%; Score 28; DB 22; Length 2007;
SQ


```

PD      17-JUN-1992.
XX
XX      31-OCT-1990;      90JP-0296708.
XX
XX      31-OCT-1990;      90JP-0296708.
XX
XX      (SHIO ) SHIONOGI & CO LTD.
XX
XX      WPT; 1992-253403/31.
XX
XX      Detection of PBP2' gene for determ. of methicillin-resistance -
PT      useful esp. for detection of methicillin-resistance
PT      Staphylococcus aureus
XX
XX      Disclosure; Fig 1; 9pp; Japanese.
PS
XX
XX      The sequence given is the PBP2' gene. This gene could be detected
CC      by the primer sequences given in AA025897-904. Due to the results of
CC      this amplification reaction resistance to methicillin in Staphylococcus
CC      aureus could be determined.
XX
XX      Sequence 2322 BP; 940 A; 324 C; 389 G; 669 T; 0 other;
XX
XX
XX      Query Match      100.0%; Score 28; DB 13; Length 2322;
XX      Best Local Similarity 100.0%; Pred. No. 0.34;
XX      Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 AAGCAAAAAGATGCCAAAGATATTCAA 28
XX      ||||||||||||||||||||||||||||
XX      954 AAGCAAAAAGATGCCAAAGATATTCAA 981

```

Search completed: December 10, 2002, 17:32:35
Job time : 184.547 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 : Search time 130.391 Seconds
(without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579A-21
Perfect score: 20
Sequence: 1 gtagtgatatacttggcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_101002:*
1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	24	ABK85911 Methicillin resist
2	20	100.0	20	24	ABK85921 Methicillin resist
3	20	100.0	39	24	ABK85928 Methicillin resist
4	20	100.0	59	20	AAK05905 Oligonucleotide pro
5	20	100.0	59	20	AAK15477 Probe mecA932-59R
6	20	100.0	89	20	AAK05906 Oligonucleotide pro
7	20	100.0	89	20	AAK15478 Probe mecA945-89
8	20	100.0	108	20	AAK15487 Probe mecA913-1020
9	20	100.0	1789	16	AAK04536 Staphylococcus aur

C 10	20	100.0	2007	13	AAQ28599 Encodes penicillin
C 11	20	100.0	2007	17	AAT28568 Bacterial antibiot
C 12	20	100.0	2007	19	AAV68337 Penicillin binding
C 13	20	100.0	2007	22	ABA76993 Antibiotic resista
C 14	20	100.0	2028	24	ABN92247 Staphylococcus epi
C 15	20	100.0	2110	14	AAK35213 Sequence of the me
C 16	20	100.0	2322	13	AAQ25905 pBP2', syntheic
C 17	20	100.0	2455	16	AAT04538 Staphylococcus aur
C 18	20	100.0	2456	22	AAH01187 Staphylococcus aur
C 19	17.4	87.0	369	24	ABO85506 Arabidopsis thalia
C 20	17.4	87.0	2961	21	AAK48316 Arabidopsis thalia
C 21	16.8	84.0	350	24	ABQ85831 Enterococcus thalia
C 22	16.8	84.0	16484	20	AAK13095 Drosophila melanog
C 23	16.4	82.0	2052	23	ABL07785 Drosophila melanog
C 24	16.4	82.0	4437	23	ABL07784 Drosophila melanog
C 25	16	80.0	199	21	AAK10590 Fusarium venenatum
C 26	15.8	79.0	696	21	AAAA4046 Human secreted exp
C 27	15.8	79.0	1187	24	ABQ38096 Oligonucleotide fo
C 28	15.8	79.0	1187	24	ABQ38097 Oligonucleotide fo
C 29	15.8	79.0	1598	23	ABL21005 Drosophila melanog
C 30	15.8	79.0	1722	23	ABL29687 Drosophila melanog
C 31	15.8	79.0	3423	23	ABL24346 Drosophila melanog
C 32	15.8	79.0	3829	23	ABL21004 Drosophila melanog
C 33	15.8	79.0	4010	23	ABL29686 Drosophila melanog
C 34	15.8	79.0	8738	23	ABL11376 Human nervous syst
C 35	15.8	79.0	9151	22	ABA14677 Human nervous syst
C 36	15.8	79.0	9153	22	ABA14676 Human musculoskele
C 37	15.8	79.0	19866	22	AAI37522 Hipolar affective
C 38	15.8	79.0	160271	22	AAF85750 Human chromosome 1
C 39	15.8	79.0	160271	22	AAF85750 Human chromosome 1
C 40	15.8	79.0	160271	22	AAK04858 Human chromosome 1
C 41	15.8	79.0	160271	22	AAK04864 Human chromosome 1
C 42	15.8	79.0	160271	22	AAK06667 Human chromosome 1
C 43	15.8	79.0	160271	22	AAH40997 160kb fragment of
C 44	15.8	79.0	160271	22	AAH23764 Human chromosome 1
C 45	15.8	79.0	160271	22	AAF85116 Nucleotide sequenc

ALIGNMENTS

RESULT 1
ABK85911
ID ABK85911 standard; DNA: 20 BP.
AC ABK85911:
XX
DT 16-AUG-2002 (first entry)
XX
DE Methicillin resistant Staphylococcus aureus detection primer #1.
XX
KW Methicillin resistant Staphylococcus Aureus; MRSA; primer: SS;
KW mecA; probe.
XX
OS Staphylococcus aureus.
XX
PN EP1160333-A2.
XX
PD 05-DEC-2001.
XX
PF 29-MAY-2001; 2001EP-0112100.
XX
PR 29-MAY-2000; 2000JP-0163149.
XX
PR 09-JUN-2000; 2000JP-0179394.
XX
PA (TORI) TOSOH CORP.
XX
PI Taya T, Ishiguro T, Saito J;
XX
XX WPI; 2002-395832/43.
XX
XX New oligonucleotide specific for the mecA methicillin-resistance gene,
XX
XX useful for cleavage, detection and amplification of the gene or related

PT mRNA -
XX Claim 1; Page 16; 28pp; English.
XX
CC This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in
CC Staphylococcus aureus) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the mecA gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the mecA gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 3 C; 4 G; 9 T; 0 other;
Query Match 100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTAGTGAATATCTTGGC 20
Db 1 GTTAGTGAATATCTTGGC 20
RESULT 2
ABK85921
ID ABK85921 standard; DNA: 20 BP.
XX
AC ABK85921;
XX
DT 16-AUG-2002 (first entry)
XX
DE Methicillin resistant Staphylococcus aureus detection primer #21.
XX
KW Methicillin resistant Staphylococcus Aureus; MRSA; primer; ss;
XX
XX mecA; probe.
XX
XX Staphylococcus aureus.
XX
XX
XX EPI160333-A2.
XX
PD 05-DEC-2001.
XX
PF 29-MAY-2001; 2001EP-0112100.
XX
PR 29-MAY-2000; 2000JP-0163149.
XX
PR 09-JUN-2000; 2000JP-0179394.
XX
PA (TOYJ) TOSOH CORP.
XX
PI Taya T, Ishiguro T, Salto J;
XX
DR WPI: 2002-395832/43.
XX
XX New oligonucleotide specific for the mecA methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related
PT mRNA -
XX
XX Claim 5; Page 19; 28pp; English.
XX
CC This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in

CC Staphylococcus aureus) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the mecA gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the mecA gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 3 C; 4 G; 9 T; 0 other;
Query Match 100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTAGTGAATATCTTGGC 20
Db 1 GTTAGTGAATATCTTGGC 20
RESULT 3
ABK85928
ID ABK85928 standard; DNA: 39 BP.
XX
AC ABK85928;
XX
DT 16-AUG-2002 (first entry)
XX
DE Methicillin resistant Staphylococcus aureus cleavage probe #3.
XX
DE Methicillin resistant Staphylococcus Aureus; MRSA; primer; ss;
XX
KW mecA; probe.
XX
XX Staphylococcus aureus.
XX
XX
XX
XX Key Location/Qualifiers
FH modified_base 39
FT /*tag= a
FT /note= "Amidated"
XX
XX EPI160333-A2.
XX
PD 05-DEC-2001.
XX
PF 29-MAY-2001; 2001EP-0112100.
XX
PR 29-MAY-2000; 2000JP-0163149.
XX
PR 09-JUN-2000; 2000JP-0179394.
XX
PA (TOYJ) TOSOH CORP.
XX
PI Taya T, Ishiguro T, Salto J;
XX
DR WPI: 2002-395832/43.
XX
XX New oligonucleotide specific for the mecA methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related
PT mRNA -
XX
XX Example 2; Page 22; 28pp; English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in
CC Staphylococcus aureus) or its derived RNA. The invention also comprises

CC a detection method employing an RNA amplification process, using RNA
CC derived from the meca gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the meca gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC *Staphylococcus aureus* (MRSA) cleaving probe used in the detection
CC method of the invention.

XX Sequence 39 BP; 5 A; 7 C; 4 G; 23 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTAGTGAATATCTTTGCC 20
|||||
Db 1 GTTAGTGAATATCTTTGCC 20

RESULT 4
AAK05905/c
ID AAK05905 standard; RNA; 59 BP.

XX AAK05905;

DT 07-MAY-1999 (first entry)

XX Oligonucleotide probe meca932-59R.

XX Hybridization; RNase H; scissile linkage; nucleic acid detection;

KW gene detection; polyamine; probe; ss.

XX Synthetic.

XX MO9901570-A2.

PN 14-JAN-1999.

XX 03-JUL-1998; 98WO-CA00631.

XX 22-JUN-1998; 98US-0090273.

PR 03-JUL-1997; 97US-0051827.

PR 18-MAY-1998; 98US-0086021.

XX (IDBI-) ID BIOMEDICAL CORP.

PI Bryan RN, Cloney LP, Farnworth BA, Marostemaki AJ;

DR WPI; 1999-106070/09.

PT Increasing the hybridization rate between two nucleic acids - using
PP ribonuclease H (RNase H) and/or a polyamine, useful for detecting
XX nucleic acids of interest in a sample

XX Example 1; Page 15; 45pp; English.

XX The invention relates to methods of increasing the hybridization rate
CC between two nucleic acids. One method comprises construction of two
CC nucleic acids and a polyamine, and hybridizing both nucleic acids
CC together, under suitable conditions. Also provided is a similar method
CC involving two nucleic acids with RNase H, where both nucleic acids do
CC not contain a scissile linkage, and if one nucleic acid is DNA, then the
CC other is RNA. The methods are useful for (in)directly detecting nucleic

CC acids of interest in a sample. They may be applied to short and long
CC nucleic acids. The acceleration of rate reactions in gene detection
CC assays, using RNase H and/or polyamines (under conditions of low salt
CC concentration), produces a lower background and, therefore, a greater
CC signal to noise ratio. Sequences AAK05903-914 represent oligonucleotide
CC probes used in the course of the invention.

XX Sequence 59 BP; 30 A; 8 C; 9 G; 12 U; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTAGTGAATATCTTTGCC 20
|||||
Db 54 GTTAGTGAATATCTTTGCC 35

RESULT 5
AAK15477/c

XX AAK15477 standard; RNA; 59 BP.

XX AAK15477;

DT 07-MAY-1999 (first entry)

XX Probe meca932-59R for detecting an antibiotic resistant meca gene.

XX Antibiotic resistant meca gene; transmission; treatment;

KW methicillin resistant; *Staphylococcus*; probe; ss.

XX Synthetic.

XX *Staphylococcus* sp.

XX MO9901572-A2.

PN 14-JAN-1999.

XX 03-JUL-1998; 98WO-CA00633.

XX 22-JUN-1998; 98US-0090276.

PR 03-JUL-1997; 97US-0051643.

PR 18-MAY-1998; 98US-0086020.

XX (IDBI-) ID BIOMEDICAL CORP.

PI Bekkaoui F, Cloney LP;

DR WPI; 1999-106072/09.

PT Method for determining the presence of an antibiotic resistant meca
PP gene in a sample - using a scissile link containing nucleic acid
XX probe for antibiotic resistant meca gene

XX Example 1; Page 16; 59pp; English.

XX The present sequence represents a probe used for determining the
CC presence of an antibiotic resistant meca gene in a biological sample.
CC The method provides a means for the rapid detection, for both
CC the prevention of transmission and treatment of, methicillin resistant
CC *Staphylococcus* species.

XX Sequence 59 BP; 30 A; 8 C; 9 G; 12 U; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTAGTGAATATCTTTGCC 20
|||||
Db 54 GTTAGTGAATATCTTTGCC 35

```

RESULT 6
AA05906
ID AAX05906 standard; DNA: 89 BP.
XX
AC AAX05906;
XX
DT 07-MAY-1999 (first entry)
XX
DE Oligonucleotide probe cmeCA915-89.
XX
KW Hybridization: RNase H; scissile linkage; nucleic acid detection;
XX gene detection; polyamine; probe; ss.
XX
OS Synthetic.
XX
PN MO9901570-A2.
XX
PD 14-JAN-1999.
XX
PF 03-JUL-1998; 98WO-CA00631.
XX
PR 22-JUN-1998; 98US-0090273.
XX 03-JUL-1997; 97US-0051827.
XX 18-MAY-1998; 98US-0086021.
XX
PA (IDBI-) ID BIOMEDICAL CORP.
XX
PI Bryan RM, Cloney LP, Farnworth BA, Marostemaki AJ;
XX
DR WPI: 1999-106070/09.
XX
PT Increasing the hybridization rate between two nucleic acids - using
XX ribonuclease H (RNase H) and/or a polyamine, useful for detecting
XX nucleic acids of interest in a sample
XX
PS Example 1; Page 15; 45pp; English.
XX
CC The invention relates to methods of increasing the hybridization rate
XX between two nucleic acids. One method comprises construction of two
XX nucleic acids and a polyamine, and hybridizing both nucleic acids
XX together, under suitable conditions. Also provided is a similar method
XX involving two nucleic acids with RNase H, where both nucleic acids do
XX not contain a scissile linkage, and if one nucleic acid is DNA, then the
XX other is RNA. The methods are useful for (in)directly detecting nucleic
XX acids of interest in a sample. They may be applied to short and long
XX nucleic acids. The acceleration of rate reactions in gene detection
XX assays, using RNase H and/or polyamines (under conditions of low salt
XX concentration), produces a lower background and, therefore, a greater
XX signal to noise ratio. Sequences AAX05903-914 represent Oligonucleotide
XX probes used in the course of the invention.
XX
SQ Sequence 89 BP; 20 A; 13 C; 13 G; 43 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACTGAAATATCTTGCC 20
   |||||||
DB 18 GTTACTGAAATATCTTGCC 37

RESULT 7
AAX15478
ID AAX15478 standard; DNA: 89 BP.
XX
AC AAX15478;
XX
DT 07-MAY-1999 (first entry)
XX
DE Probe cmeCA945-89 for detecting an antibiotic resistant meca gene.
XX
KW Antibiotic resistant meca gene; transmission; treatment;

```

```

KW methicillin resistant; Staphylococcus; probe; ss.
XX
OS Synthetic.
XX
OS Staphylococcus sp.
XX
PN MO9901572-A2.
XX
PD 14-JAN-1999.
XX
PF 03-JUL-1998; 98WO-CA00633.
XX
PR 22-JUN-1998; 98US-0090276.
XX 03-JUL-1997; 97US-0051643.
XX 18-MAY-1998; 98US-0086020.
XX
PA (IDBI-) ID BIOMEDICAL CORP.
XX
PI Bekkaoui F, Cloney LP;
XX
DR WPI: 1999-106072/09.
XX
PT Method for determining the presence of an antibiotic resistant meca
XX gene in a sample - using a scissile link containing nucleic acid
XX probe for antibiotic resistant meca gene
XX
PS Claim 5; Page 16; 59pp; English.
XX
CC The present sequence represents a probe used for determining the
XX presence of an antibiotic resistant meca gene in a biological sample.
XX The method provides a means for the rapid detection, for both
XX the prevention of transmission and treatment of, methicillin resistant
XX Staphylococcus species.
XX
SQ Sequence 89 BP; 20 A; 13 C; 13 G; 43 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACTGAAATATCTTGCC 20
   |||||||
DB 18 GTTACTGAAATATCTTGCC 37

RESULT 8
AAX15487/C
ID AAX15487 standard; DNA: 108 BP.
XX
AC AAX15487;
XX
DT 07-MAY-1999 (first entry)
XX
DE Probe meCA913-1020 for detecting an antibiotic resistant meca gene.
XX
KW Antibiotic resistant meca gene; transmission; treatment;
XX methicillin resistant; Staphylococcus; probe; ss.
XX
OS Synthetic.
XX
OS Staphylococcus sp.
XX
PN MO9901572-A2.
XX
PD 14-JAN-1999.
XX
PF 03-JUL-1998; 98WO-CA00633.
XX
PR 22-JUN-1998; 98US-0090276.
XX 03-JUL-1997; 97US-0051643.
XX 18-MAY-1998; 98US-0086020.
XX
PA (IDBI-) ID BIOMEDICAL CORP.
XX
PI Bekkaoui F, Cloney LP;

```

XX WP1: 1999-106072/09.
 DR
 XX
 PT Method for determining the presence of an antibiotic resistant mecA
 PT gene in a sample - using a scissile link containing nucleic acid
 PT probe for antibiotic resistant mecA gene
 XX
 PS Claim 4; Page 17; 59pp; English.
 XX
 CC The present sequence represents a probe used for determining the
 CC presence of an antibiotic resistant mecA gene in a biological sample.
 CC The method provides a means for the rapid detection, for both
 CC the prevention of transmission and treatment of, methicillin resistant
 CC Staphylococcus species.
 CC
 SQ Sequence 108 BP; 53 A; 14 C; 16 G; 25 T; 0 other;
 Query Match 100.0%; Score 20; DB 20; Length 108;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 GTTACTGAAATCTTTGCC 20
 |||||||
 Db 74 GTTACTGCAATATCTTTGCC 55
 RESULT 9
 AAT04536/C
 ID AAT04536 standard; cDNA to mRNA; 1789 BP.
 XX
 AC AAT04536;
 XX
 DT 11-APR-1996 (first entry)
 XX
 DE Staphylococcus aureus 'mecA protein coding sequence.
 XX
 KW methicillin-resistant Staphylococcus aureus; MRSA; 'mecA protein;
 KW antibiotic resistance; ds.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT 1..1608
 FT CDS /*tag= a
 FT /product= 'mec_A_protein
 FT
 XX
 JP07209294-A.
 XX
 11-AUG-1995.
 X
 PF 10-JAN-1994; 94JP-0012226.
 XX
 PR 10-JAN-1994; 94JP-0012226.
 XX
 PA (DENK-) DENKA SEIKEN KK.
 PA (KAWA/) KAWANO M.
 PA (MITU) MITSUBISHI CHEM CORP.
 XX
 DR WP1: 1995-313917/41.
 DR P-FSD8; AAR80035.
 XX
 PT New 'mec A protein and DNA encoding it - used for the detection of
 PT methicillin-resistant Staphylococcus aureus
 PT
 XX
 PS Claim 5; Page 11-13; 15pp; Japanese.
 XX
 CC The present sequence codes for the 'mec A protein which controls
 CC methicillin resistance in methicillin-resistant Staph. aureus. The
 CC 'mec A protein (mol. wt. 40000) is useful for preparation of
 CC antiserum specific for MRSA, thereby allowing methicillin-resistant
 CC and methicillin-sensitive strains to be distinguished. The coding
 CC sequence was obtained by PCR amplification of the mec A sequence
 CC (see AAT04538) using primers AAT04537 and AAT04539.

CC N.B. In the sequence listing of the patent specification, the
 CC sequence length is stated to be 1785 bp.
 XX
 SQ Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;
 Query Match 100.0%; Score 20; DB 16; Length 1789;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 GTTACTGAAATCTTTGCC 20
 |||||||
 Db 581 GTTACTGCAATATCTTTGCC 562
 RESULT 10
 AAQ28599/C
 ID AAQ28599 standard; DNA; 2007 BP.
 XX
 AC AAQ28599;
 XX
 DT 19-FEB-1993 (first entry)
 XX
 DE Encodes penicillin binding protein PBP2A-27R.
 XX
 KW penicillin; antibiotic; bacteria; methicillin; staphylococci;
 KW soluble; chelating peptide; MRS infection; methicillin resistant;
 KW strain.
 XX
 OS Staphylococcus aureus strain 27R.
 XX
 FH Key Location/Qualifiers
 FT 1..2007
 FT CDS /*tag= a
 FT
 XX
 EP505151-A.
 XX
 23-SEP-1992.
 XX
 PF 18-MAR-1992; 92EP-0302298.
 XX
 PR 19-MAR-1991; 91US-0672704.
 XX
 PA (ELIL) LILLY & CO ILLI.
 XX
 PI Blaszcak LC, Skatrud PL, Smith MC, Wu CYE;
 XX
 DR WP1: 1992-318034/39.
 XX
 PT Polynucleotide cpd. encoding PBP 2A-27R protein or its deriv. -
 PT contains PBP isolated from Staphylococcus aureus and is used to
 PT treat methicillin resistant staphylococci
 XX
 PS Disclosure; Page 14; 101pp; English.
 XX
 CC This sequence encodes a PBP2a penicillin binding protein isolated
 CC from S. aureus strain 27R. A cDNA library was constructed from
 CC S. aureus DNA in lambda phage EMPL3. Packaging extracts from this were
 CC then used to infect E. coli CJ236. Plaques were screened for the
 CC presence of the mecA-27R gene by a probe produced by PCR amplification
 CC of the mecA gene using primers Q28600/1. Positive plaques were purified
 CC and digested with HindIII, and this fragment digested with XbaI and
 CC cloned into M13amp18 and M13amp19 for sequencing.
 XX
 SQ Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
 Query Match 100.0%; Score 20; DB 13; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 GTTACTGAAATCTTTGCC 20
 |||||||
 Db 980 GTTACTGCAATATCTTTGCC 961

```
RESULT 11
AAT28568/c
ID AAT28568 standard; DNA: 2007 BP.
XX
AC AAT28568;
XX
DF 01-APR-1997 (first entry)
XX
DE Bacterial antibiotic resistance gene, meca, probe.
XX
KM Detection: probe; amplification primer; bacterial pathogen: pneumonia;
KM Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
KM Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
KM Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
KM Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
KM Haemophilus influenzae; Moraxella catarrhalis; septicemia; meningitis;
KM infection; intra-abdominal infection; skin infection;
XX bacterial resistance; beta-lactam antibiotic; ds.
XX
: Synthetic.
A
PN MO9608582-A2.
PD 21-MAR-1996.
XX
PF 12-SEP-1995; 95MO-CA00528.
XX
PR 12-SEP-1994; 94US-0304732.
XX
PA (BERG/) BERGERON M G.
PA (OUEL/) OUELLETTE M.
PA (ROY/) ROY P H.
XX
PI Bergeron MG, Ouellette M, Roy PH:
XX
DR WPI; 1996-179953/18.
XX
PT Method for the detection of bacterial species using probes and
PT primers - allows detection and quantification of antibiotic
PT resistant bacteria in patients, the environment and food
XX
PS Claim 91; Page 144-145; 216pp; English.
XX
CC The sequences given in AAT28568-76 represent fragments derived from
CC bacterial antibiotic resistance genes which were used as probes in the
CC method of the invention for the detection of bacterial species in a
CC sample. The method of the invention comprises using probes and/or
CC amplification primers which are specific, ubiquitous and sensitive for
CC determining the presence and/or amount of nucleic acids from selected
CC bacterial species in any sample, where the bacterial nucleic acid
CC comprises a selected target region hybridisable with the probes or
CC primers. The method comprises contacting the sample with the probes or
CC primers or primers and detecting the presence and/or amount of hybridised
CC primers or amplification products as and indication of the presence
CC and/or amount of the bacterial species. This method may be used to
CC detect commonly encountered bacterial pathogens, e.g. Escherichia coli,
CC Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis,
CC Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus
CC epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus,
CC Streptococcus pyogenes, Haemophilus influenzae and Moraxella
CC catarrhalis. These bacterial species are associated with approx. 90% of
CC urinary tract infections and with a high percentage of other severe
CC infections including septicemia, meningitis, pneumonia, intra-abdominal
CC infections, skin infections and other severe respiratory tract
CC infections. The method may also be used to evaluate a bacterial
CC resistance to beta-lactam antibiotics.
XX
SQ Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 17; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 GTTAGTTGAATATCTTGCC 20
|||
Db 980 GTTAGTTGAATATCTTGCC 961

RESULT 12
AAV68337/c
ID AAV68337 standard; DNA: 2007 BP.
XX
AC AAV68337;
XX
DF 21-JUN-1999 (first entry)
XX
DE Penicillin binding protein PBP2A meca-27R gene of S. aureus 27R.
XX
KM Penicillin binding protein: PBP2A-27R; meca-27R gene;
KM methicillin resistance; antibiotic; assay; purification; ss.
XX
OS Staphylococcus aureus.
XX
PN EP875578-A2.
XX
PD 04-NOV-1998.
XX
PF 18-MAR-1992; 92EP-0302298.
XX
PR 19-MAR-1991; 91US-0672704.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Blaszcak LC, Skatrud PL, Smith MC, Wu CE;
XX
DR WPI; 1998-559443/48.
XX
DR P-PSDB; AAM81149.
XX
PT New Staphylococcus aureus soluble penicillin-binding proteins and
PT their derivatives - useful for screening for compounds effective
PT against methicillin resistant organisms
XX
PS Disclosure; Page 14-16; 97pp; English.
XX
CC This meca-27R gene encodes penicillin binding protein 2A (PBP2A-27R)
CC responsible for the methicillin resistance of Staphylococcus aureus
CC strain 27R. The invention provides new PBPs of formula SP-L-PBP2As,
CC where: SP is 0 or a signal peptide (preferably from the ampc, ompA or
CC beta-lactamase gene product); L is Met-Val or a compound of formula
CC Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see
CC AAM81151-58) of formula (His)x-(Ala)y-(His)z and A=an amino acid,
CC x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above
CC polypeptide where each monomer unit is the same or different; Pro
CC is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see
CC AAM81159-62). Also claimed are polynucleotides encoding specific
CC soluble PBP2A compounds. The new PBP2A-27R proteins are useful for
CC assaying for agents useful as antibiotics against methicillin
CC resistant Staphylococcus strains by creating a kinetically inert
CC complex between a support-immobilised transistion ion and a modified
CC soluble PBP2A protein comprising a chelating agent, which screens
CC for agents which bind to PBP2A proteins (disclosed). Soluble forms
CC of PBP2A-27R protein facilitate crystallisation as they lack their
CC transmembrane association region, and so are useful for x-ray
CC crystallography studies of the protein, assisting in the design of
CC antibiotic compounds against methicillin resistant Staphylococcus
CC strains (disclosed). The chelating peptide operably linked to the
CC PBP2A-27R proteins is useful for purifying PBPs.
XX
SQ Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 19; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTAGTTGAATATCTTGCC 20
```

Db 980 CTTAGTTCGATATCTTTGCC 961

RESULT 13
ABA76993/c
ID ABA76993 standard; DNA; 2007 BP.

AC	ABA76993;
XX	
DT	28-JAN-2002 (first entry)

DE Antibiotic resistance detection polynucleotide SEQ ID NO 169.

KW Detection; bacterial species; animal; food; environment;
antibiotic resistance; ds.

OS Unidentified.

DN NZ501596-A.

D 29-JUN-2001.

PF 12-SEP-1995; 95NZ-0501596.

PR 12-SEP-1995; 95NZ-0501596.

PA (IDI-) IDI INFECTIO DIAGNOSTIC INC.

PI Bergeron MC, Ouellette M, Roy PH;

WP1: 2001-615034/71.

PT Method for detecting target bacterial species in a sample, comprises detecting the presence or amount of bacterial nucleic acid amplified by a primer derived from bacterial DNA, specific for the target bacterial

PS Claim 16; Page 159-160; 168pp; English.

CC The invention relates to detecting target bacterial species suspected to
CC be present in a sample, comprising contacting nucleic acids of target
CC bacterial species with an amplification primer pair derived from a
CC bacterial DNA fragment (ABA76825-ABA7661) specific for the target
CC bacterial species but ubiquitous for different strains, amplifying the
CC nucleic acid and detecting the presence or amount of an amplified
CC sequence as an indication of the presence or amount of the target
CC bacterial species. The invention includes primers and probes
CC (ABA76862-ABA76584) against the target bacterial species, especially

SQ Sequence 2007 BP: 855 A; 270 C; 341 G; 541 T; 0 other;

Query Match	100.0%	Score 20:	DB 22;	Length 2007;
Best Local Similarity	100.0%	Pred. No.	3.6;	
Matches 20; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY 1 GTTAGTGAATATCTTGGC 20
 |||||
 Db 980 GTTAGTGAATATCTTGGC 961

RESULT 14
ABN92247/c
ID ABN92247 standard; DNA; 2028 BP.

AC ABN92247;

DT 24-JUL-2002 (first entry)

DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.

Staphylococcus epidermidis; open reading frame; OKR; bacterial infection;

XX
XIX
XVIII
XVII
XVI
XV
XIV
XIII
XII
XI
X
IX
VIII
VII
VI
V
IV
III
II
I

XX
OS
slapny lococ

050360370-BL
FN
XX

PD 30-APR-2002.
XX

PE 13-AUG-1998; 9805-0134001.
XY

PR 14-AUG-1997; 97US-055779P.
PR 08-NOV-1997; 97US-064964P

XX
XX
(GENO-) GENOME THERAPEUTICS

XX
XX
Don't forget to see TA Buch D.

XX
XX
FMT: 2003-2012EE 1A1

DR P-PSDB; ABP39702.
yy

PT	Novel isolated nu
PT	Novel isolated nu

PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
PT polypeptide, useful for diagnosing and treating bacterial infections -
XX
PS Disclosure; SEQ ID 1710; 267pp; English.

ABN90512 to ABN93374 represent *Shaptylococcus epidermidis* open reading frame (ORF) nucleic acid sequences that encode the amino acid sequences given in ABP5124 to ABP37960. The *S. epidermidis* sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly *S. epidermidis* infections. The sequences can be used to screen for compounds able to interfere with the *S. epidermidis* life cycle or inhibit *S. epidermidis* infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.

sq sequence 2028 BP; 861 A; 273 C; 346 G; 547 T; 1 other;

Query Match	100.0%	Score 20:	DB 24:	Length 2028:
Best Local Similarity	100.0%:	Pred. NO. 3.6:		
Matches 20: Conservative	0:	Mismatches	0:	Indels 0:

QY 1 GTTAGTGAATATCTTGC 20
|||||
Db 1001 GTTAGTGAATATCTTGC 982

RESULT 15
AAQ35213/c
ID AAQ35213 standard; DNA; 2110 BP.

AC AAQ35213;

DT 06-JUN-1993 (first entry)

DE Sequence of the *mecA* gene.

KW Methicillin-resistant staphylococci; detection; primer; PCR; ss.

XX XX

```

OS      Staphylococcus aureus .
XX
FH      Key          Location/Qualifiers
FT      CDS          105..2110
FT                                     /tag=a
XX
PN      EP527628-A.
XX
PD      17-FEB-1993.
XX
PE      10-AUG-1992;   92EP-0307307.
XX
PR      13-AUG-1991;   91US-0744770.
XX
PA      (ELIL ) LILLY & CO ELI.
PI
PL      Skatrud PL, Unal S;
XX
DR      MPI: 1993-054352/07.
NR      P-PSDB: AAR30845.
!
f       Detection of methicillin-resistant staphylococci - using
PT       polymerase chain reaction method, and DNA primers, for rapid,
PT       sensitive and accurate detection
XX
PS      Disclosure: Pages 7-10; 16pp; English.
XX
CC      The inventors claim a method for detecting methicillin-resistant
CC      staphylococcal infections which involves the use of the PCR primed
CC      by fragments of the Staphylococcus meca gene. More specifically, the
CC      initial primers used are nucleotides 141-160 and the inverse
CC      complement of nucleotides 1929-1952 of the S. aureus meca gene. The
CC      interior primers are nucleotides 568-593 and the inverse complement
CC      of 1647-1670 of the S. aureus meca gene.
SO      Sequence 2110 BP: 896 A; 290 G; 350 G; 574 T; 0 other;
XX
Query Match          100.0%; Score 20; DB 14; Length 2110;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches    20; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
OY      1 GTTACTGATATCTTTGCC 20
        |||||||
db      1084 GTTAGTGAATATCTTTGCC 1065

```

```
Search completed: December 10, 2002, 17:32:33
Job time : 131.391 secs
```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 : Search time 27.2626 Seconds
(without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579A-21

Perfect score: 20

Sequence: 1 gtagttagaatatcgtgcc 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_patents.NA.*
1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCITUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	2007	2	US-08-743-637B-169 Sequence 169, App
C 2	20	100.0	2007	3	US-08-526-840B-169 Sequence 169, App
C 3	20	100.0	2028	4	US-09-134-001C-1710 Sequence 1710, Ap
C 4	15.8	79.0	15393	4	US-09-453-702B-191 Sequence 191, App
C 5	15.4	77.0	792	4	US-09-134-001C-2275 Sequence 2275, Ap
C 6	15.2	76.0	1348	4	US-08-936-165A-186 Sequence 186, App
C 7	15.1	76.0	37948	4	US-09-251-645-11 Sequence 11, Appl
C 8	14.8	74.0	489	4	US-09-812-484-30 Sequence 30, Appl
C 9	14.4	72.0	645	5	PCR-US96-05320A-766 Sequence 766, App
C 10	14.4	72.0	1998	4	US-09-280-116-222 Sequence 222, App
C 11	14.4	72.0	3996	4	US-09-332-295-3 Sequence 3, Appl
C 12	14.4	72.0	3996	4	US-09-709-979-3 Sequence 3, Appl
C 13	14.4	72.0	3997	4	US-09-208-742-1 Sequence 1, Appl
C 14	14.2	71.0	571	4	US-08-858-207A-262 Sequence 262, App
C 15	14.2	71.0	695	4	US-09-200-934-6 Sequence 6, Appl
C 16	14.2	71.0	954	4	US-09-134-001C-1156 Sequence 1156, Ap
C 17	14.2	71.0	1029	4	US-09-134-001C-2361 Sequence 2361, Ap
C 18	14.2	71.0	1668	1	US-08-463-090B-1 Sequence 3, Appl
C 19	14.2	71.0	1863	2	US-08-455-073A-3 Sequence 3, Appl
C 20	14.2	71.0	2240	1	US-08-148-058A-12 Sequence 12, Appl
C 21	14.2	71.0	2240	1	US-08-478-042-12 Sequence 12, Appl
C 22	14.2	71.0	2240	1	US-08-645-215-12 Sequence 12, Appl
C 23	14.2	71.0	2240	2	US-08-466-604-12 Sequence 12, Appl
C 24	14.2	71.0	2291	2	US-08-725-736D-1 Sequence 1, Appl
C 25	14.2	71.0	2291	2	US-09-162-368B-1 Sequence 1, Appl
C 26	14.2	71.0	2291	3	US-09-161-877B-1 Sequence 1, Appl
C 27	14.2	71.0	2304	1	US-08-464-266-1 Sequence 1, Appl

C 28	14.2	71.0	2304	1	US-08-464-272-1 Sequence 1, Appl
C 29	14.2	71.0	2304	4	US-08-464-514-1 Sequence 1, Appl
C 30	14.2	71.0	2304	4	US-08-486-403-1 Sequence 1, Appl
C 31	14.2	71.0	3115	4	US-09-221-017B-849 Sequence 849, App
C 32	14.2	71.0	5224	4	US-09-033-428-2 Sequence 2, Appl
C 33	14.2	71.0	5224	4	US-09-033-556-5 Sequence 5, Appl
C 34	14.2	71.0	5278	4	US-08-961-527-227 Sequence 227, App
C 35	14.2	71.0	5365	4	US-08-961-527-77 Sequence 77, Appl
C 36	14.2	71.0	5917	4	US-09-780-175-17 Sequence 17, Appl
C 37	14.2	71.0	25165	4	US-09-453-702B-39 Sequence 39, Appl
C 38	14	70.0	393	2	US-08-853-659A-14 Sequence 14, Appl
C 39	14	70.0	639	4	US-09-221-017B-741 Sequence 741, App
C 40	14	70.0	15512	2	US-08-853-659A-5 Sequence 5, Appl
C 41	14	70.0	15512	2	US-08-853-659A-8 Sequence 8, Appl
C 42	14	70.0	15512	2	US-08-853-659A-63 Sequence 63, Appl
C 43	14	70.0	15512	2	US-08-853-659A-66 Sequence 66, Appl
C 44	14	70.0	24701	2	US-08-853-659A-2 Sequence 2, Appl
C 45	14	70.0	24701	2	US-08-853-659A-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-743-637B-169/c
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586, 90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ. ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0%; Score 20; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGTGAATATCTTGCC 20
|||||
Db 980 GTTAGTGAATATCTTGCC 961

RESULT 2
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUFLETTE, Marc
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586, 90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169
Query Match 100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGTGAATATCTTGCC 20
|||||
Db 980 GTTAGTGAATATCTTGCC 961
RESULT 3
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 20; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTGAATATCTTGCC 20
|||||
Db 1001 GTTAGTGAATATCTTGCC 982

RESULT 4
US-09-453-702B-191/c
; Sequence 191, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723e1 Sequences of E. coli 0157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296, 95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15393
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 191:

OY 1 GTTACTGATATCTTGCC 20
|||||
DB 33968 GTCACTGACATCTTGCC 33949

RESULT 8
US-09-812-484-30/c
; Sequence 30, Application US/09812484
; Patent No. 6444430
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Au-Young, Janice
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: NDR2-RELATED PROTEINS
; FILE REFERENCE: PC-0038 CIP
; CURRENT APPLICATION NUMBER: US/09/812,484
; CURRENT FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO: 30
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6444430 701938896H1
US-09-812-484-30

Query Match 74.0%; Score 14.8; DB 4; Length 489;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTACTGATATCTTG 18
|||||
DB 113 GTTACTGATATCGCTG 96

RESULT 9
PCT-US96-05320A-766
; Sequence 766, Application PC/TUS9605320A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences
; APPLICANT: 9410 Key West Avenue
; APPLICANT: Rockville, MD 20850
; APPLICANT: United States of America
; APPLICANT: Johns Hopkins University
; APPLICANT: 720 Rutland Avenue
; APPLICANT: Baltimore, MD 21205
; APPLICANT: United States of America
; APPLICANT: Mark D. Adams
; APPLICANT: Owen White
; APPLICANT: Hamilton O. Smith
; APPLICANT: J. Craig Venter
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome,
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20003-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; OPERATING SYSTEM: MSOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05320A
; FILING DATE: April 22, 1996
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: June 7, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Eric K. Steffe
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.014PC01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 766:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 645 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US96-05320A-766

Query Match 72.0%; Score 14.4; DB 5; Length 645;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTAGTTGATATCTTT 17
|||||
DB 616 TTAGTTGATATCGTT 631

RESULT 10
US-09-280-116-222
; Sequence 222, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 222
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: ubiquitin carboxyl-terminal hydrolases family 2
; NAME/KEY: misc_feature
; LOCATION: (1)..(1998)
; OTHER INFORMATION: n - a, t, c or g
US-09-280-116-222

Query Match 72.0%; Score 14.4; DB 4; Length 1998;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTACTGATATCTTT 16
|||||
DB 1432 GTTACTGATATCTTT 1447

RESULT 11
US-09-332-295-3/c
; Sequence 3, Application US/09332295
; Patent No. 6303372
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Joerg
; TITLE OF INVENTION: CIP130 INHIBITS CELL CYCLE PROGRESSION
; FILE REFERENCE: 200130.456 / 1513.003
; CURRENT APPLICATION NUMBER: US/09/332,295
; CURRENT FILING DATE: 1999-06-11

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 ; Search time 25.9:18 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-21

Perfect score: 20
Sequence: 1 gtagtggaatattcttgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	10	US-09-865-579A-11
2	20	100.0	20	10	US-09-865-579A-21
3	20	100.0	39	10	US-09-865-579A-28
4	20	100.0	2007	10	US-09-452-559-169
5	17.4	87.0	369	10	US-09-770-791-376
6	16.8	84.0	350	10	US-09-770-791-701
7	16.4	84.0	16484	9	US-09-070-927A-158
8	16.4	82.0	1374	9	US-09-938-842A-4922
9	15.8	79.0	19866	10	US-09-764-877-3887
10	15.4	77.0	442	10	US-09-924-035A-602
11	15.4	77.0	635	10	US-09-770-149-654
12	15.4	77.0	1200	10	US-09-770-149-230
13	15.4	77.0	1200	10	US-09-887-576-739
14	15.4	77.0	2000	9	US-09-938-842A-4405
15	15.4	77.0	2507	10	US-09-925-301-397
16	15.2	76.0	699	10	US-09-815-242-4621
17	15.2	76.0	699	10	US-09-925-637-451
18	15.2	76.0	708	10	US-09-815-242-8576
19	15.2	76.0	708	10	US-09-815-242-8902

C 20	15.2	76.0	1348	10	US-09-939-980-186	Sequence 186, App
C 21	15.2	76.0	4431	10	US-09-817-514A-3	Sequence 3, Appl1
C 22	15.2	76.0	7053	10	US-09-070-927A-78	Sequence 78, Appl
C 23	15.2	76.0	12022	10	US-09-070-927A-117	Sequence 117, Appl
C 24	15.2	76.0	29607	10	US-09-764-877-3626	Sequence 3626, App
C 25	15	75.0	28	10	US-09-865-579A-22	Sequence 22, Appl1
C 26	15	75.0	27360	10	US-09-070-927A-164	Sequence 164, App
C 27	14.8	74.0	87	10	US-09-864-761-19866	Sequence 19866, A
C 28	14.8	74.0	385	10	US-09-878-574-322	Sequence 322, App
C 29	14.8	74.0	391	10	US-09-878-574-3251	Sequence 3251, Ap
C 30	14.8	74.0	446	10	US-09-864-761-3085	Sequence 3085, Ap
C 31	14.8	74.0	507	10	US-09-783-590-6033	Sequence 6033, Ap
C 32	14.8	74.0	574	10	US-09-864-761-8082	Sequence 8082, Ap
C 33	14.8	74.0	1160	12	US-10-062-254-285	Sequence 285, App
C 34	14.8	74.0	3115	9	US-09-736-457-802	Sequence 802, App
C 35	14.8	74.0	3115	9	US-09-902-941-802	Sequence 802, App
C 36	14.8	74.0	3563	10	US-09-764-877-3956	Sequence 3956, Ap
C 37	14.8	74.0	4637	9	US-09-736-457-804	Sequence 804, App
C 38	14.8	74.0	4637	9	US-09-902-941-804	Sequence 804, App
C 39	14.8	74.0	32192	10	US-09-764-877-3657	Sequence 3657, Ap
C 40	14.6	73.0	7287	10	US-09-070-927A-210	Sequence 210, App
C 41	14.4	72.0	363	10	US-09-867-701-2366	Sequence 2366, App
C 42	14.4	72.0	500	10	US-09-917-800A-529	Sequence 529, App
C 43	14.4	72.0	2010	10	US-09-887-576-232	Sequence 232, Appl
C 44	14.4	72.0	3996	12	US-10-147-268-3	Sequence 3, Appl1
C 45	14.4	72.0	21761	10	US-09-764-847-1680	Sequence 1680, Ap

ALIGNMENTS

RESULT 1
US-09-865-579A-11
Sequence 11, Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
APPLICANT: Saito, Junichi
TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
FILE REFERENCE: 9558-003-27 US/09/865, 579A
CURRENT APPLICATION NUMBER: 2001-05-29
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide capable of binding specifically to meca gene
US-09-865-579A-11
Query Match 100.0%; Score 20; DB 10; Length 20;
Best local similarity 100.0%; Pred. No. 0.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 1 GTTAGTTGAATATCTTGGC 20
Db 1 GTTAGTTGAATATCTTGGC 20
RESULT 2
US-09-865-579A-21
Sequence 21, Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:

```

; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; 09-865-579A-21
```

```

Query Match          100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 GTTAGTGAATATCTTTGCC 20
    |||||||
DB 1 GTTAGTGAATATCTTTGCC 20
```

```

RESULT 3
US-09-865-579A-28
; Sequence 28, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-865-579A-28
```

```

Query Match          100.0%; Score 20; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 GTTAGTGAATATCTTTGCC 20
    |||||||
DB 1 GTTAGTGAATATCTTTGCC 20
```

```

RESULT 4
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
```

```

; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287/31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169
```

```

Query Match          100.0%; Score 20; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 GTTAGTGAATATCTTTGCC 20
    |||||||
DB 980 GTTAGTGAATATCTTTGCC 961
```

```

RESULT 5
US-09-770-791-376/c
; Sequence 376, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(369)
; OTHER INFORMATION: n - A,T,C or G
US-09-770-791-376
```


COUNTRY:

Matches 17; Conservative 0; Mismatch 0

0; Gaps 0;

```
OY      2 TTACTGATATCTTTC 19
      ||||| ||||| |||||
Db      1338 TTAGTTAATATCTTTC 1355

RESULT 9
US-09-764-877-3887
; Sequence 3887, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3887
; LENGTH: 19866
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3887

Query Match      79.0%; Score 15.8; DB 10; Length 19866;
Best Local Similarity 89.5%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 GTTAGTGATATCTTTC 19
      ||||| ||||| |||||
Db      1311 CTCTGTGATATCTTTC 1329

RESULT 10
US-09-924-035A-602
; Sequence 602, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
; APPLICANT: Grilach, Jörn
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924,035A
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,784
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 602
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-924-035A-602

Query Match      77.0%; Score 15.4; DB 10; Length 442;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      2 TTACTGATATCTTTC 18
      ||||| ||||| |||||
Db      80 TTGGTTGATATCTTTC 96

RESULT 11
US-09-770-149-654/C
; Sequence 654, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
```

```
      APPLICANT: Yu, Yang
      APPLICANT: Rameaka, Joshua G.
      APPLICANT: Page, Amy
      APPLICANT: Mathew, Abraham V.
      APPLICANT: Ledford, Brooke L.
      APPLICANT: Moessner, Jeffrey P.
      APPLICANT: Haas, William David
      APPLICANT: Garcia, Carlos A.
      APPLICANT: Krickler, Maja
      APPLICANT: Slader, Ted
      APPLICANT: Davis, Keith R.
      APPLICANT: Allen, Keith
      APPLICANT: Hoffman, Neil
      APPLICANT: Hurban, Patrick
      TITLE OF INVENTION: Expressed Sequences of Arabidopsis
      FILE REFERENCE: 2024 (PARA-013PRV)
      CURRENT APPLICATION NUMBER: US/09/770,149
      CURRENT FILING DATE: 2001-01-26
      PRIOR APPLICATION NUMBER: 60/178,506
      PRIOR FILING DATE: 2000-01-27
      NUMBER OF SEQ ID NOS: 999
      SOFTWARE: FastSeq for Windows Version 4.0
      SEQ ID NO 230
      LENGTH: 706

US-09-770-149-654

Query Match      77.0%; Score 15.4; DB 10; Length 635;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      2 TTACTGATATCTTTC 18
      ||||| ||||| |||||
Db      556 TTGCTTGATATCTTTC 540

RESULT 12
US-09-770-149-654/C
; Sequence 230, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
      TITLE OF INVENTION: Expressed Sequences of Arabidopsis
      FILE REFERENCE: 2024 (PARA-013PRV)
      CURRENT APPLICATION NUMBER: US/09/770,149
      CURRENT FILING DATE: 2001-01-26
      PRIOR APPLICATION NUMBER: 60/178,506
      PRIOR FILING DATE: 2000-01-27
      NUMBER OF SEQ ID NOS: 999
      SOFTWARE: FastSeq for Windows Version 4.0
      SEQ ID NO 230
      LENGTH: 706
```

```

; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-230

```

```

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 10; Length 706;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 3 TACTGCAATATCTTTGC 19
    ||||| ||||| |||||
Db 106 TACTGCAAAATCTTTGC 90

```

```

RESULT 13
US-09-887-576-739

```

```

; Sequence 739, Application US/09887576
; Patent No. US2002014407A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001U1
; CURRENT APPLICATION NUMBER: US/09/887,576
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 739
; LENGTH: 1200
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-739

```

```

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 10; Length 1200;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 2 TTACTGCAATATCTTTG 18
    ||||| ||||| |||||
b 697 TTACTTAATATCTTTG 713

```

```

RESULT 14
US-09-938-842A-4405
; Sequence 4405, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepes, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379

```

```

; SEQ ID NO 4405
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4405

```

```

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 9; Length 2000;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 2 TTACTGCAATATCTTTG 18
    ||||| ||||| |||||
Db 1500 TTACTTAATATCTTTG 1516

```

```

RESULT 15
US-09-925-301-397

```

```

; Sequence 397, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 397
; LENGTH: 2507
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2469)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2496)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2504)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2505)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-397

```

```

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 10; Length 2507;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 4 AGTGAATATCTTTGCC 20
    ||||| ||||| |||||
Db 877 AGTGAAGATCTTTGCC 893

```

```

Search completed: December 11, 2002, 06:07:24
Job time : 31.9218 secs

```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 : Search time 1076.75 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-20

Perfect score: 21
Sequence: 1 tttctttctctataatg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estopl:*
7: em_estro:*
8: em_hlc:*
9: qb_est1:*
10: qb_est2:*
11: qb_hlc:*
12: qb_est3:*
13: qb_est4:*
14: qb_est5:*
15: em_estfun:*
16: em_estom:*
17: qb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrl:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_pod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	92.4	459	17	AZ792877 2M0045107
2	19.4	92.4	554	17	AZ271915 RPCI-23-1
3	18.4	87.6	107	13	B3391473 B3391473
4	18.4	87.6	183	9	AA481540 aa35f12.9
5	18.4	87.6	232	17	AZ033426 RPCI-23-3
6	18.4	87.6	320	9	AU271259 AU271259

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL COMMENT
AZ792877	2M0045107R	Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG2M0045107 R, DNA sequence.	AZ792877	1	GI:12937256	GSS.	house mouse.	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid Inserts	Unpublished (2000)	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL COMMENT
AZ792877	2M0045107R	Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG2M0045107 R, DNA sequence.	AZ792877	1	GI:12937256	GSS.	house mouse.	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid Inserts	Unpublished (2000)	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: 1 column: 07
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 459.
Location/Qualifiers

FEATURES

1. 459

source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="U06C2M0045107"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b/AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

168 a 67 c 70 g 154 t

Query Match 92.4%; Score 19.4; DB 17; Length 459;
Best Local Similarity 95.2%; Pred. No. 3e+04;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCCTTTTCCTATTATG 21
|||||
Db 68 TTTTCCTTTTCCTATTATG 88

RESULT 2
A2271915

LOCUS A2271915 554 bp DNA linear GSS 26-JUL-2000
DEFINITION RPCI-23-146L23.TJ RPCI-23 Mus musculus genomic clone RPCI-23-146L23
, DNA sequence.

CESSION A2271915
KEYWORDS A2271915.1 GI:9485532
SOURCE GSS.
ORGANISM house mouse.
MUS musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 554)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akkurat,
B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Kroll, M., de Jong, P.,
and Fraser, C. M.

AUTHORS Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-146L23.TV
Contact: Shaying Zhao

TITLE The Institute for Genomic Research
JOURNAL Department of Eukaryotic Genomics
COMMENT 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igf.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@edj.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 146 row: L column: 23
Seq primer: SP6
Class: BAC ends.

FEATURES

source

Location/Qualifiers
1. 554
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="RPCI-23-146L23"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site: 1;
EcoRI; Site: 2; EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 127 a 123 c 136 g 168 t
ORIGIN

Query Match 92.4%; Score 19.4; DB 17; Length 554;
Best Local Similarity 95.2%; Pred. No. 2.7e+04;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCCTTTTCCTATTATG 21
|||||
Db 409 TTTTCCTTTTCCTATTATG 429

RESULT 3
BJ391473/c

LOCUS BJ391473 107 bp mRNA linear EST 08-MAR-2002
DEFINITION BJ391473 Dictyostelium discoideum cDNA library, SF Dictyostelium
discoideum cDNA clone dds24e03 5', mRNA sequence.

ACCESSION BJ391473
VERSION BJ391473.1 GI:19302559
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.

REFERENCE Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
1 (bases 1 to 107)
Urushihara, H., Tanaka, Y., Kohara, Y., and Shin-i, T.

AUTHORS Full length cDNA of Dictyostelium discoideum at the slug stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasi Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES Location/Qualifiers
1. 107
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone_lib="dds24e03"
/clone_lib="Dictyostelium discoideum cDNA library, SF"
/sex="mat A"
/dev_stage="Slug stage"
BASE COUNT 64 a 0 c 9 g 34 t
ORIGIN

Query Match 87.6%; Score 18.4; DB 13; Length 107;
Best Local Similarity 95.0%; Pred. No. 1e+05;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCCTTTTCCTATTAT 20

```

DB      107 TTTTCTTTCTCTATTAA 88
|||||
RESULT  4
LOCUS   AA481540
DEFINITION AA481540 183 bp mRNA linear EST 14-ANG-1997
          aa35f12.s1 NCI_CGAP_CCB1 Homo sapiens cDNA clone IMAGE:815279 3',
          mRNA sequence.
ACCESSION AA481540
VERSION   AA481540.1 GI:2211092
KEYWORDS EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 183)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
           Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
           Ph.D., Gerald Marti, M.D.
           cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
           cDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/ILMIL at:
           www.bio.liml.gov/bbrp/image/image.html
           Seq primer: -41m13 fwd. 5' from Amersham
           High quality sequence stop: 176.
           Location/Qualifiers
             1..183
               /organism="Homo sapiens"
               /db_xref="GDB:6034365"
               /db_xref="taxon:9606"
               /clone_image="815279"
               /clone_lib="NCI-CGAP_CCB1"
               /lisse_type="germlinal center B cell"
               /lab_host="DH10B"
               /note="Vector: pUT3D-Pac (Pharmacia) with a modified
               polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
               was prepared from human tonsillar cells enriched for
               germinal center B cells by flow sorting (CD20+, IgD-),
               provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
               (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
               primed with a Not I - oligo(dT) primer
               15'-GTGACCAATCTGACAGCGGAGCGCCGCTCATTTTCTTTCTTTT-3'
               1. Double-stranded cDNA was ligated to Eco RI adaptors
               (Pharmacia), digested with Not I and cloned into the Not I
               and Eco RI sites of the modified pUT3D vector. Library
               went through one round of normalization, and was
               constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      58 a      35 c      34 g      56 t
ORIGIN
Query Match      87.6%; Score 18.4; DB 9; Length 183;
Best Local Similarity 95.0%; Pred. No. 8.1e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 TTTTCTTTCTCTATTAA 20
Db      6 TTTTCTTTCTGATTAA 25

```

```

ACCESSION A2033426
VERSION   A2033426.1 GI:7117769
KEYWORDS GSS.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
           1 (bases 1 to 232)
REFERENCE 1 (bases 1 to 232)
AUTHORS   Zhao, S., Nierman, W., Feldblum, T., Maick, J., Shatsman, S., Akincet,
           B., Levins, M., McGann, S., Tsengaye, G., Geor, K., Krol, M., de Jong, P.,
           and Fraser, C. M.
           Mouse BAC End Sequences from Library RPCI-23
           Unpublished (1999)
COMMENT   Other GSSs: RPCI-23-361N2.TV
           Contact: Shaying Zhao
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr., Rockville, MD 20850, USA
           Tel: 301 838 0200
           Fax: 301 838 0208
           Email: szhao@tigr.org
           Clones are derived from the mouse BAC library RPCI-23. For BAC
           library availability, please contact Pieter de Jong
           (pieterdejong.med.bufileo.edu). Clones may be purchased from
           BACPAC Resources (http://bacpac.med.bufileo.edu/orderingframe.htm)
           or from Resea ch Genetics (info@resgen.com). BAC end page:
           http://www.tigr.org/tdb/bac-ends/mouse/bac_end_intro.html
           Seq primer: Sp6
           Class: BAC ends.
           Location/Qualifiers
             1..232
               /organism="Mus musculus"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone_image="RPCI-23-361N2"
               /clone_lib="RPCI-23"
               /sex="Female"
               /lab_host="DH10B"
               /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1:
               EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
               brain genomic DNA was isolated and partially digested
               with a combination of EcoRI and EcoRI Methylase. Size
               selected DNA was cloned into the pBAC3.6 vector at the
               EcoRI sites. The ligation products were transformed into
               DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      40 a      35 c      23 g      130 t      4 others
ORIGIN
Query Match      87.6%; Score 18.4; DB 17; Length 232;
Best Local Similarity 95.0%; Pred. No. 7.3e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 TTTTCTTTCTCTATTAA 20
Db      48 TTTTCTTTCTTATTAA 67

```

```

RESULT  6
LOCUS   AU271259
DEFINITION AU271259 VS Dictyostellium discoideum cDNA clone VSK473 3', mRNA
          sequence.
ACCESSION AU271259
VERSION   AU271259.1 GI:20530057
KEYWORDS EST.
SOURCE    Dictyostellium discoideum.
ORGANISM  Dictyostellium discoideum
           Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
           1 (bases 1 to 320)
REFERENCE 1 (bases 1 to 320)
AUTHORS   Urushihara, H., Morio, T., Saito, T., Kori, E., Ochiai, H., Maeda, M.,
           Takeuchi, T., Kohara, Y., and Tanaka, Y.
           Population analysis of cDNAs from unicellular and multicellular

```

JOURNAL
COMMENT

stages of Dictyostelium discoideum
Unpublished (2002)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES
source

1..320
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSK473"
/clone_1lb="VS"
/sex="mat A"
/dev_stage="vegetative"
BASE COUNT 126 a 43 c 33 g 90 t 28 others
ORIGIN

Query Match 87.6%; Score 18.4; DB 9; Length 320;
Best Local Similarity 95.0%; Pred. No. 6.3e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAT 20
||||| ||||| ||||| |||||
Db 49 TTTCTTTTCTCTATTAT 68

RESULT 7
LOCUS AQ236558 322 bp DNA linear GSS 29-SEP-1998
DEFINITION HS_2033_B2_P05_r7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2033 COL=10 Row=L, DNA sequence.
ACCESSION AQ236558
VERSION AQ236558.1 GI:3661959
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 322)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GC, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2033 row: L column: 10
Class: BAC ends
High quality sequence stop: 322.
Location/Qualifiers

FEATURES
source
1..322
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-2033 COL=10 Row=L"
/clone_1lb="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeLoBAC11; BAC clones in
E-Coli DH10B"
BASE COUNT 121 a 58 c 42 g 101 t
ORIGIN

Query Match 87.6%; Score 18.4; DB 17; Length 322;
Best Local Similarity 95.0%; Pred. No. 6.3e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAT 20
||||| ||||| ||||| |||||
Db 52 TTTCTTTTCTCTATTAT 33

RESULT 8
LOCUS AU271258 325 bp mRNA linear EST 10-MAY-2002
DEFINITION AU271258 VS Dictyostelium discoideum cDNA clone VSK473 5', mRNA
sequence.
ACCESSION AU271258
VERSION AU271258.1 GI:20530056
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
Eukaryota; Mycelozoa; Dictyostelid; Dictyostelium.
1 (bases 1 to 325)
Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
Takeuchi,I., Kohara,Y. and Tanaka,Y.
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
Unpublished (2002)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers

FEATURES
source
1..325
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSK473"
/clone_1lb="VS"
/sex="mat A"
/dev_stage="vegetative"
BASE COUNT 126 a 45 c 35 g 105 t 14 others
ORIGIN

Query Match 87.6%; Score 18.4; DB 9; Length 325;
Best Local Similarity 95.0%; Pred. No. 6.3e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAT 20
||||| ||||| ||||| |||||
Db 51 TTTCTTTTCTCTATTAT 70

RESULT 9
LOCUS BJ336009 358 bp mRNA linear EST 05-MAR-2002
DEFINITION BJ336009 Dictyostelium discoideum cDNA library, Ar Dictyostelium
discoideum cDNA clone dda52k07 5', mRNA sequence.
ACCESSION BJ336009
VERSION BJ336009.1 GI:19166139
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
Eukaryota; Mycelozoa; Dictyostelid; Dictyostelium.
1 (bases 1 to 358)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
stage
Unpublished (2002)
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics

FEATURES
source
1..358
/organism="Dictyostelium discoideum"
/db_xref="taxon:9606"
/clone="Plate-2033 COL=10 Row=L"
/clone_1lb="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeLoBAC11; BAC clones in
E-Coli DH10B"
BASE COUNT 121 a 58 c 42 g 101 t
ORIGIN

1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: lshn@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. 358
/organism="Dicyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone_lib="Dicyostelium discoideum cDNA library, AF"
/sex="mat A"
/dev_stage="Aggregation stage"

BASE COUNT 144 a 53 c 35 g 106 t 20 others
ORIGIN

Query Match 87.6%; Score 18.4; DB 13; Length 358;
Best Local Similarity 95.0%; Pred. No. 6e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/ 1 TTTCTTTTCTCTATTAT 20
|||||
Db 82 TTTTCTTTCTCTATTAT 101

RESULT 10
LOCUS AZ111107 379 bp DNA linear GSS 09-MAY-2000
DEFINITION RPI-23-469P1.TJ RPI-23 Mus musculus genomic clone RPI-23-469P1,
DNA sequence.
ACCESSION AZ111107
VERSION AZ111107.1 GI:7764165
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS
1 (bases 1 to 379)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S., Akiret,
B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPI-23
Unpublished (1999)
Other-GSS: RPI-23-469P1.TV

TITLE
JOURNAL
COMMENT
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
or from Resea ch Genetics (http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html)
Plate: 469 row: P column: 1
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers

FEATURES
source
1. 379
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="RPI-23-469P1"
/clone_lib="RPI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site: 1;
EcoRI; Site: 2; EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size

BASE COUNT 67 a 86 c 46 g 180 t
ORIGIN
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

Query Match 87.6%; Score 18.4; DB 17; Length 379;
Best Local Similarity 95.0%; Pred. No. 5.8e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/Y 1 TTTCTTTTCTCTATTAT 20
|||||
Db 94 TTTCTTTTCTCTATTAT 113

RESULT 11
LOCUS BF354467/c 392 bp mRNA linear EST 22-NOV-2000
DEFINITION MR2-HT0758-070800-009-e05 HT0758 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF354467
VERSION BF354467.1 GI:11313541
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 392)
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Bioness, M.R.,
Nagai, M.A., da Silva, W. Jr., Zagro, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663

TITLE
JOURNAL
MEDLINE
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-HT0758-070800-009-e05&t3=2000-08-07&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 391.
Location/Qualifiers

FEATURES
source
1. 392
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0758"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site: 1; SmaI;
Site: 2; SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 120 a 81 c 103 t 1 others
ORIGIN

Query Match 87.6%; Score 18.4; DB 12; Length 392;
Best Local Similarity 95.0%; Pred. No. 5.8e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/Y 2 TTTCTTTTCTCTATTAT 21


```

Db      51 TTTCTTATCTCTATTATG 32
|||||
RESULT 12
LOCUS   A2281155
DEFINITION A2281155 416 bp DNA linear GSS 26-JUL-2000
          RPCI-23-138B7.TJ RPCI-23 Mus musculus genomic clone RPCI-23-138B7,
          DNA sequence.
ACCESSION A2281155
VERSION   A2281155.1 GI:9500057
KEYWORDS GSS.
SOURCE    house mouse.
ORGANISM Mus musculus
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 416)
AUTHORS   Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatsman,S., Akinet
          ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
          and Fraser,C.M.
TITLE     Mouse BAC End Sequences from Library RPCI-23
JOURNAL   Unpublished (1999)
COMMENT   Other-GSSs: RPCI-23-138B7.TV
          Contact: Shaying Zhao
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: szhao@tigr.org
          Clones are derived from the mouse BAC library RPCI-23. For BAC
          library availability, please contact Pieter de Jong
          (pieter@edj.med.bufileo.edu). Clones may be purchased from
          BACPAC Resources (http://bacpac.med.bufileo.edu/orderingframe.htm)
          or from Resea ch Genetics (info@resgen.com). BAC end page:
          http://www.tigr.org/tdb/bac-ends/mouse/bac_end_intro.html
          Plate: 138 row: B column: 7
          Seq primer: SP6
          Class: BAC ends.
FEATURES
Source    Location/Qualifiers
          1..416
             /organism="Mus musculus"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="RPCI-23-138B7"
             /clone_11b="RPCI-23"
             /sex="Female"
             /lab_host="DH10B"
             /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1:
             EcoRI; Site_2: EcoRI; female C57BL/6J mouse kidney and/or
             brain genomic DNA was isolated and partially digested
             with a combination of EcoRI and EcoRI Methylase. Size
             selected DNA was cloned into the pBAC3.6 vector at the
             EcoRI sites. The ligation products were transformed into
             DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 124 a 80 c 66 g 146 t
ORIGIN
Query Match 87.6%; Score 18.4; DB 17; Length 416;
Best Local Similarity 95.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TTTCTTTTCTCTATTAT 20
Db 269 TTTCTTTTCTCTACTAT 288

```

```

VERSION   BG238677.1 GI:12773750
KEYWORDS EST.
SOURCE    soybean.
ORGANISM Glycine max
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
          Glycine.
REFERENCE 1 (bases 1 to 438)
AUTHORS   Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
          ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
          Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
          ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
          ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
          ,R., Waterston,R. and Wilson,R.
TITLE     Public Soybean EST Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Shoemaker R/Public Soybean EST Project
          Public Soybean EST Project
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available through: ResGen, Invitrogen Corp. 2130
          South Memorial Parkway Huntsville, AL 35801 For further information
          call: (800)-533-4363 or contact via email: ccut@resgen.com.
FEATURES
Source    Location/Qualifiers
          1..438
             /organism="Glycine max"
             /db_xref="taxon:3847"
             /clone="GENOME SYSTEMS CLONE ID: Gm-c1043-3121"
             /clone_11b="Gm-c1043"
             /tissue-type="Hypocotyl and Plumule, germinating seeds"
             /lab_host="DH10B"
             /note="vector: pRTTpac (Pharmacia); Site_1: EcoRI;
             Site_2: NotI; This cDNA library was constructed from mRNA
             isolated from hypocotyl and plumule tissues of seeds
             germinated for three days of the cultivar Williams.
             Complementary DNA was synthesized from mRNA using a primer
             consisting of a poly(dT) sequence with a NotI restriction
             site. EcoRI adapters were ligated to the blunt-ended cDNA
             fragments followed by digestion with EcoRI and NotI. The
             cDNA fragments were directionally cloned into the
             EcoRI-NotI restriction site of the pRTT3-Pac vector. The
             ligated cDNA fragments were transformed into DH10B host
             cells (Gibco BRL). This library was constructed by Dr.
             Randy Shoemaker."
BASE COUNT 124 a 85 g 155 t 1 others
ORIGIN
Query Match 87.6%; Score 18.4; DB 12; Length 438;
Best Local Similarity 95.0%; Pred. No. 5.5e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TTTCTTTTCTCTATTAT 20
Db 61 TTTCTTTTCTCTATTAT 80

```

```

RESULT 13
LOCUS   BG238677
DEFINITION BG238677 438 bp mRNA linear EST 28-NOV-2001
          sab54b01.y1 Gm-c1043 glycine max cDNA clone GENOME SYSTEMS CLONE
          ID: Gm-c1043-3121 5', mRNA sequence.
ACCESSION BG238677

```

```

RESULT 14
LOCUS   BJ354059/c
DEFINITION BJ354059 Dictyostellium discoideum cDNA library, Af Dictyostellium
          discoideum cDNA clone dda32k07 3', mRNA sequence.
ACCESSION BJ354059
VERSION   BJ354059.1 GI:19253653
KEYWORDS EST.
SOURCE    Dictyostellium discoideum.
ORGANISM Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
REFERENCE 1 (bases 1 to 438)
          Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.

```

TITLE Full length cDNA of Dictyostelium discoideum at the aggregation stage
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
 1. .438
 /organism="Dictyostelium discoideum"
 /strain="Ax4"
 /db_xref="taxon:44689"
 /clone="ddas2k07"
 /clone_lib="Dictyostelium discoideum cDNA library, AF"
 /sex="mat A"
 /dev_stage="Aggregation stage"
 /dev_stage 41 C 59 g 204 t 1 others

BASE COUNT 133 a 133 a 41 C 59 g 204 t 1 others
 TIGIN

Query Match 87.6%; Score 18.4; DB 13; Length 438;
 Best Local Similarity 95.0%; Pred. No. 5.5e+04;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTAA 20
 |||||
 Db 357 TTTTCTTTTCTCTATTAA 338

RESULT 15
 AO363486/c 439 bp DNA linear GSS 16-DEC-1999
 LOCUS nbxb0059C14r CUGI Rice BAC Library Oryza sativa genomic clone
 DEFINITION
 ACCESSION AO363486
 VERSION AO363486
 KEYWORDS GSS.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 439)
 Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Rice Genome
 Unpublished (1998)
 On Dec 15, 1999 this sequence version replaced gl:4213141.
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Seq primer: GGAAACAGCTATGACCATG
 Class: BAC ends
 High quality sequence stop: 339.
 Location/Qualifiers
 1. .439
 /organism="Oryza sativa"
 /strain="Japonica"
 /cultivar="Nipponbare"
 /db_xref="taxon:4530"
 /clone="nbxb0059C14r"
 /clone_lib="CUGI Rice BAC Library"
 /tissue_type="leaf"
 /lab_host="E. coli DH10B"
 /note="Vector: pBelobAC11; site_1: HindIII; site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics

FEATURES
 source

and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

BASE COUNT 174 a 69 c 90 g 106 t
 TIGIN

Query Match 87.6%; Score 18.4; DB 17; Length 439;
 Best Local Similarity 95.0%; Pred. No. 5.5e+04;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTAA 20
 |||||
 Db 357 TTTTCTTTTCTCTATTAA 338

Search completed: December 10, 2002, 22:49:55
 Job time : 1080.75 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 : Search time 182.547 Seconds
(without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28
Sequence: 1 caactaactatgatgctaagttaaa 28

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

otal number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N.Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	ABK85925	Methicillin resist
2	28	100.0	108	AAK15487	Probe mecA913-1020
3	28	100.0	1789	AAAT04536	Staphylococcus aur
4	28	100.0	2007	AAQ28599	Encodes penicillin
5	28	100.0	2007	AAT28568	Bacterial antibiotic
6	28	100.0	2007	AAV68337	Penicillin binding
7	28	100.0	2007	ABA65993	Antibiotic resista
8	28	100.0	2028	ABN92247	Staphylococcus epi
9	28	100.0	2110	AAO35213	Sequence of the me

10	28	100.0	2322	13	AAQ25805	PBP2', Synthetic.
11	28	100.0	2455	16	AAAT04538	Staphylococcus aur
12	28	100.0	2456	22	AAH01187	Staphylococcus aur
13	25	89.3	89	20	AAK05906	Oligonucleotide pro
14	25	89.3	89	20	AAK15478	Probe mecA945-89
15	20.6	73.6	13206	19	AAV52166	Streptococcus pneu
16	20.6	73.6	16995	19	AAV52215	Streptococcus pneu
17	20	71.4	1166	21	AAK47557	Streptococcus pneu
18	20	71.4	1168	21	AAK34492	Arabidopsis thalia
19	19.6	70.0	2229	21	AAK39154	Arabidopsis thalia
20	19	67.9	747	20	ABN68422	Streptococcus poly
21	19	67.9	737	20	AAK99638	Nucleic acid seque
22	19	67.9	1635	20	AAK99510	Nucleic acid seque
23	19	67.9	2996	19	AAV52293	Streptococcus pneu
24	19	67.9	11309	19	AAV52241	Streptococcus pneu
25	19	67.9	12505	23	ABL07020	Drosophila melanog
26	19	67.9	134499	21	AAK22286	BAC containing rep
27	18.8	67.1	5711	24	ABO71041	Listeria monocytog
28	18.8	67.1	2944528	24	ABAO3041	Listeria monocytog
29	18.8	67.1	3011208	24	ABO69245	Listeria innocua D
30	18.6	66.4	336	22	AAK39087	Novel human diapo
31	18.6	66.4	2529	23	ABL19336	Drosophila melano
32	18.6	66.4	2821	23	ABL19338	Drosophila melano
33	18.6	66.4	3094	23	ABL27444	Drosophila melano
34	18.6	66.4	7962	23	ABL1516	Drosophila melano
35	18.6	66.4	7962	23	ABL19762	Drosophila melano
36	18.6	66.4	11443	19	AAV52182	Streptococcus pneu
37	18.4	65.7	1208	21	AAK33603	Arabidopsis thalia
38	18.4	65.7	4404	23	ABL29720	Drosophila melano
39	18.4	65.7	4622	24	ABK81410	DNA encoding small
40	18.4	65.7	6084	24	ABK12230	Drosophila melano
41	18.4	65.7	8076	24	ABK39955	Human chemically p
42	18.4	65.7	8136	24	ABK39957	Human chemically p
43	18.4	65.7	8136	24	ABL32555	Human immune syste
44	18	64.3	462	24	ABL3633	Human immune syste
45	18	64.3	588	24	ABO27036	Oligonucleotide fo

ALIGNMENTS

RESULT 1
ID ABK85925 standard; DNA; 28 BP.
XX
AC ABK85925:
XX
16-AUG-2002 (first entry)
XX
DE Methicillin resistant Staphylococcus aureus detection primer #25.
XX
XX Methicillin resistant Staphylococcus aureus; MRSA; primer; ss:
KW mecA: probe.
XX
OS Staphylococcus aureus.
XX
PN EPI160333-A2.
XX
PD 05-DEC-2001.
XX
PF 29-MAY-2001; 2001EP-0112100.
XX
PR 29-MAY-2000; 2000P-0163149.
PR 09-JUN-2000; 2000UP-0179394.
XX
PA (TOYJ) TOSOH CORP.
XX
PI Taya T, Ishiguro T, Saito J;
XX
DR WPI: 2002-395832/43.
XX
PT New oligonucleotide specific for the mecA methicillin-resistance gene,
useful for cleavage, detection and amplification of the gene or related

```

PT mRNA -
XX Claim 6; Page 21; 28pp; English.
PS
XX
CC This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in
CC Staphylococcus aureus) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the mecA gene as template. Also disclosed is a detection
CC method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant S. aureus in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the mecA gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
XX
SO Sequence 28 BP; 12 A; 5 C; 3 G; 8 T; 0 other;

Query Match      100.0%; Score 28; DB 24; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAACCTAACTATTGATGCTAAAGTTCAAA 28
   ||||||||||||||||||||||||||||
DB 1 CAACCTAACTATTGATGCTAAAGTTCAAA 28

RESULT 2
AAK15487
ID AAK15487 standard; DNA; 108 BP.
XX
AC AAK15487;
XX
DT 07-MAY-1999 (first entry)
XX
DE Probe mecA913-1020 for detecting an antibiotic resistant mecA gene.
XX
KM Antibiotic resistant mecA gene; transmission; treatment:
XX methicillin resistant; Staphylococcus; probe; ss.
XX
S Synthetic.
Staphylococcus sp.
..X
PN WO9901572-A2.
XX
PD 14-JAN-1999.
XX
PF 03-JUL-1998; 98WO-CA00633.
XX
PR 22-JUN-1998; 98US-0090276.
PR 03-JUL-1997; 97US-0051643.
PR 18-MAY-1998; 98US-0086020.
XX
PA (IDH1-) ID H1OMEDICAL CORP.
XX
PI Bekkaoul F, Cloney LP;
XX
DR WP1; 1999-106072/09.
XX
PT Method for determining the presence of an antibiotic resistant mecA
PT gene in a sample - using a scissile link containing nucleic acid
XX
PS Claim 4; Page 17; 59pp; English.
XX

```

```

CC The present sequence represents a probe used for determining the
CC presence of an antibiotic resistant mecA gene in a biological sample.
CC The method provides a means for the rapid detection, for both
CC the prevention of transmission and treatment of, methicillin resistant
CC Staphylococcus species.
XX
SO Sequence 108 BP; 53 A; 14 C; 16 G; 25 T; 0 other;

Query Match      100.0%; Score 28; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAACCTAACTATTGATGCTAAAGTTCAAA 28
   ||||||||||||||||||||||||||||
DB 67 CAACCTAACTATTGATGCTAAAGTTCAAA 94

RESULT 3
AAT04536
ID AAT04536 standard; cDNA to mRNA; 1789 BP.
XX
AC AAT04536;
XX
DT 11-APR-1996 (first entry)
XX
DE Staphylococcus aureus 'mecA protein coding sequence.
XX
KM methicillin-resistant Staphylococcus aureus; MRSA; 'mecA protein;
XX antibiotic resistance; ds.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT CDS 1..1608
FT /*tag= a
FT /product= 'mec_A-protein
PN JP07209294-A.
XX
PD 11-AUG-1995.
XX
PF 10-JAN-1994; 94JP-(*)2226.
XX
PR 10-JAN-1994; 94JP-0012226.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KAMA/) KAMANO M.
PA (MITU) MITSUBISHI CHEM CORP.
XX
DR WP1; 1995-313917/41.
DR P-PSDB; AAR80035.
XX
PT New 'mec A protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
XX
PS Claim 5; Page 11-13; 15pp; Japanese.
XX
CC The present sequence codes for the 'mec A protein which controls
CC methicillin resistance in methicillin-resistant Staph. aureus. The
CC 'mec A protein (mol. wt. 40000) is useful for preparation of
CC antiserum specific for MRSA, thereby allowing methicillin-resistant
CC and methicillin-sensitive strains to be distinguished. The coding
CC sequence was obtained by PCR amplification of the mec A sequence
CC (see AAT04538) using primers AAT04537 and AAT04539.
CC N.B. In the sequence listing of the patent specification, the
CC sequence length is stated to be 1785 bp.
XX
SO Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;

Query Match      100.0%; Score 28; DB 16; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 CAACCTAACTATTGATGCTAAAGTTCAAA 28
        ||||||||||||||||||||||||||||
Db       574 CAACCTAACTATTGATGCTAAAGTTCAA 601

RESULT 4
ID      AAQ285599 standard; DNA; 2007 BP.
XX
XX      AAQ285599:
AC
XX      19-FEB-1993 (first entry)
DT
XX      Encodes penicillin binding protein PBP2A-27R.
DE
XX      Penicillin: antibiotic; bacteria; methicillin; staphylococci;
KW      soluble; chelating peptide; MRS infection; methicillin resistant;
KM      strain.
XX
XX      Staphylococcus aureus strain 27R.
NS
X
X      Key Location/Qualifiers
FH      1..2007
FT      CDS /*tag= a
XX
XX      EP505151-A.
XX
XX      23-SEP-1992.
PD
XX      18-MAR-1992; 92EP-0302298.
PP
XX      19-MAR-1991; 91US-0672704.
PR
XX      (ELIL ) LILLY & CO ELI.
PA
XX      Blaszczak IC, Skatrud PL, Smith MC, Wu CY;
PI      WPI; 1992-318034/39.
DR
XX
XX      Polynucleotide cpd. encoding PBP 2A-27R protein or its deriv. -
PT      contains PBP isolated from Staphylococcus aureus and is used to
PR      treat methicillin resistant staphylococci
XX
XX      Disclosure: Page 14; 101pp; English.
PS
XX
XX      This sequence encodes a PBP2A penicillin binding protein isolated
CC      from S. aureus strain 27R. A cDNA library was constructed from
CC      S. aureus DNA in lambda phage EMBL3. Packaging extracts from this were
CC      then used to infect E. coli CJ236. Plaques were screened for the
CC      presence of the meca-27R gene by a probe produced by PCR amplification
CC      of the meca gene using primers Q28600.1. Positive plaques were purified
CC      and digested with HindIII, and this fragment digested with XbaI and
CC      cloned into M13mp18 and M13mp19 for sequencing.
XX
XX      Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other:

Query Match 100.0%; Score 28; DB 13; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 CAACCTAACTATTGATGCTAAAGTTCAAA 28
        ||||||||||||||||||||||||||||
Db       973 CAACCTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 5
ID      AAT28568 standard; DNA; 2007 BP.
XX
XX      AAT28568:
AC
XX      01-APR-1997 (first entry)
DT
XX

```

DE Bacterial antibiotic resistance gene, meca, probe.

XX
KW Detection; probe; amplification primer; bacterial pathogen; pneumonia;
KW Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
KW Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
KW Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
KW Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
KW Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis;
KW Infection; intra-abdominal infection; skin infection;
KM bacterial resistance; beta-lactam antibiotic; ds.
XX
OS Synthetic.
XX
PN W09608582-A2.
PD
FD 21-MAR-1996.
XX
PF 12-SEP-1995; 95WO-CA00528.
PR 12-SEP-1994; 94US-0304732.
XX
PA (BERG/) BERGERON M G.
PA (OUEL/) OUELLETTE M.
PA (ROYP/) ROY P H.
PI Bergeron MG, Ouellette M, Roy PH;
XX
DR WP1: 1996-179953/18.
PS
XX
PT Method for the detection of bacterial species using probes and
PT primers - allows detection and quantification of antibiotic
PT resistant bacteria in patients, the environment and food
XX
XX
PS Claim 91; Page 144-145; 216pp; English.

The sequences given in AAT28560-76 represent fragments derived from bacterial antibiotic resistance genes which were used as probes in the method of the invention for the detection of bacterial species in a sample. The method of the invention comprises using probes and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from selected bacterial species in any sample, where the bacterial nucleic acid comprises a selected target region hybridisable with the probes or primers. The method comprises contacting the sample with the probes or primers and detecting the presence and/or amount of hybridised products or amplification products as and indication of the presence and/or amount of the bacterial species. This method may be used to detect commonly encountered bacterial pathogens, e.g. Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus pyogenes, Haemophilus influenzae and Moraxella catarrhalis. These bacterial species are associated with approx. 90% of urinary tract infections and with a high percentage of other severe infections including septicaemia, meningitis, pneumonia, intra-abdominal infections, skin infections and other severe respiratory tract infections. The method may also be used to evaluate a bacterial resistance to beta-lactam antibiotics.

SO Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;

Query Match 100.0%; Score 28; DB 17; Length 2007;
Best Local Similarity 100.0%; Pred. NO. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAACCTACTATTGATGTAAAGTTCAA 28
|||||
DB 973 CAACCTACTATTGATGTAAAGTTCAA 1000

RESULT 6
AAV68337 standard; DNA; 2007 BP.

XX	AAV68337;
AC	
XX	21-JUN-1999 (first entry)
DT	
XX	penicillin binding protein PBP2A mecA-27R gene of S. aureus 27R.
DE	
XX	penicillin binding protein; PBP2A-27A: mecA-27R gene;
KW	methicillin resistance; antibiotic assay; purification: ss.
XX	
OS	Staphylococcus aureus.
PN	
XX	EP875578-A2.
XX	
PD	04-NOV-1998.
XX	
PF	18-MAR-1992: 92EP-0302298.
XX	
PR	19-MAR-1991: 91US-0672704.
XX	
\	(ELIL) LILLY & CO ELI.
A	
PI	Biaszczak LC, Skatrud PL, Smith MC, Wu CE;
XX	
DR	WPI: 1998-559443/48.
DR	P-PDSB: AAW81149.
XX	
PT	New Staphylococcus aureus soluble penicillin-binding proteins and
PT	their derivatives - useful for screening for compounds effective
PT	against methicillin resistant organisms
PS	
XX	Disclosure: Page 14-16; 97pp; English.
XX	
CC	This mecA-27R gene encodes penicillin binding protein 2A (PBP2A-27R)
CC	responsible for the methicillin resistance of Staphylococcus aureus
CC	strain 27R. The invention provides new PBPs of formula SP-I-PBP2As,
CC	where: SP is 0 or a signal peptide (preferably from the ampc, ompA or
CC	beta-lactamase gene product); I is Met-Vai or a compound of formula
CC	Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see
CC	AA81151-58) of formula (His)x(Aiy)(His)z and A=an amino acid,
CC	x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above
CC	polypeptide where each monomer unit is the same or different; Pro
CC	is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see
CC	AA81159-62). Also claimed are polynucleotides encoding specific
CC	soluble PBP2A compounds. The new PBP2A-27R proteins are useful for
CC	assaying for agents useful as antibiotics against methicillin
CC	resistant Staphylococcus strains by creating a kinetically inert
CC	complex between a support-immobilised transition ion and a modified
CC	soluble PBP2A protein comprising a chelating agent, which screens
CC	for agents which bind to PBP2A proteins (disclosed). Soluble forms
CC	of PBP2A-27R protein facilitate crystallisation as they lack their
CC	transmembrane association region, and so are useful for x-ray
CC	crystallography studies of the protein, assisting in the design of
CC	antibiotic compounds against methicillin resistant Staphylococcus
CC	strains (disclosed). The chelating peptide operably linked to the
CC	PBP2A-27R proteins is useful for purifying PBPs.
SQ	
XX	Sequence 2007 BP: 855 A: 272 C: 341 G: 539 T: 0 other:
Query Match	100.0%; Score 28; DR 19; Length 2007;
Best Local Similarity	100.0%; Pred. No. 0.028;
Matches 28: Conservative 0: Mismatches 0: Indels 0: Gaps 0:	
OY	1 CAACTAACTATTGATGCTAAAGTTCAAA 28
DB	973 CAACTAACCTATTGATGCTAAAGTTCAAA 1000
RESULT 7	
ABA76993	
ID	ABA76993 standard: DNA: 2007 BP.
XX	
XX	ABA76993:

XX	28-JAN-2002	(first entry)
DT		
XX	Antibiotic resistance detection polynucleotide seq	ID NO 169.
DE		
XX	Detection: bacterial species; animal; food; environment;	
KW	antibiotic resistance; ds.	
KW	antibiotic resistance; ds.	
XX	Unidentified.	
OS		
XX	NZ501596-A.	
PN		
XX	29-JUN-2001.	
PD		
XX	12-SEP-1995:	95NZ-0501596.
PF		
PR	12-SEP-1995:	95NZ-0501596.
XX		
PA	(IDI-1) IDI INFECTIO DIAGNOSTIC INC.	
XX		
PI	Bergeron MG, Ouellette M, Roy PH;	
XX		
DR	WPI: 2001-615034/71.	
XX		
PT	Method for detecting target bacterial species in a sample, comprising	
PT	detecting the presence or amount of bacterial nucleic acid amplified by	
PT	a primer derived from bacterial DNA, specific for the target bacterial	
PT	species	
XX		
PS	Claim 16; Page 159-160; 168pp; English.	
XX		
CC	The invention relates to detecting target bacterial species suspected to	
CC	be present in a sample, comprising contacting nucleic acids of target	
CC	bacterial species with an amplification primer pair derived from a	
CC	bacterial DNA fragment (ABA76825-ABA76861), specific for the target	
CC	bacterial species but ubiquitous for different strains, amplifying the	
CC	nucleic acid and detecting the presence or amount of an amplified	
CC	sequence as an indication of the presence or amount of the target	
CC	bacterial species. The invention includes primers and probes	
CC	(ABA76862-ABA76984) against the target bacterial species, especially	
CC	<i>E.coli</i> , <i>K.pneumoniae</i> , <i>P.aeruginosa</i> , <i>P.mirabilis</i> , <i>S.pneumoniae</i> ,	
CC	<i>S.aureus</i> , <i>S.epidermidis</i> , <i>E.faecalis</i> , <i>S.saprophyticus</i> , <i>S.pyogenes</i> ,	
CC	<i>H.influenzae</i> , <i>M.catalitidis</i> and/or group A <i>Streptococci</i> producing	
CC	exotoxin A gene spe A, suspected to be present in a sample which is	
CC	obtained from human patients, animals, environment or food, and which	
CC	consists of one or more bacterial colonies. Oligonucleotide	
CC	probes and primers complementary to the bacterial genes encoding	
CC	resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadB,	
CC	aac(1), aac(2), aac(3), aac(4), mecA, vanA, vanH, vanX, satA, aacA-aph, vat,	
CC	vgA, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify	
CC	commonly encountered and clinically important resistance genes. The	
CC	invention provides a rapid method of bacterial identification that can be	
CC	achieved, which reduces the time currently required for the	
CC	identification of pathogens in the clinical laboratory.	
XX		
SO	Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other:	
	Query Match	100.0%; Score 28; DB 22; Length 2007;
	Best Local Similarity	100.0%; Pred. No. 0.028;
	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 CAACTAACTATGATGCTAAAGTTCAA 28	
DB	973 CAACTAACTATGATGCTAAAGTTCAA 1000	
RSUJ.T 8		
ID	ABN922247	
XX	ABN922247 standard; DNA: 2028 BP.	
AC	ABN922247;	
XX		
DT	24-JUL-2002 (first entry)	

XX	Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.
DE	
XX	Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX	antibacterial; gene therapy; gene; ds.
KW	Staphylococcus epidermidis.
XX	
XX	US6380370-B1.
PM	
XX	
XX	30-APR-2002.
XX	
XX	13-AUG-1998; 98US-0134001.
PF	
PR	14-AUG-1997; 97US-055779P.
PR	08-NOV-1997; 97US-064964P.
XX	
PA	(GENO-) GENOME THERAPEUTICS CORP.
XX	
XX	Doucette-Stamm LA, Bush D;
XX	
XX	WPI: 2002-381255/41.
DR	P-PSDB: ABP39702.
XX	
XX	Novel isolated nucleic acid encoding a Staphylococcus epidermidis
PT	polypeptide, useful for diagnosing and treating bacterial infections -
PS	Disclosure: SEQ ID 1710; 267pp; English.
XX	
XX	ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC	frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC	given in ABP5124 to ABP37960. The S. epidermidis sequences have
CC	antibacterial activity and can be used in gene therapy. The sequences
CC	can also be used in the diagnosis and treatment of bacterial infections,
CC	particularly S. epidermidis infections. The sequences can be used to
CC	screen for compounds able to interfere with the S. epidermidis life
CC	cycle or inhibit S. epidermidis infection.
CC	N.B. the sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from the
CC	USPTO web site.
XX	
XX	Sequence 2028 BP: 861 A; 273 C; 346 G; 547 T; 1 other:
S0	
	Query Match 100.0%; Score 28; DB 24; Length 2028;
	Best Local Similarity 100.0%; Pred. No. 0.028;
	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CAACTAACATATGATGCTAAACTTCAA 28
JB	994 CACTAACTATTGATGCTAAACTTCAA 1021
	RESULT 9
	AAQ35213
DD	AAQ35213 standard; DNA: 2110 BP.
XX	
XX	AAQ35213:
XX	
XX	06-JUN-1993 (first entry)
DT	
XX	Sequence of the mec A gene.
DE	
XX	Mechicillin-resistant staphylococci; detection; primer; PCR; ss.
KW	
OS	Staphylococcus aureus.
XX	
XX	Key location/Qualifiers
FT	CDS 105..2110
FT	/*tag=a
XX	
XX	EP527628-A.
XX	
XX	17-FEB-1993.
ND	

[illegible]

```
XX The sequence given is the PBP2' gene. This gene could be detected
CC by the primer sequences given in AA025897-904. Due to the results of
CC this amplification reaction resistance to methicillin in Staphylococcus
CC aureus could be determined.
XX
SQ Sequence 2322 BP: 940 A; 324 C; 389 G; 669 T; 0 other;
Query Match 100.0%; Score 28; DB 13; Length 2322;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAACCTACTATTGATGCTAAAGTTCAA 28
DB 979 CAACCTACTATTGATGCTAAAGTTCAA 1006
RESULT 11
AA04538
ID AA04538 standard; cDNA to mRNA: 2455 BP.
X
X AA04538;
AX 11-APR-1996 (first entry)
DT
XX Staphylococcus aureus mecA protein coding sequence.
DE
XX methicillin-resistant Staphylococcus aureus; MRSA; 'mece protein;
KW antibiotic resistance; ds.
XX Staphylococcus aureus.
OS
XX
XX Key location/Qualifiers
FH 134..2146
FT CDS /tag= a
FT /product= mec_A-protein
XX
XX JP07209294-A.
XX
XX 11-AUG-1995.
XX
XX 10-JAN-1994; 94JP-00122226.
XX
XX 10-JAN-1994; 94JP-00122226.
XX
XX (DENK-) DENKA SEIKEN KK.
XX (KAWA-) KAWANO M.
XX (MITU) MITSUBISHI CHEM CORP.
XX
XX WPI: 1995-313917/41.
XX P-PSDB; AAR80036.
XX
XX New 'mec A protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
XX
XX Example 2; Page 8-10; 15pp; Japanese.
XX
XX The present sequence codes for the mec A protein. DNA coding for
CC the 'mec A protein, which controls methicillin resistance in
CC methicillin-resistant Staph. aureus (MRSA), was obtained by PCR
CC amplification of the mec A sequence using primers AA04537 and
CC AA04539. The 'mec A protein (mol. wt. 40000) is useful for
CC preparation of antiserum specific for MRSA, thereby allowing
CC methicillin-resistant and methicillin-sensitive strains to be
CC distinguished.
XX
XX Sequence 2455 BP: 997 A; 344 C; 401 G; 713 T; 0 other;
Query Match 100.0%; Score 28; DB 16; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAACCTACTATTGATGCTAAAGTTCAA 28
```

```
DB 1112 CAACCTACTATTGATGCTAAAGTTCAA 1139
|||||
RESULT 12
AA01187
ID AA01187 standard; DNA: 2456 BP.
XX
XX AA01187;
XX
XX 24-JUL-2001 (first entry)
DT
XX
XX Staphylococcus aureus nucleotide sequence SEQ ID NO:1178.
DE
XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitica;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial;
KW vaccine; primer; ds.
XX
XX Staphylococcus aureus.
OS
XX
XX WO200123604-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-CA01150.
XX
XX 28-SEP-1999; 99CA-2283458.
XX
XX 19-MAY-2000; 2000CA-2307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
XX Placard FJ, Roy PH;
XX
XX WPI: 2001-24506/25.
XX
XX Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
XX archaeal, bacterial, fungal and parasitica species in a test sample -
XX
XX Disclosure: Page 1048-1049; 1580pp; English.
XX
XX The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitica species, genus, family and group. A nucleic acid (I)
CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexa nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (I) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AA00010 to AA002304 represent nucleotide sequences and primers/probes
XX which are given in the exemplification of the present invention.
XX
XX Sequence 2456 BP: 1001 A; 344 C; 396 G; 715 T; 0 other;
```



```

XX 31-OCT-1996: 96US-0029960.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
PI Kunsch CA, Rosen CA;
DR WPI: 1998-272225/24.
XX
XX Computer-readable medium with recorded Streptococcus pneumoniae
PT polynucleotide sequences - useful in diagnostic kits and assays, and
PT pharmaceutical compositions and vaccines for Streptococcus
PT pneumoniae
XX
XX Claim 1: Page 332-339; 1409pp; English.
XX
XX The present invention describes a computer readable medium which has
CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)
CC recorded on it, or a representative fragment or a sequence at least 95%
CC identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in
CC SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
CC Streptococcus pneumoniae. The present invention also describes an
CC isolated nucleic acid molecule encoding a homologue of any of the
CC fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the
CC nucleic acid molecule is produced by a process comprising: (a) screening
CC a genomic DNA library using as a probe a target sequence defined by any
CC of the sequences in SEQ ID NO:1 to 391, identifying members of the
CC library which contain sequences that hybridise to the target sequence and
CC isolating the nucleic acid molecules from the members; or (b) isolating
CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid
CC molecules whose nucleotide sequence is homologous to amplification
CC primers derived from the fragment of the S. pneumoniae genome to prime
CC the amplification and isolating the amplified sequences. The computer
CC readable medium can be used in a computer-based system for identifying
CC fragments of the S. pneumoniae genome of commercial importance, or
CC expression modulating fragments of the S. pneumoniae genome. Products
CC from the present invention can be used in diagnosis kits and assays, and
CC pharmaceutical compositions and vaccines for S. pneumoniae.
XX
SQ Sequence 13206 BP; 4016 A; 2929 C; 2473 G; 3786 T; 2 other:
Query Match 73.6%; Score 20.6; DB 19; Length 13206;
Best Local Similarity 85.2%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 AACTACTATTGATGCTAAAGTTCAA 28
  ||||||| ||||| |||||||||
  777 AACTACTATTGATGCTAAAGTTCA 751

```

Search completed: December 10, 2002, 17:32:46
 Job time : 188.547 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 : Search time 36.2905 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28
Sequence: 1 caactaactatgctgctaaagtcca 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

ctal number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_MA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	10	US-09-865-579A-25
2	28	100.0	2007	10	US-09-452-599-169
3	19.2	68.6	491	10	US-09-560-863-992
4	18.2	65.0	475	12	US-10-062-254-359
5	18	64.3	462	10	US-09-770-444-398
6	18	64.3	3645	10	US-09-815-242-4853
7	18	64.3	3807	10	US-09-815-242-9015
8	18	64.3	7067	10	US-09-764-877-3222
9	18	64.3	7311	10	US-09-815-242-4779
10	18	64.3	18846	10	US-09-815-242-8898
11	17.6	62.9	466	10	US-09-880-107-1287
12	17.6	62.9	510	10	US-09-777-364-1720
13	17.6	62.9	551	10	US-09-920-300A-290
14	17.6	62.9	551	12	US-10-033-528-290
15	17.6	62.9	585	10	US-09-962-436-3
16	17.6	62.9	1500	10	US-09-842-552-83
17	17.6	62.9	1737	10	US-09-815-242-8403
18	17.6	62.9	6176	10	US-09-823-109-6
19	17.6	62.9	640681	10	US-09-790-988-1

c	20	17.4	62.1	1482	10	US-09-070-927A-842	Sequence 842, App
c	21	17.4	62.1	3212	10	US-09-070-927A-428	Sequence 428, App
c	22	17.4	62.1	174493	10	US-09-804-471A-3	Sequence 3, App11
c	23	17	60.7	462	10	US-09-287-070-3	Sequence 3, App11
c	24	17	60.7	508	10	US-09-287-070-10	Sequence 10, App1
c	25	17	60.7	843	9	US-09-938-842A-2426	Sequence 2426, App
c	26	17	60.7	1311	10	US-09-815-242-7057	Sequence 7057, App
c	27	17	60.7	1359	9	US-09-938-842A-1312	Sequence 1312, App
c	28	17	60.7	1889	10	US-09-287-070-4	Sequence 4, App11
c	29	17	60.7	1936	10	US-09-954-456-1138	Sequence 1138, App
c	30	17	60.7	5530	10	US-09-070-927A-206	Sequence 206, App
c	31	16.8	60.0	405	9	US-10-046-935-1092	Sequence 1092, App
c	32	16.8	60.0	405	9	US-09-878-178-1092	Sequence 1092, App
c	33	16.8	60.0	485	10	US-09-922-217-505	Sequence 505, App
c	34	16.8	60.0	485	10	US-09-833-263-505	Sequence 505, App
c	35	16.8	60.0	486	10	US-09-070-927A-744	Sequence 744, App
c	36	16.8	60.0	1268	10	US-09-070-927A-401	Sequence 401, App
c	37	16.8	60.0	2000	9	US-09-938-842A-3175	Sequence 3175, App
c	38	16.8	60.0	2000	9	US-09-938-842A-4603	Sequence 4603, App
c	39	16.8	60.0	2388	10	US-09-815-242-7124	Sequence 7124, App
c	40	16.8	60.0	2435	10	US-09-823-038A-40	Sequence 40, App1
c	41	16.8	60.0	143068	10	US-09-967-768A-316	Sequence 316, App
c	42	16.6	59.3	258	10	US-09-923-876-1148	Sequence 1148, App
c	43	16.6	59.3	2000	9	US-09-938-842A-3189	Sequence 3189, App
c	44	16.6	59.3	2000	9	US-09-938-842A-3326	Sequence 3326, App
c	45	16.6	59.3	2132	12	US-10-044-090-659	Sequence 659, App

ALIGNMENTS

RESULT 1
US-09-865-579A-25
Sequence 25, Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
APPLICANT: Saito, Junichi
TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865, 579A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-865-579A-25
Query Match 100.0%, Score 28; DB 10; length 28;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 CAACCTAAGTATGATGCTAAAGTTCAA 28
1 CAACCTAAGTATGATGCTAAAGTTCAA 28
RESULT 2
US-09-452-599-169
Sequence 169, Application US/09452599
Patent No. US20020055101A1
GENERAL INFORMATION:
APPLICANT: Bergeron, Michel G.

```
; APPLICANT: Ouclette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patenlin Ver. 2.1
; LENGTH: 2007
; SEQ ID NO 169
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169
```

```
Query Match 100.0%; Score 28; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 CAACAACTATTGATGCTAAAGTCAAA 28
Db 973 CAACAACTATTGATGCTAAAGTCAAA 1000
```

```
RESULT 3
US-09-560-863-992
; Sequence 992, Application US/09560863
; Patent No. US20020110809A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020110809A1el Human Polynucleotides and the
; FILE REFERENCE: LEX-0018-USA
; CURRENT APPLICATION NUMBER: US/09/560,863
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/132,408
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 992
; LENGTH: 491
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(491)
; OTHER INFORMATION: n = A,T,C or G
US-09-560-863-992
```

```
Query Match 68.6%; Score 19.2; DB 10; Length 491;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 4 CTAACTATTGATGCTAAAGTCAAA 27
Db 296 CTAACTTTGCTGCTAAAGTCAAA 319
```

```
RESULT 4
US-10-062-254-359
; Sequence 359, Application US/10062254
; Patent No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
```

```
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hanke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved in Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 359
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (36)
; NAME/KEY: unsure
; LOCATION: (285)
; NAME/KEY: unsure
; LOCATION: (298)
; NAME/KEY: unsure
; LOCATION: (368)
; NAME/KEY: unsure
; LOCATION: (440)
; NAME/KEY: unsure
; LOCATION: (463)
; NAME/KEY: unsure
; LOCATION: (475)
US-10-062-254-359
```

```
Query Match 65.0%; Score 18.2; DB 12; Length 475;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 2 AACTAACTATTGATGCTAAAGTCA 25
Db 429 AACTAACCAATATGCTAAAGTCA 452
```

```
RESULT 5
US-09-770-444-398/C
; Sequence 398, Application US/09770444
; Patent No. US2002023280A1
```

```

: GENERAL INFORMATION:
: APPLICANT: Gorlach, Jörn
: APPLICANT: An, Yong-Qiang
: APPLICANT: Hamilton, Carol M.
: APPLICANT: Price, Jennifer L.
: APPLICANT: Raines, Tracy M.
: APPLICANT: Yu, Yang
: APPLICANT: Rameaka, Joshua G.
: APPLICANT: Hage, Amy
: APPLICANT: Mathew, Abraham V.
: APPLICANT: Ledford, Brooke L.
: APPLICANT: Woessner, Jeffrey P.
: APPLICANT: Haas, William David
: APPLICANT: Garcia, Carlos A.
: APPLICANT: Kricker, Maja
: APPLICANT: Stader, Fred
: APPLICANT: Davis, Keith R.
: APPLICANT: Allen, Keith
: APPLICANT: Hoffman, Neil
: APPLICANT: Hurban, Patrick
: TITLE OF INVENTION: Expressed Sequences of Arabidopsis
: FILE REFERENCE: 2027 (PARA-016PRV)
: CURRENT APPLICATION NUMBER: US/09/770,444
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/178,502
: NUMBER OF SEQ ID NOS: 999
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 398
: LENGTH: 462
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: US-09-770-444-398

Query Match          64.3% Score 18: DB 10: Length 462:
Best Local Similarity 80.8% Pred. No. 80:
Matches 21: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

QY 3 ACTAAGTATTGATGCTAAAGTTCAAA 28
    ||||||| ||||| |||||
Db 139 ACTAAGTATTGATGCTAATTTCAGA 114

RESULT 6
US-09-815-242-4853
: Sequence 4853, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Karl L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9015
: LENGTH: 3807
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(3807)
: US-09-815-242-9015

Query Match          64.3% Score 18: DB 10: Length 3807:
Best Local Similarity 80.8% Pred. No. 1e+02:
Matches 21: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

QY 3 ACTAAGTATTGATGCTAAAGTTCAAA 28
    ||||||| ||||| |||||
Db 933 ACAAGCTATTATGATGAAGCTCAA 958

RESULT 8
```

```

: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4853
: LENGTH: 3645
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
: US-09-815-242-4853

Query Match          64.3% Score 18: DB 10: Length 3645:
Best Local Similarity 80.8% Pred. No. 1e+02:
Matches 21: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

QY 3 ACTAAGTATTGATGCTAAAGTTCAAA 28
    ||||||| ||||| |||||
Db 771 ACAAGCTATTATGATGAAGCTCAA 796

RESULT 7
US-09-815-242-9015
: Sequence 9015, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Karl L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9015
: LENGTH: 3807
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(3807)
: US-09-815-242-9015

Query Match          64.3% Score 18: DB 10: Length 3807:
Best Local Similarity 80.8% Pred. No. 1e+02:
Matches 21: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

QY 3 ACTAAGTATTGATGCTAAAGTTCAAA 28
    ||||||| ||||| |||||
Db 933 ACAAGCTATTATGATGAAGCTCAA 958

RESULT 8
```

```
US-09-764-877-3222/c
; Sequence 3222, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3222
; LENGTH: 7067
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3222
```

```
Query Match      64.3%; Score 18; DB 10; Length 7067;
Best Local Similarity 80.8%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      3 ACTACTATGATGCTTAAGTTCAA 28
      ||| ||||| ||| ||||| |||||
Db      5626 ACTTACTATGAGAGCTTAAGTTCAA 5601
```

```
RESULT 9
US-09-815-242-4779
; Sequence 4779, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21,078
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23,625
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4779
; LENGTH: 7311
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4779
```

```
Query Match      64.3%; Score 18; DB 10; Length 7311;
Best Local Similarity 80.8%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      3 ACTACTATGATGCTTAAGTTCAA 28
      ||| ||||| ||| ||||| |||||
```

```
Db      273 ACAAGCTATTATGATAAGCTCAA 298
```

```
RESULT 10
US-09-815-242-8898
; Sequence 8898, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8898
; LENGTH: 18846
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(18846)
US-09-815-242-8898
```

```
Query Match      64.3%; Score 18; DB 10; Length 18846;
Best Local Similarity 80.8%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      3 ACTAAGCTATTATGCTTAAGTTCAA 28
      ||| ||||| ||| ||||| |||||
Db      11799 ACAAGCTATTATGATAAGCTCAA 11824
```

```
RESULT 11
US-09-880-107-1287
; Sequence 1287, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Schert, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
```

```
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1287
LENGTH: 466
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA476754
US-09-880-107-1287
```

```
Query Match          62.9%; Score 17.6; DB 10; Length 466;
Best local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      5  TAACATGATGCTAAAGTCAA 28
DB      303  TACGATTGAGCTTAAGCTGCAA 326
```

```
RESULT 12
US-09-777-564-1720/c
Sequence 1720, Application US/09777564
Patent No. US20020022591A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493
CURRENT APPLICATION NUMBER: US/09/777,564
CURRENT FILING DATE: 2001-02-03
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: FastSeq for Window Version 4.0
SEQ ID NO 1720
LENGTH: 510
TYPE: DNA
ORGANISM: Homo sapiens
US-09-777-564-1720
```

```
Query Match          62.9%; Score 17.6; DB 10; Length 510;
Best local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      2  AACTAATGATGCTAAAGTTC 25
DB      203  AACTGACTTCTGATCATTAAGTTC 180
```

```
RESULT 13
US-09-920-300A-290
Sequence 290, Application US/09920300A
Patent No. US20020136728A1
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 290
LENGTH: 551
TYPE: DNA
ORGANISM: Homo sapiens
US-09-920-300A-290
```

```
Query Match          62.9%; Score 17.6; DB 10; Length 551;
Best local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      2  AACTAATGATGCTAAAGTTC 25
DB      490  AACTGACTTCTGATCATTAAGTTC 513
```

```
RESULT 14
US-10-033-528-290
Sequence 290, Application US/10033528
Patent No. US20020131971A1
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 290
LENGTH: 551
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-528-290
```

```
Query Match          62.9%; Score 17.6; DB 12; Length 551;
Best local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      2  AACTAATGATGCTAAAGTTC 25
DB      490  AACTGACTTCTGATCATTAAGTTC 513
```

```
RESULT 15
US-09-962-436-3/c
Sequence 3, Application US/09962436
Patent No. US20020081301A1
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using SI
TITLE OF INVENTION: Sels
FILE REFERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 585
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: n=a,t,g or c
US-09-962-436-3
```

```
Query Match          62.9%; Score 17.6; DB 10; Length 585;
Best local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      5  TAACATGATGCTAAAGTCAA 28
DB      298  TACGATTGAGCTTAAGCTGCAA 275
```

```
Search completed: December 11, 2002, 06:14:07
Job time : 42.2905 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 : Search time 38.1676 Seconds
(without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28
Sequence: 1 caactaactatgtagctaaagtcaaa 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/1na/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/1na/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/1na/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/1na/PCrus.COMB.seq:*
6: /cgn2_6/ptodata/1/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	2007	2	US-08-743-637B-169
2	28	100.0	2007	3	US-08-526-840B-169
3	28	100.0	2028	4	US-09-134-001C-1710
4	20.6	73.6	13206	4	US-08-961-527-33
5	20.6	73.6	16995	4	US-08-961-527-82
6	19	67.9	2996	4	US-08-961-527-260
7	19	67.9	11309	4	US-08-961-527-108
8	18.6	66.4	226	4	US-09-235-451-40
9	18.6	66.4	11443	4	US-08-961-527-49
10	17.8	63.6	3946	4	US-09-453-702B-103
11	17.4	62.1	548	4	US-08-642-274D-21
12	17.4	62.1	548	4	US-08-952-014C-21
13	17.4	62.1	851	4	US-08-961-527-361
14	17.4	62.1	1074	4	US-09-134-001C-382
15	17.4	62.1	2914	3	US-09-002-298-4
16	17.4	62.1	4398	4	US-08-961-527-293
17	17.4	62.1	8898	4	US-08-961-527-69
18	17.4	62.1	38564	4	US-09-734-673-3
19	17	60.7	2495	4	US-08-961-527-255
20	17	60.7	4290	4	US-08-961-527-25
21	17	60.7	11887	4	US-08-924-629C-4
22	16.8	60.0	998	4	US-08-961-527-146
23	16.8	60.0	2667	4	US-09-227-357-62
24	16.8	60.0	5183	1	US-09-134-001C-195
25	16.8	60.0	5183	2	US-08-459-568-3
26	16.8	60.0	5868	3	US-08-399-411-3
27	16.8	60.0	5868	4	US-08-516-859A-3
					US-09-586-472-3

28	16.8	60.0	5868	4	US-09-528-706-3	Sequence 3, Appl1
29	16.8	60.0	72604	4	US-09-268-992-7	Sequence 7, Appl1
30	16.8	60.0	72604	4	US-09-657-474-7	Sequence 7, Appl1
31	16.6	59.3	741	4	US-09-134-001C-2455	Sequence 2455, Ap
32	16.6	59.3	1599	1	US-08-143-219-27	Sequence 27, Appl1
33	16.6	59.3	8648	4	US-09-415-946-2	Sequence 2, Appl1
34	16.6	59.3	17341	4	US-09-415-946-1	Sequence 1, Appl1
35	16.6	59.3	31880	4	US-09-453-702B-242	Sequence 242, App
36	16.4	58.6	453	4	US-09-134-001C-881	Sequence 881, App
37	16.4	58.6	562	4	US-09-328-111-468	Sequence 468, App
38	16.4	58.6	903	4	US-09-134-001C-1620	Sequence 1620, Ap
39	16.4	58.6	2167	3	US-08-961-083-83	Sequence 83, Appl1
40	16.4	58.6	2810	4	US-09-105-390-6	Sequence 6, Appl1
41	16.4	58.6	2884	1	US-08-148-209A-5	Sequence 5, Appl1
42	16.4	58.6	14735	4	US-08-961-527-171	Sequence 171, App
43	16.4	58.6	15363	4	US-08-961-527-139	Sequence 139, App
44	16.4	58.6	19702	4	US-08-961-527-7	Sequence 7, Appl1
45	16.4	58.6	51259	3	US-08-781-891-209	Sequence 209, App

ALIGNMENTS

RESULT 1
US-08-743-637B-169
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGFRON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/743,637B
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586, 90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414)277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0% Score 28; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAACTAATTGATGCTAAAGTTCAAA 28
DB 973 CAACTAATTGATGCTAAAGTTCAAA 1000

RESULT 2
US-08-526-840B-169
Sequence 169, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: APPLICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: B50586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169
Query Match
Best Local Similarity 100.0%; Score 28; DB 3; Length 2007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CAACTAATTGATGCTAAAGTTCAAA 28
DB 973 CAACTAATTGATGCTAAAGTTCAAA 1000
RESULT 3
US-09-134-001C-1710
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: CTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match
Best Local Similarity 100.0%; Score 28; DB 4; Length 2028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAACTAATTGATGCTAAAGTTCAAA 28
DB 994 CAACTAATTGATGCTAAAGTTCAAA 1021

RESULT 4
US-08-961-527-33/C
Sequence 33, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 13206 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-33

Query Match
Best Local Similarity 85.2%; Score 20.6; DB 4; Length 13206;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTACTATTGATGCTAAAGTTCAAA 28
||||||| ||||| ||||| ||||| |||||
DB 777 AACTACTATTGATGATTAAGTTCAGA 751

RESULT 5

US-08-961-527-82/C
; Sequence 82, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1695 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-82
Query Match 73.6%; Score 20.6; DB 4; Length 1695;
Best local Similarity 85.2%; Pred. No. 3.6;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 AACTACTATTGATGCTAAAGTTCAAA 28
||||||| ||||| ||||| ||||| |||||
DB 456 AACTACTATTGATGATTAAGTTCAGA 430
RESULT 6
US-08-961-527-260
; Sequence 260, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2996 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-08-961-527-260

Query Match 67.9%; Score 19; DB 4; Length 2996;
Best local Similarity 81.5%; Pred. No. 15;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACTACTATTGATGCTAAAGTTCAAA 28
||||||| ||||| ||||| ||||| |||||

DB 2181 AACTACTATTGATGATTAAGTTCAGA 2207

RESULT 7

US-08-961-527-108/C
; Sequence 108, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11309 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

```

; TOPOLOGY: linear
US-08-961-527-108
Query Match
Best Local Similarity 67.9%; Score 19; DB 4; Length 11309;
Best Match 81.5%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACTACTATTGATGCTAAAGTTCA 28
   ||||| ||||| ||||| |||||
DB 9189 AATTACTTATGATGATTAAGTTCC 9163

RESULT 8
US-09-235-451-40
; Sequence 40, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 226
; TYPE: DNA
; ORGANISM: R. rattus
US-09-235-451-40

Query Match
Best Local Similarity 66.4%; Score 18.6; DB 4; Length 226;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAAGTACTATTGATGCTAAAGTTTC 25
   ||||| ||||| ||||| |||||
DB 70 CAAGTACTTGTGATGCTGAAGTTTC 94

RESULT 9
US-08-961-527-49
; Sequence 49, Application US/08961527
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11443 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-49

Query Match
Best Local Similarity 66.4%; Score 18.6; DB 4; Length 11443;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTACTATTGATGCTAAAGTTCA 26
   ||||| ||||| ||||| |||||
DB 10721 AATTACTTATGATGATTAAGTTCA 10745

RESULT 10
US-09-453-702B-103/c
; Sequence 103, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Bialtner, Frederick R.
; Perna, Nicole T.
; Plunkett, Guy
; TITLE OF INVENTION: No. 6365723e1 Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-DEC-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296,95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3946
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-453-702B-103

Query Match
Best Local Similarity 63.6%; Score 17.8; DB 4; Length 3946;
```

Best Local Similarity 90.5%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AACTACTATGTGCTTAAAG 22
|||||
DB 3539 AACTACTGTGATGTTAAAG 3519

RESULT 11

US-08-642-274D-21
; Sequence 21, Application US/08642274D
; Patent No. 6200749
; GENERAL INFORMATION:
; APPLICANT: Shiloh, Yosef
; TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO
; FILE REFERENCE: 22900003
; CURRENT APPLICATION NUMBER: US/08/642,274D
; CURRENT FILING DATE: 1996-05-03
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 21
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: genomic
US-08-642-274D-21

Query Match 62.1%; Score 17.4; DB 4; Length 548;
Best Local Similarity 77.8%; Pred. No. 61;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 AACTACTATGTGCTTAAAGTCAAA 28
|||||
DB 206 ACCTAAACATGATGTTAAAGTTTAA 232

RESULT 12

US-08-952-014C-21
; Sequence 21, Application US/08952014C
; Patent No. 6265158
; GENERAL INFORMATION:
; APPLICANT: Shiloh, Yosef
; TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE AND ITS
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6265158thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,014C
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I
; REGISTRATION NUMBER: 30,995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 810-539-5050
; TELEFAX: 810-539-5055
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 548 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-952-014C-21

Query Match 62.1%; Score 17.4; DB 4; Length 548;
Best Local Similarity 77.8%; Pred. No. 61;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 AACTACTATGTGCTTAAAGTCAAA 28
|||||
DB 206 ACCTAAACATGATGTTAAAGTTTAA 232

RESULT 13

US-08-961-527-361
; Sequence 361, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; OPERATING SYSTEM: HP Vectra 486/33
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 361:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 851 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-361

Query Match 62.1%; Score 17.4; DB 4; Length 851;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 AACTACTATGTGCTTAAAGTCAAA 28
|||||
DB 6 AATTAAGTATGATGATTAAGTCAAG 32

RESULT 14

US-09-134-001C-382
; Sequence 382, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

```

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 382
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-382

```

```

Query Match      62.1%; Score 17.4; DB 4; Length 1074;
Best Local Similarity 77.8%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Oy      2  AACTACTATTGATGCTAAAGTTCAA 28
      ||||| ||||| || || || |||
      ,  671  AACTAAATATTGTGTGAAGATGAAA 697

```

```

RESUI.T 15
US-09-002-298-4
; Sequence 4, Application US/09002298
; Patent No. 6046001
; GENERAL INFORMATION:
; APPLICANT: Handman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN FATTY ACID BETA-OXIDATION ENZYMES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,298
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0453 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-4166
; TELEFAX: 650-855-0555
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2714 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVARUT02
; CLONE: 2595635
US-09-002-298-4

```

```

Query Match      62.1%; Score 17.4; DB 3; Length 2714;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy      2  AACTACTATTGATGCTAAAGTTCAA 28
      ||||| ||||| ||||| ||||| |||||
Db      1945  AACTGACTGTCTGCTAAAGACACAAA 1971

```

Search completed: December 10, 2002, 22:54:57
Job time : 48.2926 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 ; Search time 1435.66 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28
Sequence: 1 caactaactatgctgctaaagtcaaa 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

otal number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estlum:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	ID	Description
1	21.6	77.1	471	12	BF611176
2	21.6	77.1	497	12	BG160008
3	21.6	77.1	505	13	BJ041404
4	21.6	77.1	511	13	BJ059576
5	21.6	77.1	512	13	BJ060237
6	21.6	77.1	727	13	BK398481

Result	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	BF611176	471 bp mRNA	EST 14-DEC-2000									
2	BF611176	471 bp mRNA	EST 14-DEC-2000									
3	BF611176	471 bp mRNA	EST 14-DEC-2000									
4	BF611176	471 bp mRNA	EST 14-DEC-2000									
5	BF611176	471 bp mRNA	EST 14-DEC-2000									
6	BF611176	471 bp mRNA	EST 14-DEC-2000									

ALIGNMENTS

BF611176 471 bp mRNA linear EST 14-DEC-2000
IMAGE:3430204 5', mRNA sequence.
BF611176
EST.
African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 471)
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person,
B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Waterston, R. and Wilson, R.
Washu Xenopus EST project, 1999
Unpublished (1999)
Other ESTs: dd76b03.x2
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estevatson.wustl.edu
Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.


```

VERSION      BJ059576.1 GI:17492916
KEYWORDS     EST.
SOURCE       African clawed frog.
ORGANISM     Xenopus laevis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
              Xenopodinae; Xenopus.
REFERENCE    1 (bases 1 to 511)
AUTHORS      Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
              ,Y.
TITLE        Expressed genes in X. laevis embryo
JOURNAL      Unpublished (2001)
COMMENT      Contact: Tadasu Shin-i
              Center For Genetic Resource Information
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6856
              Fax: 81-559-81-6855
              Email: tshin@genes.nig.ac.jp.
              Location/Qualifiers
                1..511
                /organism="Xenopus laevis"
                /db_xref="taxon:8355"
                /clone_lib="X1063a03"
                /clone_lib="NIBB Mochii normalized Xenopus tailbud
                library"
                /tissue_type="whole embryo"
                /dev_stage="stage 25"
                /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
                were oligo-dT primed and directionally cloned. Staging
                according to Nieuwkoop and Faber. Library is subtracted
                and was constructed by N. Garrett and A.M. Zorn,
                (Wellcome/CRC Institute)."
BASE COUNT   143 a 104 c 98 g 165 t 1 others
ORIGIN
Query Match 77.1%; Score 21.6; DB 13; Length 511;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
    ||||| || ||||| ||||| |||||
Db 285 CAGCTAATTAAATGATGCTAAAGTCAAA 312

RESULT 5
LOCUS      BJ060237 512 bp mRNA linear EST 11-DEC-2001
DEFINITION laevis cDNA clone X1065d05 5', mRNA sequence.
ACCESSION  BJ060237
VERSION     BJ060237.1 GI:17496967
KEYWORDS   EST.
SOURCE      African clawed frog.
ORGANISM   Xenopus laevis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
              Xenopodinae; Xenopus.
REFERENCE    1 (bases 1 to 512)
AUTHORS      Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
              ,Y.
TITLE        Expressed genes in X. laevis embryo
JOURNAL      Unpublished (2001)
COMMENT      Contact: Tadasu Shin-i
              Center For Genetic Resource Information
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6856
              Fax: 81-559-81-6855
              Email: tshin@genes.nig.ac.jp.
              Location/Qualifiers
                1..512
                /organism="Xenopus laevis"

```

```

/db_xref="taxon:8355"
/clone="X1065d05"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT   145 a 101 c 101 g 164 t 1 others
ORIGIN
Query Match 77.1%; Score 21.6; DB 13; Length 512;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
    ||||| || ||||| ||||| |||||
Db 267 CAGCTAATTAAATGATGCTAAAGTCAAA 294

RESULT 6
LOCUS      BM398481/C 727 bp mRNA linear EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA (large fraction)
ACCESSION  BM398481
VERSION     BM398481.1 GI:18198534
KEYWORDS   EST.
SOURCE      Tetrahymena thermophila.
              Tetrahymena thermophila.
              Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
              Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE    1 (bases 1 to 727)
AUTHORS      Turkewitz,A.P., Karier,K.M., Jahn,C., Ortas,E., Kirk,K.E., Frankel
              ,J. and Klobuchar,L.
TITLE        EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
              Molecular Genetics and Cell Biology
              University of Chicago
              920 E. 58th Street, Chicago, IL 60637, USA
              Tel: 773 702 4374
              Fax: 773 702 3172
              Email: apturkew@midway.uchicago.edu
              Seq primer: 73.
              Location/Qualifiers
                1..727
                /organism="Tetrahymena thermophila"
                /strain="CU428.1"
                /db_xref="taxon:5911"
                /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                /note="Vector: Bluescript SK+; Details on library
                preparation can be found in Chilcoat and Turkewitz (2001)
                Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT   260 a 94 c 141 g 232 t
ORIGIN
Query Match 77.1%; Score 21.6; DB 13; Length 727;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
    ||||| || ||||| ||||| |||||
Db 216 CAACTAATCTTGATGCTCAATTCAA 189

RESULT 7
LOCUS      A0876537 504 bp DNA linear GSS 09-NOV-1999
DEFINITION HS_2001_B2_G05_MR CIT Approved Human Genomic Sperm Library D Homo

```


ACCESSION	sapientis genomic clone Plate=2001 Col=10 Row=N, DNA sequence.		
VERSION	A0876537		
KEYWORDS	A0876537.1 GI:6308004		
SOURCE	GSS.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 504)		
TITLE	Malleras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and		
JOURNAL	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome		
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)		
COMMENT	99380589		
	Contact: Mahalras GG, Wallace JC, Hood L		
	High Throughput Sequencing Center		
	401 Queen Anne Avenue North, Seattle, WA 98109, USA		
	Tel: (206) 616-3618		
	Fax: (206) 616-3687		
	Email: jwallace@u.washington.edu		
	Clones may be purchased from Research Genetics (info@resgen.com).		
	BAC end Web Server: http://www.htsc.washington.edu		
	Plate: 2001 row: N column: 10		
	Seq primer: M13 Reverse		
	Class: BAC ends		
	High quality sequence stop: 504.		
FEATURES	Location/Qualifiers		
source	1..504		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="Plate-2001 Col-10 Row-N"		
	/clone.lib="CIT Approved Human Genomic Sperm Library D"		
	/sex="male"		
	/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"		
BASE COUNT	115 a 139 c 78 g 158 t 14 others		
ORIGIN			
Query Match	73.6%; Score 20.6; DB 17; Length 504;		
Best Local Similarity	85.2%; Pred.No.1.7e+02;		
Matches 23; Conservative	0; Mismatches 4; Indels 0; Caps 0;		
QY 1	CAACTACTATTGATGCTAAATCTCA 27		
Db 257	CAACTACTATTGATGCTTAAGTCAAA 283		
LOCUS	BJ073806 638 bp mRNA linear EST 11-DEC-2001		
DEFINITION	BJ073806 NIBB Mochil normalized Xenopus tailbud library Xenopus laevis cDNA clone Xl.101e02 5', mRNA sequence.		
ACCESSION	BJ073806		
VERSION	BJ073806.1 GI:17503995		
KEYWORDS	EST.		
SOURCE	African clawed frog.		
ORGANISM	Xenopus laevis		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus. 1 (bases 1 to 638)		
AUTHORS	Kikayama,A., Terasaka,C., Mochil,M., Ueno,N., Shin-I,T. and Kohara,Y.		
TITLE	Expressed genes in X. laevis embryo		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Tadasu Shin-i		
	Center For Genetic Resource Information		
	National Institute of Genetics		
	1111 Yata, Mishima, Shizuoka 411-8540, Japan		
	Tel: 81-559-81-6856		

```

FEATURES
Source
    Email: tshini@genes.nig.ac.jp.
    Fax: 81-559-81-6855
    Location/Qualifiers
        1..638
            /organism="Xenopus laevis"
            /db_xref="taxon:8355"
            /clone="Xt101e02"
            /clone_1lb="NIBB Mochii normalized Xenopus tailbud library"
            /tissue_type="whole embryo"
            /dev_stage="stage 25"
            /note="Vector: pBSK3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nicwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

BASE COUNT      158 a       145 c       160 g       175 t
ORIGIN
Query Match          73.6%; Score 20.6; DB 13; Length 638;
Best Local Similarity 85.2%; Pred. No. 1.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      1 CAACTAAGTATGATGCCTAAAGTTCAA 27
         ||||| | ||||||||| |||
DB      612 CAGCTAATTGAATGACGTAAAGTCGAA 638

RESULT 9
CNS000KM/c
LOCUS
DEFINITION
Arabidopsis thaliana genome survey sequence Sp6 end of HAC F11K19
of IGF library from strain Columbia of Arabidopsis thaliana,
genomic survey sequence.
AL085934
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana.
Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 268)
Salanoubat,M., Choinsne,N., Arriguenave,F., Brottier,P., Wincker,P.,
Samson,D., Saurin,W., Weissenbach,J. and Queller,F.
Unpublished
2 (bases 1 to 268)
Genoscope.
Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage ;
BP 191 91006 Evry cedex - FRANCE (E-mail : sequele@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
    1..268
        /organism="Arabidopsis thaliana"
        /strain="Columbia"
        /db_xref="taxon:3702"
        /clone="F11K19"
        /clone_1lb="IGF"
        /note="end : SP6"

BASE COUNT      75 a       70 c       54 g       69 t
ORIGIN
Query Match          71.4%; Score 20; DB 17; Length 268;
Best Local Similarity 82.1%; Pred. No. 2.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY      1 CAACTAAGTATGATGCCTAAAGTTCAA 28
         ||||| | ||||| |||||
DB      215 CAACTCAGCTTGACGCTAAGGTTCAAA 188

RESULT 10
```

BH366114
LOCUS BH366114 394 bp DNA linear GSS 03-DEC-2001
DEFINITION CH230-75F8.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-75F8, DNA sequence.
ACCESSION BH366114
VERSION BH366114.1 GI:17296848
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 394)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shwartsbeyn
A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,E. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcorI segment
Unpublished (1999)
Other GSSs: CH230-75F8.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mai.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 75 row: F column: 8
Seq primer: SP6
Class: BAC ends.
FEATURES
Location/Qualifiers
source 1..394
/organism="Rattus norvegicus"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-75F8"
/clone_lib="CHORI-230 Segment 1"
/sex="female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"

BASE COUNT 137 a 81 c 66 g 110 t
ORIGIN
Query Match 71.4%; Score 20; DB 17; Length 394;
Best Local Similarity 82.1%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 CAACCTAATGATGCTAAAGTTCAA 28
||||| ||||| ||||| ||||| |||||
DB 92 CAACCAACTACTAATCTAAATTCAA 119

RESULT 11
LOCUS AL759527 479 bp DNA linear GSS 18-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-188A08-014624,
genomic survey sequence.
ACCESSION AL759527
VERSION AL759527.1 GI:21497875
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1

AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
and Weissshaar,B.
TITLE A pipeline for automated high-throughput generation of ESTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
JOURNAL Unpublished
REFERENCE 2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weissshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 479)
Li,Y., Rosso,M., Strizhov,N. and Weissshaar,B.
Direct Submission
Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer
Zuechlingsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene At3g47850. The
sequences are generated at the MPI for plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz.koeln.mpg.de/GABI-Kat/.

FEATURES
Location/Qualifiers
source 1..479
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-188A08-014624"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"

BASE COUNT 150 a 109 c 111 g 109 t
ORIGIN
Query Match 71.4%; Score 20; DB 17; Length 479;
Best Local Similarity 82.1%; Pred. No. 3e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 CAACCTAATGATGCTAAAGTTCAA 28
||||| ||||| ||||| ||||| |||||
DB 358 CAACCTACGCTTGACCTAAGCTTCAA 331

RESULT 12
LOCUS CNS00P03 548 bp DNA linear GSS 28-JUN-1999
DEFINITION Arabidopsis thaliana genome survey sequence T7 end of BAC F7M17 of
IGF library from strain Columbia of Arabidopsis thaliana, genomic
survey sequence.
ACCESSION AL083889
VERSION AL083889.1 GI:5285029
KEYWORDS GSS.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 548)
Salanoubat,M., Choisme,N., Artiguenave,F., Brottier,P., Wincker,P.,
Samson,D., Saurin,W., Weissenbach,J. and Queller,F.
Unpublished
2 (bases 1 to 548)
Genoscope.
Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY ccdex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr

FEATURES
 Source
 1. 548
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="F7M17"
 /clone_lib="TGF"
 /note="end : T7"

BASE COUNT
 160 a 109 c 137 g 142 t

ORIGIN
 Query Match 71.4% Score 20; DB 17; Length 548;
 Best Local Similarity 82.1% Pred. No. 3.2e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
 ||||| 1 ||||| 1111 111111
 Db 205 CAACTCACTCTTTCAGCCTTAAGTTCAAA 178

RESULT 13
 BH742194 574 bp DNA linear GSS 25-FEB-2002
 LOCUS g143b05.g1 Bobuds01 Brassica oleracea genomic clone g143b05 5', DNA
 DEFINITION sequence.
 ACCESSION BH742194
 VERSION BH742194.1 GI:18876807
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 574)
 Katar, M., O'Shaughnessy, A., Palmer, L., Bahret, A., Baker, J., Balija
 V., Cunliffe, D.M., Katzenberger, P., King, L., Kirchoff, K., Kuit, K.,
 Miller, B., Muller, S., Nascimento, L., Preston, R., Santos, L., Shah, R.,
 Zutavern, T., Dedha, N., Radniewic, P.D. and McCombie, W.R.
 Whole Genome Shotgun Reads from Brassica oleracea (2002b)
 Unpublished (2002)
 Contact: W. Richard McCombie
 Cold Spring Harbor Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: g143 row: b column: 05
 Seq primer: -210n1Rev
 Class: shotgun
 High quality sequence stop: 574.
 Location/Qualifiers
 1. 574
 /organism="Brassica oleracea"
 /db_xref="taxon:3712"
 /clone="g143b05"
 /clone_lib="Bobuds01"
 /note="Vector: M13 for .x reads, pBluescript for .b and .g
 reads; Site_1: EcoRV; Whole genome shotgun library from
 flowering buds. DNA was purified from a crude nuclear prep
 using Brassica oleracea TO1000DH3 buds provided by Thomas
 Osborn at the University of Wisconsin. Genomic DNA
 provided by Pablo Radniewicz (CSHL) and shotgun library
 prepared in McCombie lab."

BASE COUNT
 216 a 91 c 80 g 187 t

ORIGIN
 Query Match 71.4% Score 20; DB 17; Length 574;
 Best Local Similarity 82.1% Pred. No. 3.2e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
 ||||| 1 ||||| 1111 111111
 Db 539 CCAATATATTATTAAGTTCAAA 566

RESULT 14
 BH275516 621 bp DNA linear GSS 30-NOV-2001
 LOCUS CH230-83N9.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
 DEFINITION CH230-83N9, DNA sequence.
 ACCESSION BH275516
 VERSION BH275516.1 GI:17187918
 KEYWORDS GSS.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 621)
 Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
 A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
 Jong, P. and Fraser, C.M.
 Rat BAC End Sequences from Library CHORI-230 EcORI segment
 Unpublished (1999)
 Other_GSSs: CH230-83N9.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library
 availability, please contact Pieter de Jong (pdj@jorgemail.cho.org).
 Clones may be purchased from BACPAC Resources
 (<http://www.chori.org/bacpac/ordering/information.htm>). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: B3 row: N column: 9
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1. 621
 /organism="Rattus norvegicus"
 /strain="BN/SNHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-83N9"
 /clone_lib="CHORI-230 Segment 1"
 /sex="Female"
 /cell_type="Brain"
 /note="Vector: PTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
 CHORI-230 Rat (BN/SNHsd/MCW) BAC library produced by
 Pieter de Jong"

BASE COUNT
 199 a 131 c 118 g 173 t

ORIGIN
 Query Match 71.4% Score 20; DB 17; Length 621;
 Best Local Similarity 82.1% Pred. No. 3.3e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
 ||||| 1 ||||| 1111 111111
 Db 154 CAACTAACTATTGATGCTAAAGTTCAAA 181

RESULT 15
 BM397184/c 809 bp mRNA linear EST 17-JAN-2002
 LOCUS 5009-0-3-A09.t.1 Chilcoal/Turkewitz cDNA (large fraction)
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM397184
 VERSION BM397184.1 GI:18197237
 KEYWORDS EST.

SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE 1 (bases 1 to 809)
 AUTHORS Turkewitz,A.P., Karger,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
 ,J. and Klobutcher,L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: 73.
 FEATURES Location/Qualifiers
 source 1..809
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 BASE COUNT 312 a 87 c 156 g 254 t
 ORIGIN
 Query Match 71.4%; Score 20; DB 13; Length 809;
 Best Local Similarity 82.1%; Pred. No. 3.7e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 CAACTAAGTATGATGCTAAAGTTCAA 28
 ||||| | ||||| | | |||||
 Db 192 CAACTAATCTGTGATGTCATTTCAA 165

Search completed: December 10, 2002, 22:50:18
 Job time : 1439.66 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 607.084 Seconds

(without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28

Sequence: 1 caactaactatgatgtacctaagttcaaa 28

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapexl 1.0

Searched: 2054640 seqs, 14551402878 residues

otal number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBml:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	AX306866	AX306866 Sequence
2	28	100.0	1789	E09772	E09772 The base se
3	28	100.0	2007	AR089410	AR089410 Sequence
4	28	100.0	2007	AR093610	AR093610 Sequence
5	28	100.0	2322	SABBP	YU0688 Staphylococ
6	28	100.0	2322	E03736	E03736 DNA sequenc
7	28	100.0	2454	SEMECAPB	X52592 S. epidermi
8	28	100.0	2455	E09771	E09771 The base se
9	28	100.0	2456	SAHECAPB	X52593 S. aureus m
10	28	100.0	2456	AX110445	AX110445 Sequence
11	28	100.0	5596	SSK8MECA	Y13095 S. sciuri me
12	28	100.0	6368	SSK3MECA2	Y13095 S. sciuri me
13	28	100.0	9047	SAMECAPB1	Y14051 Staphylococ
14	28	100.0	21777	AB063173	AB063173 Staphyloc
15	28	100.0	26090	AB063172	AB063172 Staphyloc
16	28	100.0	39332	AB033763	AB033763 Staphyloc
17	28	100.0	58237	DB6934	DB6934 Staphylococ
18	28	100.0	68256	AB037671	AB037671 Staphyloc
19	28	100.0	290250	AP004822	AP004822 Staphyloc
20	28	100.0	298050	AP003129	AP003129 Staphyloc
21	28	100.0	349999	AP003358	AP003358 Staphyloc
22	22.2	79.3	5806	SSK3MECA1	Y13052 S. sciuri me
23	22.2	79.3	349980	AX417038	AX417038 Sequence
24	22.2	79.3	349980	AX417041	AX417041 Sequence
25	21.2	75.7	11608	AF125160	AF125160 Rattus no
26	21.2	75.7	192419	AC110094	AC110094 Rattus no
27	20.6	73.6	247	BLCOIT	X90409 B. lucorum D
28	20.6	73.6	5068	SSK1MECA	Y09223 S. sciuri me
29	20.6	73.6	6684	SSK1MECA	Y13094 S. sciuri me
30	20.6	73.6	8592	AE010503	AE010503 Fusobacte
31	20.6	73.6	10029	AE007351	AE007351 Streptoco
32	20.6	73.6	11692	AE007454	AE007454 Streptoco
33	20.6	73.6	13206	BD003713	BD003713 Polynucle
34	20.6	73.6	16995	BD003762	BD003762 Polynucle
35	20.6	73.6	120492	CXY43R8C	AI032637 Caenorhab
36	20.6	73.6	163820	AC123878	AC123878 Mus muscu
37	20.6	73.6	178521	AC126450	AC126450 Mus muscu
38	20.6	73.6	232807	SPNEU1901	AL449923 Streptoco
39	20.6	73.6	248254	SPNEU1903	AL449925 Streptoco
40	20.2	72.1	186766	AL732294	AL732294 Mus muscu
41	20.2	72.1	245087	AC091606	AC091606 Mus muscu
42	20	71.4	969	AY116864	AY116864 Arabidops
43	20	71.4	1107	AF436027	AF436027 Neotrypae
44	20	71.4	1160	AF428310	AF428310 Arabidops
45	20	71.4	1168	AY086386	AY086386 Arabidops

ALIGNMENTS

RESULT 1	AX306866	Sequence 25 from Patent Epl160333.	28 bp	DNA	Linear	PAT 14-DEC-2001
LOCUS	AX306866					
DEFINITION	AX306866					
ACCESSION	AX306866					
VERSION	AX306866.1	GI:17894688				
KEYWORDS						
SOURCE						
ORGANISM						
synthetic construct.						
synthetic construct						
artificial sequences.						
REFERENCE						
1						
AUTHORS	Taya, T., Ishiguro, T. and Saito, J.					
TITLE	Oligonucleotides and method for detection of meca gene of					
JOURNAL	methicillin-resistant Staphylococcus aureus					
	Patent: EP 1160333-A 25 05-DEC-2001;					

```

FEATURES             Tosoh Corporation (JP)
      SOURCE          Location/Qualifiers
                        1..28
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
                        /note="Primer"
BASE COUNT           12 a      5 c      3 g      8 t
ORIGIN
Query Match          100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY      1  CAACTAACTATTGATGCTAAAGTTCAAA 28
Db      1  CAACTAACTATTGATGCTAAAGTTCAAA 28

RESULT 2
E09772  E09772      1789 bp  RNA      linear  PAT 29-SEP-1997
LOCUS   The base sequence of modified meca DNA.
ACCESSION E09772
VERSION   E09772.1 GI:22026401
KEYWORDS  JP 1995209294-A/2.
SOURCE    Staphylococcus aureus.
ORGANISM  Staphylococcus aureus.
REFERENCE 1 (bases 1 to 1789)
AUTHORS   Kono, M., Hiramatsu, K., Sasazu, M., Noguchi, M. and Suguro, K.
TITLE     NOVEL 'MECA PROTEIN' CODING DNA THEREFOR, AND DETECTION METHOD FOR
JOURNAL   METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
PATENT    Patent: JP 1995209294-A 2 11-AUG-1995;
          KONO MEGUMI, MITSUBISHI CHM CORP, DENKA SEIKEN CO LTD
COMMENT   OS Staphylococcus aureus
          PN JP 1995209294-A/2
          PD 11-AUG-1995
          PF 10-JAN-1994 JP 1994012226
          PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
          MASAHISA,
          PI SUGURO KAZUYA
          PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC
          C12R1:19),
          CC (C12P21/02,C12R1:19);
          CC strandedness: Double;
          CC topology: Linear;
          FH key      Location/Qualifiers
          FT source   1..1789
          FT          /organism="Staphylococcus aureus" FT CDS
          FT          Location/Qualifiers
          FT          1..1789
          FT          /product="Modified meca".
FEATURES
      SOURCE          Location/Qualifiers
                        1..1789
                        /organism="Staphylococcus aureus"
                        /db_xref="taxon:1280"
BASE COUNT           735 a      263 c      302 g      489 t
ORIGIN
Query Match          100.0%; Score 28; DB 6; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  CAACTAACTATTGATGCTAAAGTTCAAA 28
Db      1  CAACTAACTATTGATGCTAAAGTTCAAA 601

RESULT 3
AR089410 2007 bp  DNA      linear  PAT 07-SEP-2000
LOCUS   Sequence 169 from patent US 5994066.
DEFINITION
ACCESSION AR089410

```

```

VERSION             AR089410.1 GI:10016167
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unknown.
REFERENCE            1 (bases 1 to 2007)
AUTHORS             Bergeron, M.G., Picard, F.J., Ouellette, M. and Roy, P.H.
TITLE               Species-specific and universal DNA probes and amplification primers
JOURNAL             to rapidly detect and identify common bacterial pathogens and
PATENT              associated antibiotic resistance genes from clinical specimens for
                    routine diagnosis in microbiology laboratories
                    Patent: US 5994066-A 169 30-NOV-1999;
FEATURES
      SOURCE          Location/Qualifiers
                        1..2007
                        /organism="unknown"
BASE COUNT           855 a      270 c      341 g      541 t
ORIGIN
Query Match          100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  CAACTAACTATTGATGCTAAAGTTCAAA 28
Db      1  CAACTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 4
AR093610 2007 bp  DNA      linear  PAT 08-SEP-2000
LOCUS   Sequence 169 from patent U. 6001564.
ACCESSION AR093610
VERSION   AR093610.1 GI:10020359
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS   Bergeron, M.G., Ouellette, M. and Roy, P.H.
TITLE     Species specific and universal DNA probes and amplification primers
JOURNAL   to rapidly detect and identify common bacterial pathogens and
PATENT    associated antibiotic resistance genes from clinical specimens for
          routine diagnosis in microbiology laboratories
          Patent: US 6001564-A 169 14-DEC-1999;
FEATURES
      SOURCE          Location/Qualifiers
                        1..2007
                        /organism="unknown"
BASE COUNT           855 a      270 c      341 g      541 t
ORIGIN
Query Match          100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  CAACTAACTATTGATGCTAAAGTTCAAA 28
Db      1  CAACTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 5
SABP      2322 bp  DNA      linear  BCT 12-SEP-1993
LOCUS   Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible
DEFINITION
ACCESSION Y00688
VERSION   Y00688.1 GI:46628
KEYWORDS  penicillin-binding protein.
SOURCE    Staphylococcus aureus.
ORGANISM  Staphylococcus aureus.
REFERENCE 1 (bases 1 to 2322)
AUTHORS   Song, M.D., Wach, M., Dol, M., Ishino, F. and Matsubashi, M.
TITLE     Evolution of an inducible penicillin-target protein in

```

methicillin-resistant *Staphylococcus aureus* by gene fusion
 JOURNAL FEBS Lett. 221 (1), 167-171 (1987)
 MEDLINE 87304805
 PUBMED 3305073
 REFERENCE 2 (bases 1 to 2322)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
 Harberis-Maino, L., Kayser, F. H. and Berger-Bachi, B.
 TITLE Sequence comparison of meca genes isolated from
 methicillin-resistant *Staphylococcus aureus* and *Staphylococcus*
epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT Data kindly reviewed (13.1.88) by Matsubashi.
 FEATURES
 source
 1..2322
 Location/Qualifiers
 /organism="Staphylococcus aureus"
 /db_xref="taxon:1280"
 1..2013
 /note="penicillin-binding protein (AA 1-670)"
 /codon_start=1
 /transl_table=11
 /protein_id="CAA68684.1"
 /db_xref="GI:46629"
 /db_xref="SWISS-PROT:P07944"
 /translation="MKKIKYPLILIVVVGCGIYFVASKDKKINNTIDAIEDKNEKQ
 VYKDSYISKSDNGEVEEMTERPIKIVNSGVGDINODRIKVKSKNRKRVDAQYKIK
 TVNGIDRVQVDFEEDGMKLDMDHSYIIGOMOKDSIHLENKSEKGIIDRNRY
 ELANGTIDHRLGIFPKVSKYKDKYIAKELSTSEPYINKKIKYKMIPTSFHKYK
 KMDYISDPAKKFFLTNTETESRNPICATKATSHLCYGPINSEELKQKQYGYRDA
 VIKKGLEKLDKIOHEDGYRVTIVRVDSNNTIAHTLIERKKKGKDIQLTIDAKV
 OKSIYNNKNDVSGSTAIHPOTGELLALVSTPSYDVPYPMYQMSNEEYKILTEDKKEP
 LNKFOITTSPTSGSTOKILTAMIGLNKTLIDDTSYKIDGKQKDSMGCVYNTREV
 VNGNIDLKQAISSDSNIFARVALLEGSKFEKMGKLGVEDIPDYPFYVAQISNK
 NIDNEILLADSGGGEELINVOILISTYSALENNGINAPHLKDTKMKWKNKITS
 KENILNLNCGMOQVYKTHKEDIVSYALIGKSGTAEKMGQFGRCQICMFPISYDK
 DNPNNMAINVDNODKMASTNAKISGVYDELYENGKKYDIDE"

BASE COUNT 940 a 324 c 369 g 669 t
 ORIGIN

Query Match 100.0%; Score 28; DB 1; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 0.94;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTACTATGATGCTAAAGTTCAA 28
 |||||||||||||||||||||||||||||
 Db 979 CAACTACTATGATGCTAAAGTTCAA 1006

RESULT 6
 LOCUS E03736 2322 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA sequence of PBP2' gene for determination of methicillin
 resistance.
 ACCESSION E03736
 VERSION E03736.1 GI:2171951
 KEYWORDS JP 1992169200-A/9.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2322)
 AUTHORS Murakami, Y., Nakamura, E., Teraoka, H., Wada, K., Minamide, W. and
 Murakami, K.
 TITLE DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
 JOURNAL Patent: JP 1992169200-A 9 17-JUN-1992;
 SHIONOGI & CO LTD
 OS (methicillin resistant) *staphylococcus aureus*
 PN JP 1992169200-A/9
 PD 17-JUN-1992
 PF 31-OCT-1990 JP 1990296708
 PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI,
 MINAMIDE WAKIO, MURAKAMI KAZUHIISA
 PC C1201/68, C12N15/11;

CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti_sense: No;
 FH Key Location/Qualifiers
 FT misc_feature 1..2322
 FT /note="PBP2' gene for determination of
 methicillin resistance".
 FEATURES
 source
 1..2322
 /organism="unidentified"
 /db_xref="taxon:332644"
 BASE COUNT 939 a 324 c 390 g 669 t
 ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 0.94;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTACTATGATGCTAAAGTTCAA 28
 |||||||||||||||||||||||||||||
 Db 979 CAACTACTATGATGCTAAAGTTCAA 1006

RESULT 7
 LOCUS SEMECAPB 2454 bp DNA linear BCT 12-SEP-1993
 DEFINITION S. epidermidis meca gene for PBP2' (penicillin binding protein 2').
 ACCESSION X52592.1 GI:46993
 VERSION X52592.1
 KEYWORDS meca gene; methicillin resistance; penicillin-binding protein 2'.
 SOURCE *Staphylococcus epidermidis*.
 ORGANISM *Staphylococcus epidermidis*.
 REFERENCE 1 (bases 1 to 2454)
 AUTHORS Ryffel, C.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
 Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
 REFERENCE 2 (bases 1 to 2454)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
 Harberis-Maino, L., Kayser, F. H. and Berger-Bachi, B.
 TITLE Sequence comparison of meca genes from methicillin-resistant
Staphylococcus aureus and *Staphylococcus epidermidis*
 JOURNAL Gene (1990) In press
 REFERENCE 3 (bases 1 to 2454)
 AUTHORS Ryffel, C.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
 Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
 REFERENCE 4 (bases 1 to 2454)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
 Harberis-Maino, L., Kayser, F. H. and Berger-Bachi, B.
 TITLE Sequence comparison of meca genes isolated from
 methicillin-resistant *Staphylococcus aureus* and *Staphylococcus*
epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT See also <X52593-4> and <Y00688>.
 DATA kindly reviewed (23-JUL-1990) by C. Ryffel.
 FEATURES
 source
 1..2454
 /organism="Staphylococcus epidermidis"
 /strain="WT55"
 /db_xref="taxon:1282"
 /clone="WT80/WT9"
 80..85
 /note="-35 region"
 101..105
 promoter
 promoter
 promoter

RBS	/note=" -10 region"
	130..134
precursor_RNA	/note="Ribosome binding site"
	141..2159
CDS	/note="primary transcript"
	141..2147
	/note="PBP2' (AA 1 - 668) "
	/codon_start=1
	/transl_table=1
	/protein_id="CAA36828.1"
	/db_xref="GI:"CAA36828.1"
	/db_xref="SPTREMBL:O54113"
	/translation="MKRKIVPLILVWVGFIYPASKDKELINTIDAIEDKFNKO VYKSYSISKSDNGEVEEMTERPIKTYSVKDGINIDOKRIKKRSKKRKNDAQYKIK TNCNIDRNVOFNPVRKEGCKMLDMDSVLIPGMKRQSIIHEFLSKERKIIDRRNV ELANATGAIEIGIYPRKVNSKKDYKAIAKEISISDIYIKOOMDNMWDOTDFPVLPKYTK KMDDYISDPFAKPHLTINTEBESRPYLGRATSHLGVCPIINSBELKOEKGCTKDPA VIGKRGLEKLRYDLQHEDGYRVTVVDNSNTVAHTLERKKKDGKDIOILTDAKVOR SIYNMNKNDYGSGTAIHPOTGELLALVSTPSDVYPPMYGSNEEKRLTEDKEPLL NKPEITTSPTGSTOKILTFAMIGLNKKRTLDSDSYKSIDKGMOKDSMGCVVTREVVN ENIDLAKIESDNIIFPARVALLEGSKPKPEGMKLLGVEDIPTYPYNAVLSINKNL DNELLADSGCGCEILLINPOLISAI SALENNGNINAHLIKTRKKVKKKI ISKE NILNLTJPMOOOVNKTTHKEDIRYSYAULICKSCSAELKMOGEROIOMFISTDRDN PNMMATAINYKDVODKGNASTNAKISGVYIDELIENGNNKKTIIDE"
old_sequence	441..448
	/note="altaaac was ac in [1]"
old_sequence	/citation=[1]
	641..643
	/note="agc was ac in [1]"
old_sequence	/citation=[1]
	652..653
	/note="ta was tta in [1]"
old_sequence	/citation=[1]
	731..733
	/note="caa was ca in [1]"
old_sequence	/citation=[1]
	780..781
	/note="cl was ctt in [1]"
BASE COUNT	997 a 345 c 398 g 714 t
ORIGIN	
Query Match	100.0%; Score 28; DB 1; Length 2454;
Best Local Similarity	100.0%; Pred. NO. 0.93; Mismatches
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 CACTACTATTGCATGTAAAGTTCCAAA 28
Db	1113 CAACACTACTATGGATGCTAAAGTTCAA 1140
RESULT 8	
E09771 LOCUS	E09771 2455 bp RNA linear PAT 29-SEP-1997
DEFINITION	The base sequence of meca DNA.
ACCESSION	E09771
VERSION	E09771.1 GI:22026400
KEYWORDS	JU 1995209294-A/1.
SOURCE	Staphylococcus aureus.
ORGANISM	Staphylococcus aureus Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS	Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suwuro,K.
TITLE	NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL	Patent: JP 1995209294-A 1 11-AUG-1995; OS MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
COMMENT	OS Staphylococcus aureus PN JU 1995209294-A/1 PD 11-AUG-1995 PF 10-JAN-1994 JP 1994012226 PI KONO MEGUMI, HIRAMATSU KEICHI, SASAZU MITSUNORI, PI NOGUUCHI MASAHISA,

	Pt	SUGURO KAZUYA G0IN93/53.C07K14/31,C12N1/21,C12N15/09,C12P21/02,(C12M1/21,Pc C12R1:19), PC (C12P21/02,C12R1:19); CC strandedness: Double; CC topology: Linear;	
	FH	Key	Location/Qualifiers
	FT	source	1..2455
	FT		/organism='Staphylococcus aureus' FT CDS
FEATURES	FI	134..2146	/product='meca protein'. Location/Qualifiers
source		1..2455	
		/organism='Staphylococcus aureus'	
		/db_xref='taxon:1280'	
BASE COUNT		997 a 344 c 401 g 713 t	
ORIGIN			
Query Match		100.0%; Score 28; DB 6; Length 2455;	
Best Local Similarity		100.0%; Pred. No. 0 93;	
Matches	28; Conservative	0; Mismatches	0; Indels
	Gaps	0;	0;
OY	1	CACCTAACTATTGATCGTCAAAGTTCAAA	28
Dn	1112	CACCTAACTATTGATCGTCAAAGTTCAAA	1139
LOCUS	SAHECAPB	2456 bp	DNA linear BCT 12-SEP-1993
DEFINITION	S. aureus meca gene for pbp2' (penicillin binding protein 2').	X52593	
VERSION	X52593.1 GI:46610	meca gene; methicillin resistance; penicillin-binding protein; penicillin-binding protein 2.	
KEYWORDS	Staphylococcus aureus Staphylococcus aureus Bacteria; Firmicutes; Bacillales; Staphylococcus. kvyfel,c.		
SOURCE ORGANISM	Direct Submission Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of Medical Microbiology, Gloriastr 32, CH-8028 Zurich, Switzerland (bases 1 to 2456)		
REFERENCE AUTHORS	Ryf fel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E., Barberis-Maino,L., Kayser,F.H. and Berger-Bachi,B.		
TITLE	Sequence comparison of meca genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis		
JOURNAL MEDLINE PUBMED	Gene 94 (1), 137-138 (1990) 91033056 2227446		
COMMENT	See also <X52592>, <X52594> and <Y00688>. Data kindly reviewed (23-JUL-1990) by C. Ryffel. 		
FEATURES	Source	Location/Qualifiers	
promoter		1..2456	
RBS		/organism='Staphylococcus aureus' /strain='NCRC8325, isolate=BA870' /db_xref='taxon:1280' /clone_id='EMBL-3' 80..85	
precursor_RNA		/note='-35 region' 101..105	
CD S		/note='-10 region' 130..134	
		/note='ribosome binding site' 141..2153	
		/note='primary transcript' 141..2147	
		/note='pbp2' (AA 1-668)' /codon_start=1 /transl_table=11	

[illegible]

DEFINITION	S_sciuri_meca2 gene, strain K3 (MM2).
ACCESSION	Y13095
VERSION	Y13095.1
KEYWORDS	CTORF261 gene; meca2 gene; mecI gene; mecRI gene; NTOF101; ORF142
SOURCE	Staphylococcus sciuri.
ORGANISM	Staphylococcus sciuri
REFERENCE	Bacteria: Firmicutes: Bacillales: Staphylococcus.
AUTHORS	1 (bases 1 to 6368)
TITLE	Wu, S., de Lencastre, H. and Tomasz, A.
JOURNAL	Genetic organization of the meca region in methicillin-susceptible
MEDLINE	and methicillin resistant strains of Staphylococcus sciuri
PUBMED	J. Bacteriol. 180 (2), 236-242 (1998)
REFERENCE	98101461
AUTHORS	9440511
TITLE	2 (bases 1 to 6368)
JOURNAL	Wu, S.
MEDLINE	Direct Submission
PUBMED	Submitted (08-MA-1997) S. Wu, Lab of Microbiology, The Rockefeller
REFERENCE	University, 1230 York Avenue, New York NY 10021, USA
AUTHORS	Related sequences L14020, X52593, Y09223.
TITLE	Location/Qualifiers
JOURNAL	1. 6368
MEDLINE	/organism="Staphylococcus sciuri"
PUBMED	/strain="K3 (MM2)"
REFERENCE	/sub_species="rodentius"
AUTHORS	/db_xref="taxon:1296"
TITLE	complement(1..883)
JOURNAL	/gene="CTORF261"
MEDLINE	complement(<1..784)
PUBMED	/gene="CTORF261"
REFERENCE	/codon_start=1
AUTHORS	/transl_table=1
TITLE	/protein_id="CAV73539.1"
JOURNAL	/db_xref="GI:2791913"
MEDLINE	/db_xref="SPTRMBL:054280"
PUBMED	/translation="MENTLINDMKRYLREIYNHNISRPOISKULEINKATISSIIII
REFERENCE	NKLYKSLVNEVGEGDSTKSCGRKPIILKYNHLKCYPLSDLTYSSEVYRNFTDGN
AUTHORS	IKHSTYDLPDKVKSLSIIRKIDIDQKEDTLNGLGVSTIGVVDNEQHYTLPLP
TITLE	HETGISYIAKKIKEITNYPVANEANISALYENFNINLSYNLIALSIHKIGAGAG
JOURNAL	IINNOYRGANGEGEIGKTLVSKVDNVEIFRKHIEDIFSOEA"
MEDLINE	complement(791..797)
PUBMED	/gene="CTORF261"
REFERENCE	complement(855..860)
AUTHORS	/gene="CTORF261"
TITLE	complement(878..883)
JOURNAL	/gene="CTORF261"
MEDLINE	complement(1257..1628)
PUBMED	/gene="mecI"
REFERENCE	complement(1257..1628)
AUTHORS	/gene="mecI"
TITLE	/codon_start=1
JOURNAL	/transl_table=1
MEDLINE	/product="MecI protein"
PUBMED	/protein_id="CAV73540.1"
REFERENCE	/db_xref="GI:2791914"
AUTHORS	/db_xref="SPTRMBL:054281"
TITLE	/translation="MDNKTEIISAEWVNNIIMKKYASANNIIIEFIOMORDSPKTI
JOURNAL	IRTLITLPIFKKGFIDRRKDNKIIFYLSVESDIKTKSKFINKYKKGFSNLYLNF
MEDLINE	VERKDLSDDEIEELRNILNKR"
PUBMED	complement(join(1628..3385,3392..3398,3410..3415))
REFERENCE	/gene="mecr1"
AUTHORS	complement(1628..3385)
TITLE	/gene="mecr1"
JOURNAL	/codon_start=1
MEDLINE	/transl_table=1
PUBMED	/product="MecrI protein"
REFERENCE	/protein_id="CAV73541.1"
AUTHORS	/db_xref="GI:2791915"
TITLE	/db_xref="SPTRMBL:054282"
JOURNAL	/translation="MSSFLMLCISSLLTICVFLVRLMYIKYTONIMSCHKILWLIV
MEDLINE	VSTLIPIPKYKISNFTFSKDMNRRNSDITSSVSHLDDGOSSVTKDIAINVOEFT
PUBMED	SNITVILLIIVWGSILCTIPMKAFKAPDIDIKSSLESSLNERLKVCSKMOFYKK
REFERENCE	HITISYSNIDNPVFCVAKSQIOLPTVYVETMNDKELEYIIILHELSHVASHDLINQ

LTVYFKATLFFHFRPALYISKTYLMDNDCEVOCVRNKLTLNREHRIAREESILKSLKLS
 QHINNAVAOYDILGGENSNIKERVKITALTIDSPKFRNKRITVATVGSISLTQAPLPS
 AHWODKTEIVNYSYKLLNQAPYFKPGHDSGVLYNREQAVSYNPEPSQORSPNST
 YKITYLALAFADONLILSNHTEIQOMDKHOFYPERKENOQONLNSMKYVVMNYENLKNL
 LRQDQKSYLIDLIEYGENEELSGENENYMESSLKLSAIEOVMLLKDMMQHNNHPNKAI
 NEKVENKSLKQDKEYTKYVGTGTGTGVNHNKEANGWFVGVETKQDITYEATHLKGEDNA
 NCKEKNQOISERTIKEMELI"
 gene complement(1636. .1640)
 RBS /gene="mec1"
 complement(1636. .1640)
 RBS /gene="mec1"
 complement(16392. .3398)
 RBS /gene="mecr1"
 complement(3410. .3415)
 -10_signal /gene="mecr1"
 gene 3424. .3429
 /gene="meca2"
 3424. .3429
 -35_signal /gene="meca2"
 gene 3424. .3429
 complement(3433. .3438)
 -35_signal /gene="meca2"
 complement(3433. .3438)
 gene /gene="mecr1"
 3448. .3453
 -10_signal /gene="meca2"
 3448. .3453
 RBS /gene="meca2"
 3474. .3479
 CDS /gene="meca2"
 3485. .3491
 /gene="meca2"
 /codon_start=1
 /transl_table=1
 /product="Meca2 protein"
 /protein_id="CAA73542.1"
 /db_xref="GI:2791916"
 /db_xref="SPTREMBL:O54283"
 /translation="MKRIKIVPELILVYVVGEGIFYFASKDKEINNTIDAIGDKNFKQ
 TVKDSYISGDSNGCEVEWTEERPILKIVNSLGYKVDNIIDQRKIKVSKNKKPVDAQYKIKK
 NYGNDIDRNVQCEPFAVEKEDGMKMLDWDHSVILPGHOKDQSIHLENLSBRCKTIDRNNV
 ELAINGTAAEIGIVPKNVSKKDYKALIAKELISIEDYIKQOMDMWODDPFVPLTKYKTA
 KNDYETIDPAKKEHLLTNTNETSRNPLEKATSHLIGYVGRINSPELKQKPEVKKKDDA
 VYGGKLELYIDRKKLQIHEDGRYVTVYDNRNNTIAHTLEKKKKRKGDIQLTIDKAYQKQ
 STYNNKTVSGSGTGIHPQTGELLALVSTPSYDVPENYKGSNEEYNTLEDKKEPLL
 NKQPTTTSNGSTQKILTLTAMIGLNNKTTLDDKTSYKIDCGWQKDSWCGVNTYREPVN
 GAIIDKQALFESSDNIFFARVALELQSKFEEKGMKLGVEDIPSDYFYNQISNKNIL
 DNEILTLADSGGCGEILINPVOILSYALNNNGININAPHLIKDTKNNYKNNKIISEKE
 NINLLTDGQGVQVNTKEIDYIRSYANLIGKSTAELEKMKQGETGRPIGMWISYDKON
 PHLMAIVKQIDPDKGMASYNKISGKYVDLEYNGNKKYIDE"
 gene complement(5537. .6038)
 CDS /gene="ORF142"
 complement(5537. .5965)
 /gene="ORF142"
 /codon_start=1
 /transl_table=1
 /protein_id="CAA73543.1"
 /db_xref="GI:2791917"
 /db_xref="SPTREMBL:O54520"
 /translation="MKYDQFVGETYFKTKSLHITREEELIOFATTFDDQYMHIDKEKAR
 GSRFRKISGNSMHTLISIFKLMVEGKSGVEEYVAGTQNNNNYKIFKPYPGNTLVIAEHE
 IINRKSIIKENGILVIVSTYVNEEIVEIKGEVVALINNS"
 complement(5972. .5977)
 RBS /gene="ORF142"
 complement(6010. .6015)
 -10_signal /gene="ORF142"
 gene 6033. .6038
 -35_signal /gene="ORF142"
 complement(6062. .6368)
 gene /gene="NTORF101"
 complement(6062. .>6368)
 CDS /gene="NTORF101"
 /codon_start=2
 /transl_table=11

gene	protein_id="CAAT73544.1"
	/db_xref="GI:2791918"
	/db_xref="SPTRMBL:054616"
	/translation="SFNNVVLKLALEIMPYNNNAVLPHTTSPFRKDMFTLLDYCNALIV
	NTEBAKTKTKKKVKKVAGAYELANWTYNNKKPARANOLANMGVIXDLPFTDNAMKMYHLISO"
BASE COUNT	2230 a 998 c 884 g 2256 t
ORIGIN	
Query Match	100.0%; Score 28; DB 1; Length 6368;
Best Local Similarity	100.0%; Pred. No. 0.8;
Matches 28; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
0y	1 CAACTAACTATGATGCTAAAGTTCAAA 28
Db 4457	CAACTAACTATGATGCTAAAGTTCAAA 4484
RESULT 13	
SAMECAR11	
LOCUS	9047 bp DNA linear BCT 16-JAN-1998
DEFINITION	Staphylococcus aureus mecA, mecH, mecI genes and ORF142, ORF44, ORF145 and ORF224.
ACCESSION	Y14051.1
KEYWORDS	GI:2791983
SOURCE	mecA gene; mecI gene; mecH gene; ORF142; ORF145; ORF224; ORF44; PBP2A; repressor protein; transposase.
ORGANISM	Staphylococcus aureus.
REFERENCE	Staphylococcus aureus.
AUTHORS	Bacteria; Firmicutes; Bacilliales; Staphylococcus.
TITLE	1 (bases 1 to 9047)
JOURNAL	Mu,S.
REFERENCE	Direct Submission
AUTHORS	Submitted (27-JUN-1997) S. Wu, Laboratory of Microbiology, The
TITLE	Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
JOURNAL	2 (bases 1 to 9047)
AUTHORS	Wu,S., de Lencastre,H. and Tomasz,A.
TITLE	Genetic Organization of the mecA region in methicillin-susceptible
JOURNAL	and methicillin-resistant strains of Staphylococcus sciuri
MEDLINE	J. Bacteriol. 180 (2), 236-242 (1998)
PUBMED	98101461
FEATURES	9440511
Source	Location/Qualifiers
	1..9047
	/organism="Staphylococcus aureus"
	/strain="BMS-1"
	/strain="BB270"
	/db_xref="taxon:1280"
	complement(<1..505)
	/note="ORF168"
	/codon_start=1
	/transl_table=1
	/product="putative repressor"
	/protein_id="CAAT4373.1"
	/db_xref="GI:2791984"
	/db_xref="GI:2791985"
	/translation="MYNYFDGQNVYKHSYDLPDEKVSLSIYIKKHIDIDIEKIDTYNG
	LLGVSYSIHGVYDNEQHYVTLPHFETGISTAKIKETITWVAVNEANLSATYERN
	FNHLSYNNLIALSIHKIGAGLIINOLYRGANGEGEIGKTLVSKVSDNVEIFPKI
	EDIFSOEA"
	complement(1244..1615)
	/gene="mecI"
	complement(1244..1615)
	/gene="mecI"
	complement(1244..1615)
	/gene="mecI"
	/codon_start=1
	/transl_table=1
	/product="MecI protein"
	/protein_id="CAAT4374.1"
	/db_xref="GI:2791985"
	/translation="MDKKYFISAEHEVNNIIMKKYASANNIEIQLQKQMSPKT
	IRTLITLYLKKGFIDRRKKDKIFQYYSLVESDSIKTKSNFINKYKGGFNSLVNF
	VERKDSQDELEEDLRNLNK"
	complement(1615..3372)
	/gene="mecRI"

[illegible]

```

BASE COUNT      3099 a      1469 c      1257 g      3222 t
ORIGIN
Query Match      100.0%: Score 28; DB 1; Length 9047;
Best Local Similarity 100.0%: Pred. No. 0.76;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  CACCTAACCTATGATGCTAAAGTTCAAA 28
|||||
Db      4444 CACTACTACTATTGATGCTAAAGTTCAAA 4471

RESULT 14
AB063173      21777 bp      DNA      linear      BCT 09-APR-2002
LOCUS
DEFINITION      Staphylococcus aureus DNA, type-IV staphylococcal cassette
ACCESSION      AB063173
VERSION      AB063173.1 GI:17025993
KEYWORDS
ORGANISM
SOURCE
REFERENCE
AUTHORS      1
TITLE      Hiramatsu, K., Cui, L., Kuroda, M. and Ito, T.
The emergence and evolution of methicillin-resistant Staphylococcus
aureus
JOURNAL
MEDLINE      Trends Microbiol. 9 (10), 486-493 (2001)
REFERENCE
AUTHORS      2
TITLE      Ma, X. X., Ito, T., Tiensasitorn, C., Jamklang, M., Chongtrakool, P.,
Boyle-Varva, S., Daum, R. S. and Hiramatsu, K.
Novel Type of Staphylococcal Cassette Chromosome mec Identified in
Community-Acquired Methicillin-Resistant Staphylococcus aureus
Strains
JOURNAL
MEDLINE      Antimicrob. Agents Chemother. 46 (4), 1147-1152 (2002)
REFERENCE
AUTHORS      3 (bases 1 to 21777)
TITLE      Xue, M. X., Ito, T., Hiramatsu, K. and Tiensasitorn, C.
Direct Submission
Submitted (12-JUN-2001) Teruyo Ito, Junendo University, Department
of Bacteriology, Hongo 2-1-1, Bunkyo-ku, Tokyo 113-8421, Japan
(E-mail: teruyobacter@junendo.ac.jp, Tel:81-3-5802-1041,
Fax:81-3-5684-7830)
FEATURES
Source
location/Qualifiers
1. 21777
/organism="Staphylococcus aureus"
/strain="JCS1978(8/6-3P)"
/db_xref="taxon:1280"
/note="community-acquired MRSA strain isolated at the
university of Chicago children's hospital"
301..21221
/note="302..21222 or 303..21223 or 304..21224
type-IV SCCmec of JCS1978(8/6-3P)"
301..326
/note="inverted complementary repeat(1r-1) of SCCmec of
JCS1978"
/rpt_type=inverted
complement(325..1446)
/note="ORF No. CM001"
/codon_start=1
/transl_table=11

```

```

/product="hypothetical protein"
/protein_id="BAB72122.1"
/db_xref="GI:17025994"
/translation="MKMSYQIKIIVMGPSLYNEFLHOPYITILEDYIIKIDSI,TRNLVE
KFTNNYIEILDKDIIIAKTESGQITSAALSNPQIIVNKSIEFGNCIILONPKSVI
NOIKNSPENOACEVEYPKLDLAVISNIKERSTEOLEGOVNAIKRIILALYKLTKE
SRKSIIVMLYGVSGVGTGEMSKITISECGGLFKPKROMSKNTVMFEDYIFCNNGEPS
IARDLLESNTIVILDEPDKGVNENSAFQOLPDEGIJFEDSOYKVTMNSIITISNF
KGEQIRRELDPIYYRPDDIIFERALENDEKKNILIRIILSEPRKILSDNKSILPRE
EILKOYMIKIKQIPNTRHMKLVENDINLRILISAMLN"
complement(1424..2194)
/note="ORF No. CM002"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72123.1"
/db_xref="GI:17025995"
/translation="MKLIYFDESTRASDYLIKIIQNGRESKQITETKKNOKQTSGLKGF
IGPMESKVEESLFSIEGMNGNINRTSEKYEKLTNAILSDPKMLANEELGIKFS
EYKLSYENSIAHEQITISPYLSMLDGNIVLDQEVASINKNHEETLKGYYEILAKK
MNECIIVRNKKAFAVNNYINLIDLSQMO/LIYGVKVGIIIDINQINQNAINSIGPQNV
VTSISEFTVNSPNNHOSILFMYDILLAGVEVENELSN"
2311..3741
/note="ORF No. M001"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72124.1"
/db_xref="GI:17025996"
/translation="MNFENYKFTGDKLMEKCNLSKKMFKNSMOKLEVVYKLDITRYK
SNPSATNSGYSFNLELELFYKLTILNTIEDFPVPTSAKFPDIDLEKALKNNSHFIR
YITNTIDSIDNKNDALKAQIVASENSYFTLEWISAQSCSDALSFPFNYSIDLDR
SSKIYRKLARHRIDELMEPLMEDNMVYNEFNKQLYKHQYDKENNAETPVVAHVE
HDDSKNSNENHGVTYISNKPISITKYSERTNKLIDPFIIDILNKLYLPSLNKRHNK
ITAYIIONGDESKIREKIRKMEIVKYPNVNGYFLDIEDLFTNYQRIINTIDYKGS
TEPDLONPESRIDNITNSKPLISNDKFPNIYKDFSLISKEPSNLFHINROSTHIGCN
SNQVDSFLNDLYRIHLLDKYSSKNDIEPLSKINTELTNAQLEKKEIKSTQIKDEIV
SKRVNDSWSJAKALSETLNDLNF"
3861..5651
/note="ORF No. M002"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72125.1"
/db_xref="GI:17025997"
/translation="MNNNFKQYPYFLNSNGFEVYIPKNSNDVEKIIQLSPITIEEN
KPLDSTGEVKLIITDGKNIERIEASDILTSFKLPLRIKYGAINERYIKSLVIAQS
MROSPLSKLYGVQLQSDDEGANVSLDKPFSEIOSQANEIICETHYDLOPQGT
FKGMEMYLKQVGNLLELAVIFGISALVTSFLHKNHATEFAGIIFSGGSSGKS
TAASLAVSAGNPTKGNETLFRSMATNALLEGYSNNYGIPIVFDELSAATFRDTG
LIYSTTEGQGRORSNVHGPRKPMWGTSVISTSEYSIFNDSANDGCIHVRIETNER
ETKDATNSDNIKKTYALNGHYLPIVAKYILNKREDEVITOMFREEDHMFRESLKDETN
TGIIRNFKRIYAVITTSAKILGKVLSTDIIDIANIKDPIIDYHTVSEKSIADAIDVIT
OPVAQNRGFEDEGALKNFENYGLISLKDHIIEVKMLANFEKOMLNNHQFDVANNV
NALRDGKFLADRGROTTRKSYKNSKOSJLAFVHLKLDFEFASILGILTKDSILON
WTPSNDNKAAXELFKSANEGIGPSGVHEDE"
5732..5797
/note="ORF No. M003"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72126.1"
/db_xref="GI:17025998"
/translation="MDRLLELADLVIEINQNTD"
5885..7234
/gene="ccrA"
/gene_ccrA_5885..7234
/note="ORF No. M004"
/codon_start=1
/transl_table=11
/product="cassette chromosome recombinase A"
/protein_id="BAB72127.1"

```

```

/db_xref="GI:17025999"
/translation="MKOYIGYLRQSTWKKQSLAOKAOLEIAEKHIIHINFEYSDKO
SGRDNNSGCVROMQULIOQGCODILCCYRIINRLIRNKNALIKIKCOTYVHILSVH
DCYTDMDQAFRLNLNFIISALESDNIGOVKNGJQEKAKQOCLITTAHPRDYDIIH
NGTPIINONESPTKAVAFNVIKSHGKKKIAQLLEENDYIINRQYQVARNIIMPBNIC
GRIIVQDQGNMPEPSIVSANYEDQARBLQKQTKQTSBNOJOKKIKPCSCNATLI
NMTIRKKNHTRTYVVCPRKNMASRFECDGKINQOTLEDKYLEVCGRPEYQORITYKI
KGAIKDIRKROIRKHHIILTOEOLIEKLAGGIIDAEFREQOTQSLROOPQRTSING
HOIOTONITIQKKFTNLNLIYPIETIHTIKDKNLIGIYKNEBILANIYNQMOSSIA"
7256..8884
/gene="ccrB"
/gene_ccrB_7256..8884
/note="ORF No. M005"
/codon_start=1
/transl_table=11
/product="cassette chromosome recombinase B"
/protein_id="BAB72128.1"
/db_xref="GI:17026000"
/translation="MOQLTKTRVGIYRVSTEMQSTEGYSIDGOINOIKEYCDPHHFE
VKDIYADBGISGKSWNRELORMILKDAEKNIDCVMIYKTRILARNTSDILKIVEDLIH
KONVEPESLSRMEVNTSSGKLMIQIIASFSFPRRNIVHNVHMGOTPRBAEGYYOON
LPICGDKIPDSKHELMINQHRANIVKYIFESVAKGHCYRKIANLNNKGVYTKKKQPF
SISITTYILANPEYTGKIQPAKIKDMSKRRKGLNDKPVIAEGKHSPIINDLMDKVO
MRKQVSOQPVQVHKGNTNLGIIHCPQCGAPMAASNTNTLKDGTKRKIRIYSCSNF
RNKQSKVCSANSVRADYIEDYVMKQILEIVSDVYTORVAVRQENKVDGALHDI
AYKQOQYDEVQTKLNNLIKTEIDNPDLSYIRPSIQYKEQOLNDITNOIINQKQONE
DKSLFDKQIKSLQHLIFHDIKHEKSLKLYIVSDIRIDIKKQGNKKQFYVTKL
NNEIILKFNKKQJDEVALHSSLSLFLPQTLVLT"
9406..9756
/note="ORF No. M006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72130.1"
/db_xref="GI:17026002"
/translation="MKTITQELKQITTHLPQLSNNEACECALEMAENILPEPFIND
SPLVHLLETIYINDELHELSTIYFELTANNOLISVGIYLDHFMDFLYLTDONTIIL
DEHLLKQGGQDHE"
9843..10154
/note="ORF No. M007"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72131.1"
/db_xref="GI:17026003"
/translation="MKINRYITRGINESIPDLQILLMHNVKKDNQDPHTDYLIFKL
QEDENILSTHEQEQPTYKLEYHYHYEKNONALPKKYYVIREDDVAFYVYMLPREE
Y"
10166..10675
/note="ORF No. M008"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72133.1"
/db_xref="GI:17026003"
/translation="MMNTIKSGITHEALIESDQEHRYLLKKTMPKKAQCTVITMYPH
LDGVSLDITTYLILNOLANSRGAVLYLVNLFSLIKRIPENLKIINKYEDHTDIIHLM
KAISSDTVILAYGAIVAKRPVYIDRVQVMEKLPHKKAKVALLNPVNETIMHLPNK
ARQKIWLS"
10676..12334
/note="ORF No. M009"
/codon_start=1
/transl_table=11
/complement(12557..13543)
/gene="mecr1"
/pseudo
complement(12557..13543)
/gene="mecr1"
/note="ORF No. CM003"
/codon_start=1

```

gene /product-"signal transducer protein MecRI"
13643..15649
/gene-"meca"
CDS 13643..15649
/gene-"meca"

Query Match 100.0%; Score 28; DB 1; Length 2177;
Best Local Similarity 100.0%; Pred No. 0.66;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTACTATGATGCTAAAGTTCAA 28
|||||
Db 14615 CAACTACTATGATGCTAAAGTTCAA 14642

RESULT 15
AB063172 26090 bp DNA linear BCT 09-APR-2002
LOCUS Staphylococcus aureus DNA, type-IV staphylococcal cassette
DEFINITION AB063172
chromosome mec, strain:CA05(JCSC1968).
CCSSION AB063172
KEYWORDS AH063172.2 GI:19352029
SOURCE .
ORGANISM Staphylococcus aureus (strain:JCSC 1968 (CA05)) DNA.
REFERENCE Staphylococcus aureus
1 Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS Hiramatsu,K., Cui,L., Kuroda,M. and Ito,T.
TITLE The emergence and evolution of methicillin-resistant Staphylococcus
aureus
JOURNAL Trends Microbiol. 9 (10), 486-493 (2001)
MIDLIN 2
REFERENCE 21482917
AUTHORS Ma,X.X., Ito,T., Tienasaitorn,C., Jamklang,M., Chongtrakool,P.,
Boyle-Vavra,S., Daum,R.S. and Hiramatsu,K.
TITLE Novel Type of Staphylococcal Cassette Chromosome mec Identified in
Community-Acquired Methicillin-Resistant Staphylococcus aureus
Strains
JOURNAL Antimicrob. Agents Chemother. 46 (4), 1147-1152 (2002)
MIDLIN 3
REFERENCE 21895198
AUTHORS (bases 1 to 26090)
Xue,M.X., Ito,T., Hiramatsu,K. and Tienasaitorn,C.
TITLE Direct Submission
Submitted (12-JUN-2001) Teruyo Ito, Juntendo University, Department
of Bacteriology; Hongo 2-1-1, Bunkyo-ku, Tokyo 113-8421, Japan
(E-mail:teruybac@med.juntendo.ac.jp, Tel:81-3-5802-1041,
Fax:81-3-5684-7830)
COMMENT On Mar 11, 2002 this sequence version replaced gi:17025971.
FEATURES
source location/Qualifiers
1..26090
/organism="Staphylococcus aureus"
/strain="JCSC 1968 (CA05)"
/db_xref="taxon:1280"
/note="community-acquired MRSA strain isolated at the
University of Chicago children's hospital"
misc_feature 976..25224
/note="977..25225 or 978..25226 or 979..25227
type IV SCCmec of JCSC1968 (CA05)"
976..1001
/note="Inverted complementary repeat(IR-L) of SCCmec of
JCSC1968"
repeat_region /rpt_type="inverted
complement(1280..1900)
/note="ORF No. CQ001"
CDS /codon_start=1
/transl_table=11
/product-"hypothetical protein"
/protein_id="BAB72101.1"
/db_xref="GI:17025972"
/translation="MKFTVEVEVLEHLVKAYKRGAKPTYPHENLYRGRNHSISGIGDL
LGAVLSRLGVOIFTDPLSMIDKSLRYPDLICEDNEIKNILEYKMDLGYQKRD
FDYCKRKEEMISNIVGKOCVLSRKREKIPKNIADIDKFHVYIYSENNGPKRFDEEI

CDS
2653..3657
/note="ORF No. Q001"
/codon_start=1
/transl_table=11
/product-"hypothetical protein"
/protein_id="BAB72102.1"
/db_xref="GI:17025973"
/translation="MIDPICISSYIRVADEESI,TIHAATTHIHANPVSGIRDAI
KINASTIYSGESDDMIGYKNMNRHTRPOHNDIYVCNLIKVIATPCHTPESISFL
TDEGAGVPMGLFSGDFLEVDIGRPDLLEAAVVEGISIGAKOMKSIPIIDLP
DYIOLPMGHGASPCGKSLGAIPTSLGKGTINNAFSENNATFIDLIISQAPPH
HFAOMKKTINQFGMLYOPPTYVPATSTNGLTDFDLKSKEVYIGHIEGIIINPYDNFI
NOIGWYLNNOENINLIGDYHLVSKATHNLTLYLMDIMCOLDISYHKLKFKHILFIYKT
complement(4281..5771)
/note="ORF No. CQ002"
/codon_start=1
/transl_table=11
/product-"hypothetical protein"
/protein_id="BAB72103.1"
/db_xref="GI:17025974"
/translation="MHRESKYIEYKSRKGLSNDIMSTYSAPANTEGGTIYCIPEEK
IEDKPYFVSQVDEPEKMIEDFMNLLYGRSKYSNDIMSTYSAPANTEGGTIYCIPEEK
EAPYSKPIYVDNKKDLVTKRVDADRINATEBEYFMIVNSODDIDITELLDNYSDL
NIESIENYRKLLKNTNDRYANMSQDLMDLGAVRKDRSSKQYKMTACLLFEG
KYNALISDRPGFOLDYFKKTNVLDITDMKDRISSGDIGNDILNVYSPFEKYLKINDI
EESFLNDLITRONYARDLKVAIREALVNTLAAHAYDTPKOSIKIVNCDDPIEFVNPNG
MKINKEDPIHGHSKDRNSILSTLFRVGSYSKASGCGPIFDVYVNRHKLKTPLEIT
MDDTVYLMKODLMKEFEKYPDLKKYIKYITIDVGSISGKALKMENNTIYOFNRMLK
KIKDNLIRKEEGEPATKYVLESKEADILRTKVKYSLEFFRK"
complement(6389..7438)
/note="ORF No. CQ003"
/codon_start=1
/transl_table=11
/product-"hypothetical protein"
/protein_id="BAB72104.1"
/db_xref="GI:17025975"
/translation="MPTLEEITIDKYNLVLYLKRVDYVEVEYEDLLLRSLSDLNEHO
KMDRFSIKRHLNSNFDYLDTEFRSINKIYSNINIMHINSQNNNRKNFPINEQ
LKSILAIKVDAMHYSNITSKALAEIKTKTOLVTKIDITLYNOSKLENEVYRKG
ISYTKLENNKYLNEIOFYNNLNOLISVLAEOEYANAFLELYLEIYAKRGO
KKTQYEFCKKLNEFIOSYVITLLIDIRLPVRLYIIRDIVDTCGEKDNRYKRTILIE
SIKAYRYVVDQIKRFRNGLESILNATLSEONMLKVIDYKATCFPREKTHNNTIE
YVSLFFKALDLKK"
7577..7867
/note="ORF No. Q0002"
/codon_start=1
/transl_table=11
/product-"hypothetical protein"
/protein_id="BAB72105.1"
/db_xref="GI:17025976"
/translation="MNKSKQOEKLYNPIIAKSIQOQVGSFPIYGLKKYNNVCSFN
DREVGRRFAYIKYTPGLPFKIVGTGKNSLDYKRGINPCNNSTPLGAGDC"
7867..9654
/note="ORF No. Q0003"
/codon_start=1
/transl_table=11
/product-"hypothetical protein"
/protein_id="BAB72106.1"
/db_xref="GI:17025977"
/translation="MSYTFEIGFPALDSFGMKETIPPKKDDSEKVVYMAPIYVA
RSDPTGVEKLIITNNNGKDIPESDILITRNLPSLIKYGSINEXYIRSLSVALOL
MRDRLPISELVGVGLIETNPPGVLSLDKVKLSIOFNSSSPYPIVDSAYDLPKPGCP
DMWPMWYIDEVYGHLLLELAVIFGISALVTSFLRKKEHLERAGILFSTQGSSTGKST
AALAVSVAGNPTKGNELFRSNWATRNLALBGLYSNNNGIPIVEDELSSTLRDTGT
LYSLAEGQGRORSNVGEVKTFRKNGTSTVISTSEYSIINDSANDGLKLVRTIEINQF
TINATNADNIKRAVALNNGVHVLVAKYILINDEVDIOMFTYKEVDEAKKIDENFT
GIKMFRRYAVITISAKILGRVSTIDIANIYDVTIDVHTFVRSRSLADAIYDTIO
FVANORGRKPSDEGALKMKPENYGLISLMDPHIEVMKIANVKKOMNNQDPODVNVVN
ALRDNCGTILADGROTKRVSVDNKGQSOLFVHLKIDVDFASITLGLTKKSLIONH
TPANDKKAKELFKSANBSIGPSGVHEDE"
9735..9800

```
/note="ORF No. 0004"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72107.1"
/db_xref="GI:17025978"
/translation="MDELIELADLVEIEINQTNQ"
9888..11237
/gene="ccra"
9888..11237
/gene="ccra"
/note="ORF No. 0005"
/codon_start=1
/transl_table=11
/product="cassette chromosome recombinase A"
/protein_id="BAB72108.1"
/db_xref="GI:17025979"
/translation="MKOVIGYLRQSTMKQOSLAQKQAEIAEKHHIOHINPYSKQ
SGRKDRSGYRQMTOLIOGGCCDILCCYRLNRLKALIKLCQTYRVHIIIVH
DGYFMDQAFEDRLKINIFSLAELESDNIGEOVRNGLOEKAKOGLITTHAPGTDYH
NCTFTINQNESTPVKAVFNVTYIKGHQYKIAQLLEBDNTYINRQPYQVRNIIINPVC
GVNNQYQYDNPFPISVSTSIYEQAQRLQKQTSDDQLKQIKPCCNATLT
NMTIRKKNHTLRVYVCPKMNASRFVDFKGINAQTLDEKVLVLCRDYQONRIYTKI
KGAIDKRIKROBNIEKHIIITQELIEKLAGGIIIDAEFPQEOSLRQOPORTSING
HOIOHTIQNIQKRFNLTYPIETIHITKDKNLGIFYFKNEPLNIIVNQMSSTA"
11259..12887
/gene="ccrB"
11259..12887
/gene="ccrB"
/note="ORF No. 0006"
/codon_start=1
/transl_table=11
/product="cassette chromosome recombinase B"
/protein_id="BAB72109.1"
/db_xref="GI:17025980"
/translation="MOQLTKRVGIYRVSTEMQSTEGYSIDQINQIKCYCDFHHFE
VKDIYADRGISGKSMNPLOMLDKAEGNIDCVMIYKTNRLARNTSDLIKIVEDLIH
KQNEFEFISERMEVNTSGKILQIOLIASFSEPERNIVENMGOTRRARQEGYQGN
LPIQYDKIPDSKHELMINQHEANIVKYIPESYAKGHGVRKIANALNHKGYVTRKGRF
SISSTIYYILANPYIGKIQPAKYKDMSEKRRKGLNDKPYIAEGKHSPIINODLMDVQ
MRKKQVSOQPOVHGKQTNLTGIIHCPOGAPMAASNTNTLKDGTKRIRYVSCSNF
RNKGSVCSSANSVRADYIEDYVAKQILEIYKSDKVIQRYVARNOENKVDGAALHHDII
AYKQOQYDEVQTKLNNLTIETDNPLTIVIRPSIQYKQKOLNDITNOINQKNOONE
DKSLFDAKQISKLQIHQDQIHMEKSRKALYLSVIDRINIRKQGNHKKQYVTLKL
NNEIIKQLPNNKQIDEVHLSSTSLFPLQTLVLTII"
13409..13759
/note="ORF No. 0007"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72110.1"
/db_xref="GI:17025981"
/translation="MKTITQELKQYITTHI.FQLSNNAWECEALEAENILPERPIND
SPLVHLTETTYTYNDDELHELSTYPLFMYANNQLISVGLDHFDMDFLTLDTONIII
DERHLKQGGQDHE"
13846..14157
/note="ORF No. 0008"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72111.1"
/db_xref="GI:17025982"
/translation="MKINRIYRGINIESIPLDIQIILIMHMEKKDNOPTDYLHI.FKL
QEDENILSTHQEQPYKLEHYHTNYEKQNALPKKYVIRDDVDAYFYVLLPBE
Y"
14169..14678
/note="ORF No. 0009"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAB72112.1"
/db_xref="GI:17025983"
```

```
Query Match          100.0%: Score 28; DB 1; Length 26090;
Best Local Similarity 100.0%: Pred. No. 0.64;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Caps 0;
OY      1 CAACTACTATTGATGCTAAAGTTCAAA 28
        |||||||
Db 18618 CAACTACTATTGATGCTAAAGTTCAAA 18645
```

Search completed: December 10, 2002, 20:17:18
Job time : 618.209 secs